

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:00:15 ; Search time 187 Seconds
(without alignments)
14.098 Million cell updates/sec

Title: US-10-719-523-5
Perfect score: 48
Sequence: 1 HHHHH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A Genesep21:.*
1: Genesep21980s:.*
2: Genesep21990s:.*
3: Genesep20000s:.*
4: Genesep2001s:.*
5: Genesep2002s:.*
6: Genesep2003as:.*
7: Genesep2003bs:.*
8: Genesep2004s:.*
9: Genesep2005s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 48 | 100.0 | 6 | 2 | AAV49221 Nickel to |
| 2 | 48 | 100.0 | 6 | 2 | AAW19161 Isoelectr |
| 3 | 48 | 100.0 | 6 | 2 | AAW18225 Purificat |
| 4 | 48 | 100.0 | 6 | 2 | AAW63024 Hexa-hist |
| 5 | 48 | 100.0 | 6 | 2 | AAW69961 Poly-His |
| 6 | 48 | 100.0 | 6 | 2 | AAW68297 Poly-His |
| 7 | 48 | 100.0 | 6 | 2 | AAW44011 Poly-His |
| 8 | 48 | 100.0 | 6 | 2 | AAE08742 Poly-His |
| 9 | 48 | 100.0 | 6 | 2 | ADV42333 Hexahisti |
| 10 | 48 | 100.0 | 6 | 2 | AAV06469 Epitope t |
| 11 | 48 | 100.0 | 6 | 2 | AAW84203 Peptide c |
| 12 | 48 | 100.0 | 6 | 2 | AAV17447 Major out |
| 13 | 48 | 100.0 | 6 | 2 | AAV09544 Human TAK |
| 14 | 48 | 100.0 | 6 | 2 | AAV33592 VH-VL dom |
| 15 | 48 | 100.0 | 6 | 2 | AAE16561 Epitope t |
| 16 | 48 | 100.0 | 6 | 2 | AAV50711 Single ch |
| 17 | 48 | 100.0 | 6 | 3 | AAV78351 His-6 pep |
| 18 | 48 | 100.0 | 6 | 3 | AAV96641 His6 tag |
| 19 | 48 | 100.0 | 6 | 3 | ABD08438 Histidine |
| 20 | 48 | 100.0 | 6 | 3 | ABD08438 His-6 pep |
| 21 | 48 | 100.0 | 6 | 3 | AAV77706 6-His pep |
| 22 | 48 | 100.0 | 6 | 3 | AAV96951 Polyhisti |
| 23 | 48 | 100.0 | 6 | 3 | AAW10788 B. subtil |
| 24 | 48 | 100.0 | 6 | 4 | AAW59857 6-His pep |

| | | | | | |
|----|----|-------|---|---|--------------------|
| 25 | 48 | 100.0 | 6 | 4 | AAE12713 Hexahis t |
| 26 | 48 | 100.0 | 6 | 4 | AAE13079 Epitope t |
| 27 | 48 | 100.0 | 6 | 4 | AAW35439 Nascent p |
| 28 | 48 | 100.0 | 6 | 4 | AAW45989 Transdomi |
| 29 | 48 | 100.0 | 6 | 4 | AAW78043 6-His epi |
| 30 | 48 | 100.0 | 6 | 4 | AAW97353 6-His epi |
| 31 | 48 | 100.0 | 6 | 4 | AAW52173 Peptide t |
| 32 | 48 | 100.0 | 6 | 4 | ABW76820 His tag. |
| 33 | 48 | 100.0 | 6 | 4 | AAW66801 6-His epi |
| 34 | 48 | 100.0 | 6 | 4 | AAE01997 Poly-His |
| 35 | 48 | 100.0 | 6 | 4 | AAW65669 His tag u |
| 36 | 48 | 100.0 | 6 | 4 | AAU00163 His Tag t |
| 37 | 48 | 100.0 | 6 | 4 | AAW62605 Metal cap |
| 38 | 48 | 100.0 | 6 | 4 | AAW62662 C-termina |
| 39 | 48 | 100.0 | 6 | 4 | AAU02090 His-tag p |
| 40 | 48 | 100.0 | 6 | 4 | AAW85699 Amino aci |
| 41 | 48 | 100.0 | 6 | 4 | ABW00924 Hexahisti |
| 42 | 48 | 100.0 | 6 | 4 | AAE08006 His tag u |
| 43 | 48 | 100.0 | 6 | 4 | AAW51720 FSH alpha |
| 44 | 48 | 100.0 | 6 | 5 | AAE26107 His tag p |
| 45 | 48 | 100.0 | 6 | 5 | AAE28476 6His pep |
| 46 | 48 | 100.0 | 6 | 5 | AAW49702 KpnI/Sali |
| 47 | 48 | 100.0 | 6 | 5 | AAU10567 Purificat |
| 48 | 48 | 100.0 | 6 | 5 | ABW32021 Synthetic |
| 49 | 48 | 100.0 | 6 | 5 | AAE23795 His6 tag |
| 50 | 48 | 100.0 | 6 | 5 | AAE28606 His pep |
| 51 | 48 | 100.0 | 6 | 5 | AAO22927 Human pap |
| 52 | 48 | 100.0 | 6 | 5 | AAU76910 C termina |
| 53 | 48 | 100.0 | 6 | 5 | AAU75289 His6 tag |
| 54 | 48 | 100.0 | 6 | 5 | AAE18829 His tag u |
| 55 | 48 | 100.0 | 6 | 5 | AAO19983 Histidine |
| 56 | 48 | 100.0 | 6 | 5 | ABW93013 Synthetic |
| 57 | 48 | 100.0 | 6 | 5 | ABW32856 His tag f |
| 58 | 48 | 100.0 | 6 | 5 | ABW71813 HIS tag p |
| 59 | 48 | 100.0 | 6 | 5 | ABW77485 AAV-hep |
| 60 | 48 | 100.0 | 6 | 5 | ADW70469 Histidine |
| 61 | 48 | 100.0 | 6 | 5 | ABW98509 Synthetic |
| 62 | 48 | 100.0 | 6 | 6 | ADA05147 Peptide S |
| 63 | 48 | 100.0 | 6 | 6 | AAE30397 6-His tag |
| 64 | 48 | 100.0 | 6 | 6 | AAO16087 Neurologi |
| 65 | 48 | 100.0 | 6 | 6 | ABW55464 Peptide S |
| 66 | 48 | 100.0 | 6 | 6 | AAO16240 Synthetic |
| 67 | 48 | 100.0 | 6 | 6 | AAO16698 PAL-781 p |
| 68 | 48 | 100.0 | 6 | 6 | ABW32676 Histidine |
| 69 | 48 | 100.0 | 6 | 6 | ABW55533 Adapter p |
| 70 | 48 | 100.0 | 6 | 6 | ABW58182 Hexa-hist |
| 71 | 48 | 100.0 | 6 | 6 | ABW58805 Mucin 1 (|
| 72 | 48 | 100.0 | 6 | 6 | ABW08057 Synthetic |
| 73 | 48 | 100.0 | 6 | 6 | ABW40361 Hexahisti |
| 74 | 48 | 100.0 | 6 | 6 | ABW38460 6-His epi |
| 75 | 48 | 100.0 | 6 | 6 | ABW58380 Histidine |
| 76 | 48 | 100.0 | 6 | 6 | AAE34362 His tag u |
| 77 | 48 | 100.0 | 6 | 6 | ABW73745 His-tag # |
| 78 | 48 | 100.0 | 6 | 6 | ABW08700 Protein a |
| 79 | 48 | 100.0 | 6 | 6 | AAE34693 His tag p |
| 80 | 48 | 100.0 | 6 | 6 | ABW55850 His tag p |
| 81 | 48 | 100.0 | 6 | 6 | ABW93302 Single ch |
| 82 | 48 | 100.0 | 6 | 6 | ABU08159 Synthetic |
| 83 | 48 | 100.0 | 6 | 6 | ABU09877 Six histi |
| 84 | 48 | 100.0 | 6 | 6 | AAE30831 His tag p |
| 85 | 48 | 100.0 | 6 | 6 | ABW56478 Interfero |
| 86 | 48 | 100.0 | 6 | 6 | AAE32846 His-tag p |
| 87 | 48 | 100.0 | 6 | 6 | ABW83551 Fusion pr |
| 88 | 48 | 100.0 | 6 | 6 | ADW94904 Interfero |
| 89 | 48 | 100.0 | 6 | 6 | ABW25838 His6x epi |
| 90 | 48 | 100.0 | 6 | 7 | ABW62463 Poly-hist |
| 91 | 48 | 100.0 | 6 | 7 | ADW09805 His6x epi |
| 92 | 48 | 100.0 | 6 | 7 | ADW16593 Poly-His |
| 93 | 48 | 100.0 | 6 | 7 | ADW87317 Polyhisti |
| 94 | 48 | 100.0 | 6 | 7 | ADW64741 Hepatiti |
| 95 | 48 | 100.0 | 6 | 7 | ADW73007 POLY-His |
| 96 | 48 | 100.0 | 6 | 7 | ADW78273 POLY-His |
| 97 | 48 | 100.0 | 6 | 7 | ADW28984 His tag. |

| | | | | | | | | | | | | | |
|-----|----|-------|---|---|----------|-----|----|-------|---|---|-----------|-----------|-----------|
| 98 | 48 | 100.0 | 6 | 7 | ABW01458 | 171 | 48 | 100.0 | 6 | 8 | ADT91376 | Adt91376 | Hexahisti |
| 99 | 48 | 100.0 | 6 | 7 | AD65097 | 172 | 48 | 100.0 | 6 | 8 | ADT71347 | Adt71347 | Marker pe |
| 100 | 48 | 100.0 | 6 | 7 | AD65097 | 173 | 48 | 100.0 | 6 | 8 | ADT91518 | Adt91518 | Hist6 tag |
| 101 | 48 | 100.0 | 6 | 7 | AD651383 | 174 | 48 | 100.0 | 6 | 8 | ADT88255 | Adt88255 | Hist6 tag |
| 102 | 48 | 100.0 | 6 | 7 | ABW02158 | 175 | 48 | 100.0 | 6 | 8 | ADT78164 | Adt78164 | C. pneumo |
| 103 | 48 | 100.0 | 6 | 7 | ADP44382 | 176 | 48 | 100.0 | 6 | 8 | ADU48662 | Adu48662 | Hist6 tag |
| 104 | 48 | 100.0 | 6 | 7 | ADP50719 | 177 | 48 | 100.0 | 6 | 8 | ADU48596 | Adu48596 | Amino aci |
| 105 | 48 | 100.0 | 6 | 7 | ADP53324 | 178 | 48 | 100.0 | 6 | 8 | ABY00768 | AbY00768 | Poly-hist |
| 106 | 48 | 100.0 | 6 | 7 | ADP70394 | 179 | 48 | 100.0 | 6 | 9 | ADV24178 | Adv24178 | Nickel ma |
| 107 | 48 | 100.0 | 6 | 7 | ADG32337 | 180 | 48 | 100.0 | 6 | 9 | ADV24326 | Adv24326 | Nickel ma |
| 108 | 48 | 100.0 | 6 | 7 | ADG98833 | 181 | 48 | 100.0 | 6 | 9 | ADV24212 | Adv24212 | Nickel ma |
| 109 | 48 | 100.0 | 6 | 7 | ADG84817 | 182 | 48 | 100.0 | 6 | 9 | ADV24579 | Adv24579 | Nickel ma |
| 110 | 48 | 100.0 | 6 | 7 | ADG46728 | 183 | 48 | 100.0 | 6 | 9 | ADV24675 | Adv24675 | Nickel ma |
| 111 | 48 | 100.0 | 6 | 7 | ADH44350 | 184 | 48 | 100.0 | 6 | 9 | ADU92041 | AdU92041 | Hist6 tag |
| 112 | 48 | 100.0 | 6 | 7 | ADH69235 | 185 | 48 | 100.0 | 6 | 9 | ADU92529 | AdU92529 | 6-His epi |
| 113 | 48 | 100.0 | 6 | 7 | ADH63030 | 186 | 48 | 100.0 | 6 | 9 | ADV98592 | Adv98592 | Hist6 tag |
| 114 | 48 | 100.0 | 6 | 7 | ADH53325 | 187 | 48 | 100.0 | 6 | 9 | ADV38214 | Adv38214 | Histidine |
| 115 | 48 | 100.0 | 6 | 7 | ADH54589 | 188 | 48 | 100.0 | 6 | 9 | ADM09034 | AdM09034 | Hist6 pep |
| 116 | 48 | 100.0 | 6 | 7 | ADH96360 | 189 | 48 | 100.0 | 6 | 9 | ADM64949 | AdM64949 | 6-His epi |
| 117 | 48 | 100.0 | 6 | 7 | ADH80639 | 190 | 48 | 100.0 | 6 | 9 | ADM23846 | AdM23846 | Novel hum |
| 118 | 48 | 100.0 | 6 | 7 | ADJ59015 | 191 | 48 | 100.0 | 6 | 9 | ADM10847 | AdM10847 | Hist6 tag |
| 119 | 48 | 100.0 | 6 | 7 | ADK41227 | 192 | 48 | 100.0 | 6 | 9 | ADM26206 | AdM26206 | Human BA4 |
| 120 | 48 | 100.0 | 6 | 7 | ADM64594 | 193 | 48 | 100.0 | 6 | 9 | ADM25792 | AdM25792 | Cleavable |
| 121 | 48 | 100.0 | 6 | 8 | ADP12240 | 194 | 48 | 100.0 | 6 | 9 | ADM22486 | AdM22486 | Hist6 tag |
| 122 | 48 | 100.0 | 6 | 8 | ADG45048 | 195 | 48 | 100.0 | 6 | 9 | ADM96889 | AdM96889 | Histidine |
| 123 | 48 | 100.0 | 6 | 8 | ADP77118 | 196 | 48 | 100.0 | 6 | 9 | ADX57833 | AdX57833 | N-termina |
| 124 | 48 | 100.0 | 6 | 8 | ADG28807 | 197 | 48 | 100.0 | 6 | 9 | ADX05063 | AdX05063 | Hist6 tag |
| 125 | 48 | 100.0 | 6 | 8 | ADH22658 | 198 | 48 | 100.0 | 6 | 9 | ADX40948 | AdX40948 | Hist6 tag |
| 126 | 48 | 100.0 | 6 | 8 | ADH19013 | 199 | 48 | 100.0 | 6 | 9 | ADY27309 | AdY27309 | Hist6 tag |
| 127 | 48 | 100.0 | 6 | 8 | ADH34697 | 200 | 48 | 100.0 | 6 | 9 | ADX85209 | AdX85209 | 6x-His ta |
| 128 | 48 | 100.0 | 6 | 8 | ADH23664 | 201 | 48 | 100.0 | 6 | 9 | ADY28266 | AdY28266 | Hist6 tag |
| 129 | 48 | 100.0 | 6 | 8 | ADH25161 | 202 | 48 | 100.0 | 6 | 9 | ADX87288 | AdX87288 | Protein I |
| 130 | 48 | 100.0 | 6 | 8 | ADJ36217 | 203 | 48 | 100.0 | 6 | 9 | ADY50198 | AdY50198 | Hist6 tag |
| 131 | 48 | 100.0 | 6 | 8 | ADJ36641 | 204 | 48 | 100.0 | 6 | 9 | ADY39758 | AdY39758 | Hist6 tag |
| 132 | 48 | 100.0 | 6 | 8 | ADJ88139 | 205 | 48 | 100.0 | 6 | 9 | ADY56834 | AdY56834 | Histidine |
| 133 | 48 | 100.0 | 6 | 8 | ADJ88087 | 206 | 48 | 100.0 | 6 | 9 | ADY34113 | AdY34113 | Hist6 tag |
| 134 | 48 | 100.0 | 6 | 8 | ADJ79526 | 207 | 48 | 100.0 | 6 | 9 | ADY34114 | AdY34114 | Hist6 tag |
| 135 | 48 | 100.0 | 6 | 8 | ADJ50909 | 208 | 48 | 100.0 | 6 | 9 | ADY53282 | AdY53282 | 6xHis tag |
| 136 | 48 | 100.0 | 6 | 8 | ADL69051 | 209 | 48 | 100.0 | 6 | 9 | ADY75189 | AdY75189 | Chlamydia |
| 137 | 48 | 100.0 | 6 | 8 | ADJ67712 | 210 | 48 | 100.0 | 6 | 9 | ADY80247 | AdY80247 | Amino aci |
| 138 | 48 | 100.0 | 6 | 8 | ADL81220 | 211 | 48 | 100.0 | 6 | 9 | ADY75177 | AdY75177 | Hexa-hist |
| 139 | 48 | 100.0 | 6 | 8 | ADJ93827 | 212 | 48 | 100.0 | 6 | 9 | ADY78382 | AdY78382 | Histidine |
| 140 | 48 | 100.0 | 6 | 8 | ADN92353 | 213 | 48 | 100.0 | 6 | 9 | ADZ03629 | AdZ03629 | Epitope c |
| 141 | 48 | 100.0 | 6 | 8 | ADM38896 | 214 | 48 | 100.0 | 6 | 9 | ADZ08744 | AdZ08744 | Recombina |
| 142 | 48 | 100.0 | 6 | 8 | ADM80159 | 215 | 48 | 100.0 | 6 | 9 | ADZ46754 | AdZ46754 | 6-His tag |
| 143 | 48 | 100.0 | 6 | 8 | ADK13663 | 216 | 48 | 100.0 | 6 | 9 | ADZ59474 | AdZ59474 | Preferred |
| 144 | 48 | 100.0 | 6 | 8 | ADM94772 | 217 | 48 | 100.0 | 6 | 9 | ADZ69433 | AdZ69433 | Hexa-His |
| 145 | 48 | 100.0 | 6 | 8 | ADM06306 | 218 | 48 | 100.0 | 6 | 9 | AEH14985 | AEH14985 | 6x-His ep |
| 146 | 48 | 100.0 | 6 | 8 | ADU06948 | 219 | 48 | 100.0 | 6 | 9 | ADZ76889 | AdZ76889 | Fusion pa |
| 147 | 48 | 100.0 | 6 | 8 | ADO32452 | 220 | 48 | 100.0 | 6 | 9 | ADZ69864 | AdZ69864 | Hist6 tag |
| 148 | 48 | 100.0 | 6 | 8 | ADO49511 | 221 | 48 | 100.0 | 6 | 9 | ADZ87785 | AdZ87785 | Novel COP |
| 149 | 48 | 100.0 | 6 | 8 | ADO04650 | 222 | 48 | 100.0 | 6 | 9 | ADZ85112 | AdZ85112 | Synthetic |
| 150 | 48 | 100.0 | 6 | 8 | ADO14230 | 223 | 48 | 100.0 | 6 | 9 | AEA23267 | AEA23267 | 6x-His ta |
| 151 | 48 | 100.0 | 6 | 8 | ADO49029 | 224 | 48 | 100.0 | 6 | 9 | AEA99867 | AEA99867 | Hist6 tag |
| 152 | 48 | 100.0 | 6 | 8 | ADO26659 | 225 | 48 | 100.0 | 6 | 9 | AEA21312 | AEA21312 | Nanoparti |
| 153 | 48 | 100.0 | 6 | 8 | ADO26661 | 226 | 48 | 100.0 | 6 | 9 | AEBO0924 | AEBO0924 | Hexahisti |
| 154 | 48 | 100.0 | 6 | 8 | ADP84150 | 227 | 48 | 100.0 | 6 | 9 | AEH13397 | AEH13397 | Hist6 tag |
| 155 | 48 | 100.0 | 6 | 8 | ADP90806 | 228 | 48 | 100.0 | 6 | 9 | AEH4084 | AEH4084 | Hist6 tag |
| 156 | 48 | 100.0 | 6 | 8 | ADP87523 | 229 | 48 | 100.0 | 6 | 9 | AEH56912 | AEH56912 | 6xHis tag |
| 157 | 48 | 100.0 | 6 | 8 | ADQ88328 | 230 | 48 | 100.0 | 6 | 9 | AEH70210 | AEH70210 | Hexahisti |
| 158 | 48 | 100.0 | 6 | 8 | ADQ96748 | 231 | 48 | 100.0 | 6 | 9 | AEH68294 | AEH68294 | Epitope c |
| 159 | 48 | 100.0 | 6 | 8 | ADRO3293 | 232 | 48 | 100.0 | 6 | 9 | AEH01718 | AEH01718 | Hist6 epi |
| 160 | 48 | 100.0 | 6 | 8 | ADQ98113 | 233 | 48 | 100.0 | 6 | 9 | AAH80401 | AAH80401 | Affinity |
| 161 | 48 | 100.0 | 6 | 8 | ADRI6247 | 234 | 48 | 100.0 | 7 | 4 | AAH503173 | AAH503173 | Human car |
| 162 | 48 | 100.0 | 6 | 8 | ADR90374 | 235 | 48 | 100.0 | 7 | 4 | AAH64363 | AAH64363 | Peptide i |
| 163 | 48 | 100.0 | 6 | 8 | ADR29322 | 236 | 48 | 100.0 | 7 | 5 | AAH14511 | AAH14511 | Tag added |
| 164 | 48 | 100.0 | 6 | 8 | ADS20226 | 237 | 48 | 100.0 | 7 | 5 | AAE25397 | AAE25397 | Hist6 tag |
| 165 | 48 | 100.0 | 6 | 8 | ADR88395 | 238 | 48 | 100.0 | 7 | 6 | ABR83552 | ABR83552 | Fusion pr |
| 166 | 48 | 100.0 | 6 | 8 | ADR72506 | 239 | 48 | 100.0 | 7 | 6 | ABU61988 | ABU61988 | Synthetic |
| 167 | 48 | 100.0 | 6 | 8 | ADR39718 | 240 | 48 | 100.0 | 7 | 8 | ADH22659 | ADH22659 | Oligohist |
| 168 | 48 | 100.0 | 6 | 8 | ADH17887 | 241 | 48 | 100.0 | 7 | 8 | ADH58901 | ADH58901 | 6xHis tag |
| 169 | 48 | 100.0 | 6 | 8 | ADR72483 | 242 | 48 | 100.0 | 7 | 8 | ADU49030 | ADU49030 | Labeling |
| 170 | 48 | 100.0 | 6 | 8 | ADH74281 | 243 | 48 | 100.0 | 7 | 9 | ADY34115 | ADY34115 | Hy tag pe |

| | | | | | | | | | | | | | |
|-----|----|-------|---|---|-----------|---------------------|-----|----|-------|----|---|-----------|----------------------|
| 244 | 48 | 100.0 | 7 | 9 | ADZ69281 | Ad69281 Hexahisti | 317 | 48 | 100.0 | 8 | 9 | ADY67556 | Ady67556 His tag. |
| 245 | 48 | 100.0 | 7 | 9 | AE834466 | Ae34466 Exemplary | 318 | 48 | 100.0 | 8 | 9 | ADZ04230 | Adz04230 Modified |
| 246 | 48 | 100.0 | 7 | 9 | AE810134 | Ae10134 Histidine | 319 | 48 | 100.0 | 8 | 9 | ADZ39458 | Adz39458 Histidine |
| 247 | 48 | 100.0 | 8 | 2 | AA877412 | AA877412 Extension | 320 | 48 | 100.0 | 8 | 9 | AE817922 | Ae17922 Peptide u |
| 248 | 48 | 100.0 | 8 | 2 | AA895539 | AA895539 Polychisti | 321 | 48 | 100.0 | 8 | 9 | AE824522 | Ae24522 N-termina |
| 249 | 48 | 100.0 | 8 | 2 | AA820036 | AA820036 C-termina | 322 | 48 | 100.0 | 8 | 9 | AE886406 | Ae886406 Amino aci |
| 250 | 48 | 100.0 | 8 | 2 | AA861479 | AA861479 A. fumiga | 323 | 48 | 100.0 | 8 | 9 | AE871113 | Ae871113 C-Adi Kin |
| 251 | 48 | 100.0 | 8 | 2 | AA861601 | AA861601 polychisti | 324 | 48 | 100.0 | 8 | 9 | AE830728 | Ae830728 C-Adi Kin |
| 252 | 48 | 100.0 | 8 | 3 | AA853237 | AA853237 MN protei | 325 | 48 | 100.0 | 8 | 9 | AE891052 | Ae891052 Lantibiot |
| 253 | 48 | 100.0 | 8 | 3 | AA803014 | AA803014 Tag fused | 326 | 48 | 100.0 | 9 | 2 | AA806142 | Aa806142 Variant a |
| 254 | 48 | 100.0 | 8 | 3 | AA809991 | AA809991 C. tetani | 327 | 48 | 100.0 | 9 | 2 | AA860080 | AA860080 Homo sapi |
| 255 | 48 | 100.0 | 8 | 3 | AA896685 | AA896685 Polychisti | 328 | 48 | 100.0 | 9 | 2 | AA828306 | AA828306 Amino aci |
| 256 | 48 | 100.0 | 8 | 3 | AA800161 | AA800161 Hexahisti | 329 | 48 | 100.0 | 9 | 2 | AA890199 | AA890199 B7-2-6His |
| 257 | 48 | 100.0 | 8 | 4 | AA813200 | AA813200 His tag u | 330 | 48 | 100.0 | 9 | 3 | AA853258 | AA853258 Human neu |
| 258 | 48 | 100.0 | 8 | 4 | AA836993 | AA836993 Peptide u | 331 | 48 | 100.0 | 9 | 3 | AA844463 | AA844463 Gly(His)8 |
| 259 | 48 | 100.0 | 8 | 4 | AA864364 | AA864364 Peptide i | 332 | 48 | 100.0 | 9 | 3 | AA879558 | AA879558 Peptide t |
| 260 | 48 | 100.0 | 8 | 4 | AA852174 | AA852174 Peptide i | 333 | 48 | 100.0 | 9 | 3 | AA815187 | AA815187 His-conta |
| 261 | 48 | 100.0 | 8 | 4 | AA848167 | AA848167 Histidine | 334 | 48 | 100.0 | 9 | 4 | AA813114 | AA813114 C-termina |
| 262 | 48 | 100.0 | 8 | 4 | AA808227 | AA808227 Tag #1 fo | 335 | 48 | 100.0 | 9 | 4 | AA882692 | AA882692 His-tag. |
| 263 | 48 | 100.0 | 8 | 4 | AA800164 | AA800164 His Tag (| 336 | 48 | 100.0 | 9 | 4 | AA864361 | AA864361 Peptide i |
| 264 | 48 | 100.0 | 8 | 4 | AA864395 | AA864395 Peptide t | 337 | 48 | 100.0 | 9 | 4 | AA897661 | AA897661 Influenza |
| 265 | 48 | 100.0 | 8 | 4 | AA811985 | AA811985 Tag #2, t | 338 | 48 | 100.0 | 9 | 5 | AA8018574 | AA8018574 E coli ou |
| 266 | 48 | 100.0 | 8 | 4 | AA851721 | AA851721 FSH alpha | 339 | 48 | 100.0 | 9 | 5 | AA8019058 | AA8019058 Mutation |
| 267 | 48 | 100.0 | 8 | 5 | AA896775 | AA896775 Divinyl e | 340 | 48 | 100.0 | 9 | 5 | AA870938 | AA870938 Plasmodu |
| 268 | 48 | 100.0 | 8 | 5 | AA8953086 | AA8953086 CYP 27C1 | 341 | 48 | 100.0 | 9 | 5 | AA809999 | AA809999 Nonapepti |
| 269 | 48 | 100.0 | 8 | 5 | AA899814 | AA899814 Membrane | 342 | 48 | 100.0 | 9 | 6 | AA872218 | AA872218 Polychisti |
| 270 | 48 | 100.0 | 8 | 5 | AA832022 | AA832022 Synthetic | 343 | 48 | 100.0 | 9 | 6 | AA872181 | AA872181 Human can |
| 271 | 48 | 100.0 | 8 | 5 | AA878663 | AA878663 His tag e | 344 | 48 | 100.0 | 9 | 6 | AA870232 | AA870232 Membrane |
| 272 | 48 | 100.0 | 8 | 5 | AA831736 | AA831736 Fish grow | 345 | 48 | 100.0 | 9 | 6 | AA889706 | AA889706 Poly-hist |
| 273 | 48 | 100.0 | 8 | 5 | AA816245 | AA816245 Polychisti | 346 | 48 | 100.0 | 9 | 6 | AA883554 | AA883554 Fusion pr |
| 274 | 48 | 100.0 | 8 | 5 | AA877832 | AA877832 His tag p | 347 | 48 | 100.0 | 9 | 6 | AA883544 | AA883544 C-termina |
| 275 | 48 | 100.0 | 8 | 5 | AA877821 | AA877821 C terminal | 348 | 48 | 100.0 | 9 | 7 | AA867705 | AA867705 Peptide 1 |
| 276 | 48 | 100.0 | 8 | 5 | AA899334 | AA899334 His6tag p | 349 | 48 | 100.0 | 9 | 7 | AA899740 | AA899740 Honeybee |
| 277 | 48 | 100.0 | 8 | 5 | AA871814 | AA871814 Peptide t | 350 | 48 | 100.0 | 9 | 8 | AA864370 | AA864370 Llg/HyHEL |
| 278 | 48 | 100.0 | 8 | 5 | AA899299 | AA899299 Brevibacti | 351 | 48 | 100.0 | 9 | 8 | AA822661 | AA822661 Oligohisti |
| 279 | 48 | 100.0 | 8 | 6 | AA873746 | AA873746 His-tag # | 352 | 48 | 100.0 | 9 | 8 | AA818298 | AA818298 Vector pe |
| 280 | 48 | 100.0 | 8 | 6 | AA8956479 | AA8956479 Interfero | 353 | 48 | 100.0 | 9 | 8 | AA8150911 | AA8150911 IFN-beta- |
| 281 | 48 | 100.0 | 8 | 6 | AA871241 | AA871241 Histidine | 354 | 48 | 100.0 | 9 | 8 | AA849032 | AA849032 Labelling |
| 282 | 48 | 100.0 | 8 | 6 | AA8883560 | AA8883560 His6-Ser2 | 355 | 48 | 100.0 | 9 | 8 | AA816338 | AA816338 Human pro |
| 283 | 48 | 100.0 | 8 | 6 | AA883553 | AA883553 Fusion pr | 356 | 48 | 100.0 | 9 | 8 | AA894950 | AA894950 human aci |
| 284 | 48 | 100.0 | 8 | 6 | AA894905 | AA894905 Interfero | 357 | 48 | 100.0 | 9 | 9 | AA880248 | AA880248 Amino aci |
| 285 | 48 | 100.0 | 8 | 6 | AA861986 | AA861986 Synthetic | 358 | 48 | 100.0 | 9 | 9 | AA818561 | AA818561 Amino aci |
| 286 | 48 | 100.0 | 8 | 7 | AA839944 | AA839944 Recombina | 359 | 48 | 100.0 | 10 | 2 | AA824523 | AA824523 N-termina |
| 287 | 48 | 100.0 | 8 | 7 | AA867262 | AA867262 His tag e | 360 | 48 | 100.0 | 10 | 2 | AA839733 | AA839733 First typ |
| 288 | 48 | 100.0 | 8 | 7 | AA832211 | AA832211 Plasmid p | 361 | 48 | 100.0 | 10 | 2 | AA873684 | AA873684 Metal-aff |
| 289 | 48 | 100.0 | 8 | 7 | AA853514 | AA853514 Bacterial | 362 | 48 | 100.0 | 10 | 2 | AA877469 | AA877469 I-domain |
| 290 | 48 | 100.0 | 8 | 7 | AA893704 | AA893704 Tag pepti | 363 | 48 | 100.0 | 10 | 2 | AA874672 | AA874672 Polychisti |
| 291 | 48 | 100.0 | 8 | 7 | AA8F86365 | AA8F86365 Human cyt | 364 | 48 | 100.0 | 10 | 2 | AA851496 | AA851496 Human DNA |
| 292 | 48 | 100.0 | 8 | 7 | AA8H34464 | AA8H34464 Armb C-te | 365 | 48 | 100.0 | 10 | 2 | AA856089 | AA856089 Human mon |
| 293 | 48 | 100.0 | 8 | 7 | AA8L01701 | AA8L01701 GUS beta- | 366 | 48 | 100.0 | 10 | 2 | AA872331 | AA872331 Protein a |
| 294 | 48 | 100.0 | 8 | 7 | AA8K41228 | AA8K41228 G-CSF rel | 367 | 48 | 100.0 | 10 | 2 | AA889262 | AA889262 N-termina |
| 295 | 48 | 100.0 | 8 | 8 | AA8F28865 | AA8F28865 His (6) t | 368 | 48 | 100.0 | 10 | 2 | AA850501 | AA850501 Dermatoph |
| 296 | 48 | 100.0 | 8 | 8 | AA8G45049 | AA8G45049 Synthetis | 369 | 48 | 100.0 | 10 | 2 | AA806610 | AA806610 Hexahisti |
| 297 | 48 | 100.0 | 8 | 8 | AA8H22660 | AA8H22660 Oligohist | 370 | 48 | 100.0 | 10 | 2 | AA894259 | AA894259 His-tag e |
| 298 | 48 | 100.0 | 8 | 8 | AA8H17890 | AA8H17890 Caspase-7 | 371 | 48 | 100.0 | 10 | 2 | AA843534 | AA843534 Leishmani |
| 299 | 48 | 100.0 | 8 | 8 | AA8H76464 | AA8H76464 Peptide o | 372 | 48 | 100.0 | 10 | 2 | AA882996 | AA882996 Human fib |
| 300 | 48 | 100.0 | 8 | 8 | AA8J77673 | AA8J77673 C-termina | 373 | 48 | 100.0 | 10 | 3 | AA851518 | AA851518 Human TFR |
| 301 | 48 | 100.0 | 8 | 8 | AA8K00112 | AA8K00112 His-tag w | 374 | 48 | 100.0 | 10 | 3 | AA828976 | AA828976 N-termina |
| 302 | 48 | 100.0 | 8 | 8 | AA8O49031 | AA8O49031 Labeling | 375 | 48 | 100.0 | 10 | 3 | AA890141 | AA890141 Leader se |
| 303 | 48 | 100.0 | 8 | 8 | AA8O98121 | AA8O98121 Peptide | 376 | 48 | 100.0 | 10 | 3 | AA877721 | AA877721 Leader se |
| 304 | 48 | 100.0 | 8 | 8 | AA8R16114 | AA8R16114 SGH16 ta | 377 | 48 | 100.0 | 10 | 3 | AA8I0776 | AA8I0776 B. subc.fil |
| 305 | 48 | 100.0 | 8 | 8 | AA8R16873 | AA8R16873 Ser-Gly-H | 378 | 48 | 100.0 | 10 | 4 | AA8I0830 | AA8I0830 Expressio |
| 306 | 48 | 100.0 | 8 | 8 | AA8R30797 | AA8R30797 ADAM33 C- | 379 | 48 | 100.0 | 10 | 4 | AA898321 | AA898321 Recombina |
| 307 | 48 | 100.0 | 8 | 8 | AA8R8396 | AA8R8396 Peptide u | 380 | 48 | 100.0 | 10 | 4 | AA8I9104 | AA8I9104 His-Tag C |
| 308 | 48 | 100.0 | 8 | 8 | AA8R49664 | AA8R49664 His tag p | 381 | 48 | 100.0 | 10 | 4 | AA872220 | AA872220 Histidine |
| 309 | 48 | 100.0 | 8 | 8 | AA8I2574 | AA8I2574 PolyHis p | 382 | 48 | 100.0 | 10 | 4 | AA897658 | AA897658 Influenza |
| 310 | 48 | 100.0 | 8 | 8 | AA8T61982 | AA8T61982 Human WSX | 383 | 48 | 100.0 | 10 | 4 | AA8B70426 | AA8B70426 Oligo-his |
| 311 | 48 | 100.0 | 8 | 9 | AA8U92045 | AA8U92045 His tag. | 384 | 48 | 100.0 | 10 | 4 | AA8B75181 | AA8B75181 Chimeric |
| 312 | 48 | 100.0 | 8 | 9 | AA8M25793 | AA8M25793 Cleavable | 385 | 48 | 100.0 | 10 | 5 | AA8E28471 | AA8E28471 Epticope t |
| 313 | 48 | 100.0 | 8 | 9 | AA8M78624 | AA8M78624 S.aureus | 386 | 48 | 100.0 | 10 | 5 | AA8U97726 | AA8U97726 Hexa-hist |
| 314 | 48 | 100.0 | 8 | 9 | AA8X18091 | AA8X18091 Peptide 1 | 387 | 48 | 100.0 | 10 | 5 | AA8B76374 | AA8B76374 Hexa-hist |
| 315 | 48 | 100.0 | 8 | 9 | AA8Y34118 | AA8Y34118 HY tag pe | 388 | 48 | 100.0 | 10 | 5 | AA8E28849 | AA8E28849 Peptide u |
| 316 | 48 | 100.0 | 8 | 9 | AA8Y34116 | AA8Y34116 HY tag pe | 389 | 48 | 100.0 | 10 | 5 | AA8B05988 | AA8B05988 Monoclonal |

| | | | | | | | | | | | | | | | |
|-----|----|-------|----|---|----------|------------|---------|-----|----|-------|----|---|----------|----------|-----------|
| 390 | 48 | 100.0 | 10 | 5 | AAU78933 | 9 | Histidi | 463 | 48 | 100.0 | 11 | 8 | ADU57742 | Adi57742 | 6x N-term |
| 391 | 48 | 100.0 | 10 | 6 | ABG75687 | 2C-methyl | | 464 | 48 | 100.0 | 11 | 8 | ADU76992 | Adi76992 | Poly-His |
| 392 | 48 | 100.0 | 10 | 6 | ABG73909 | His-tagge | | 465 | 48 | 100.0 | 11 | 8 | ADN37757 | Adi37757 | Endoplasm |
| 393 | 48 | 100.0 | 10 | 6 | ABR27276 | Human can | | 466 | 48 | 100.0 | 11 | 8 | ADO21902 | Ado21902 | Polyhisti |
| 394 | 48 | 100.0 | 10 | 6 | ABR27717 | Human can | | 467 | 48 | 100.0 | 11 | 8 | ADO49034 | Ado49034 | Labelling |
| 395 | 48 | 100.0 | 10 | 6 | ABP97469 | Vector pr | | 468 | 48 | 100.0 | 11 | 8 | ADP49312 | Adp49312 | Natriuret |
| 396 | 48 | 100.0 | 10 | 6 | AAOI6174 | 06-alkylg | | 469 | 48 | 100.0 | 11 | 8 | ADP49268 | Adp49268 | Natriuret |
| 397 | 48 | 100.0 | 10 | 6 | ABB82902 | Amino aci | | 470 | 48 | 100.0 | 11 | 8 | ADP49285 | Adp49285 | Natriuret |
| 398 | 48 | 100.0 | 10 | 6 | AAE30843 | HIS tag p | | 471 | 48 | 100.0 | 11 | 8 | ADP88411 | Adp88411 | Human int |
| 399 | 48 | 100.0 | 10 | 6 | ABR83555 | Fusion pr | | 472 | 48 | 100.0 | 11 | 8 | ADR50730 | Adr50730 | N-termi |
| 400 | 48 | 100.0 | 10 | 7 | ADC72967 | Peptide a | | 473 | 48 | 100.0 | 11 | 8 | ADT07104 | Adt07104 | His tag p |
| 401 | 48 | 100.0 | 10 | 7 | ADD68299 | C-termina | | 474 | 48 | 100.0 | 11 | 8 | ADY34244 | Ady34244 | His tag p |
| 402 | 48 | 100.0 | 10 | 7 | ADP28730 | SUR2-type | | 475 | 48 | 100.0 | 11 | 9 | ADY30851 | Ady30851 | His tag p |
| 403 | 48 | 100.0 | 10 | 7 | ADP28734 | SUR2-type | | 476 | 48 | 100.0 | 11 | 9 | ADY54245 | Ady54245 | Modified |
| 404 | 48 | 100.0 | 10 | 7 | ADP28735 | SUR2-type | | 477 | 48 | 100.0 | 11 | 9 | ADY54254 | Ady54254 | Modified |
| 405 | 48 | 100.0 | 10 | 7 | ADP28731 | SUR2-type | | 478 | 48 | 100.0 | 11 | 9 | ADY54252 | Ady54252 | Modified |
| 406 | 48 | 100.0 | 10 | 7 | ADP28733 | SUR2-type | | 479 | 48 | 100.0 | 11 | 9 | ADY60812 | Ady60812 | C-termina |
| 407 | 48 | 100.0 | 10 | 7 | ADP28732 | SUR2-type | | 480 | 48 | 100.0 | 11 | 9 | AEA27993 | Aea27993 | Poly-His |
| 408 | 48 | 100.0 | 10 | 7 | ABR83692 | C-termina | | 481 | 48 | 100.0 | 11 | 9 | AEA21677 | Aea21677 | Aspartate |
| 409 | 48 | 100.0 | 10 | 7 | ADP88580 | Protein t | | 482 | 48 | 100.0 | 11 | 9 | ABE09678 | Aeb09678 | Factor Xa |
| 410 | 48 | 100.0 | 10 | 7 | ADH44345 | Transfect | | 483 | 48 | 100.0 | 11 | 9 | ABE87456 | Aeb87456 | N-termi |
| 411 | 48 | 100.0 | 10 | 7 | ADH44345 | Transfect | | 484 | 48 | 100.0 | 12 | 2 | AAO7064 | Aao7064 | Transcrip |
| 412 | 48 | 100.0 | 10 | 7 | ADL26635 | Multiimeri | | 485 | 48 | 100.0 | 12 | 2 | AAW61549 | Aaw61549 | Endoprote |
| 413 | 48 | 100.0 | 10 | 7 | ADL26635 | C-termina | | 486 | 48 | 100.0 | 12 | 2 | AAV15775 | Aav15775 | Histidine |
| 414 | 48 | 100.0 | 10 | 8 | ADP12235 | Transfect | | 487 | 48 | 100.0 | 12 | 2 | AAW82993 | Aaw82993 | Human fib |
| 415 | 48 | 100.0 | 10 | 8 | ADG30367 | HIS tag p | | 488 | 48 | 100.0 | 12 | 3 | AAV53265 | Aav53265 | pili coat |
| 416 | 48 | 100.0 | 10 | 8 | ADH22662 | Oligohist | | 489 | 48 | 100.0 | 12 | 3 | AAV95878 | Aav95878 | Hexahisti |
| 417 | 48 | 100.0 | 10 | 8 | ADJ77679 | C-termina | | 490 | 48 | 100.0 | 12 | 4 | AAH85050 | Aah85050 | Peptide t |
| 418 | 48 | 100.0 | 10 | 8 | ADL33425 | Bacterial | | 491 | 48 | 100.0 | 12 | 4 | AAU04934 | Aau04934 | Human pla |
| 419 | 48 | 100.0 | 10 | 8 | ADO05860 | Peptide t | | 492 | 48 | 100.0 | 12 | 4 | AAU04935 | Aau04935 | Human pla |
| 420 | 48 | 100.0 | 10 | 8 | ADO49033 | Labelling | | 493 | 48 | 100.0 | 12 | 4 | AAH64365 | Aah64365 | Peptide i |
| 421 | 48 | 100.0 | 10 | 8 | ADP49278 | Natriuret | | 494 | 48 | 100.0 | 12 | 4 | AAH72438 | Aah72438 | His tag. |
| 422 | 48 | 100.0 | 10 | 8 | ADP90803 | Protein/p | | 495 | 48 | 100.0 | 12 | 5 | AAU96716 | Aau96716 | Molecular |
| 423 | 48 | 100.0 | 10 | 8 | ADQ60109 | HIS tag p | | 496 | 48 | 100.0 | 12 | 5 | AAU96774 | Aau96774 | Divinyl e |
| 424 | 48 | 100.0 | 10 | 8 | ADR29320 | Histidine | | 497 | 48 | 100.0 | 12 | 5 | ABB05983 | Abb05983 | Monoclon |
| 425 | 48 | 100.0 | 10 | 9 | ADR23840 | Linker co | | 498 | 48 | 100.0 | 12 | 5 | AAE19655 | Aae19655 | Arbiodops |
| 426 | 48 | 100.0 | 10 | 9 | ADY23887 | Novel fus | | 499 | 48 | 100.0 | 12 | 6 | ABR33565 | Abi33565 | Plasmid p |
| 427 | 48 | 100.0 | 10 | 9 | ADY34120 | HY tag pe | | 500 | 48 | 100.0 | 12 | 6 | ABP55084 | Abp55084 | Hexa-hist |
| 428 | 48 | 100.0 | 10 | 9 | ADY34119 | HY tag pe | | 501 | 48 | 100.0 | 12 | 6 | ADA26429 | Ada26429 | Synthetic |
| 429 | 48 | 100.0 | 10 | 9 | ADY34117 | HY tag pe | | 502 | 48 | 100.0 | 12 | 7 | ABB80260 | Abb80260 | Human big |
| 430 | 48 | 100.0 | 10 | 9 | AEA14998 | 10X-His e | | 503 | 48 | 100.0 | 12 | 7 | ADD95116 | Add95116 | Human GBP |
| 431 | 48 | 100.0 | 10 | 9 | ADZ69867 | GGS-His- | | 504 | 48 | 100.0 | 12 | 8 | ADP28957 | Adp28957 | Nuclear r |
| 432 | 48 | 100.0 | 10 | 9 | AEA18562 | Amino aci | | 505 | 48 | 100.0 | 12 | 8 | ADH22664 | Adh22664 | Oligohist |
| 433 | 48 | 100.0 | 10 | 9 | ABE43913 | Rhomboid | | 506 | 48 | 100.0 | 12 | 8 | ADH53866 | Adh53866 | Human cel |
| 434 | 48 | 100.0 | 11 | 2 | AAH77410 | Extension | | 507 | 48 | 100.0 | 12 | 8 | ADN02212 | Adn02212 | Vector pQ |
| 435 | 48 | 100.0 | 11 | 2 | AAW61480 | A. fumiga | | 508 | 48 | 100.0 | 12 | 8 | ADL09056 | Adl09056 | Human big |
| 436 | 48 | 100.0 | 11 | 2 | AAW53171 | C-termina | | 509 | 48 | 100.0 | 12 | 8 | ADO49035 | Ado49035 | Labelling |
| 437 | 48 | 100.0 | 11 | 2 | AAW80426 | Linker us | | 510 | 48 | 100.0 | 12 | 8 | ADP88406 | Adp88406 | Human int |
| 438 | 48 | 100.0 | 11 | 2 | AAV05815 | Non-toxic | | 511 | 48 | 100.0 | 12 | 8 | ADU59684 | Adu59684 | GBP-4 rel |
| 439 | 48 | 100.0 | 11 | 2 | AAV42688 | Polyhisti | | 512 | 48 | 100.0 | 12 | 9 | ADV66855 | Adv66855 | Vector pP |
| 440 | 48 | 100.0 | 11 | 2 | AAW70581 | Amino aci | | 513 | 48 | 100.0 | 12 | 9 | ADX40941 | Adx40941 | HIS tag p |
| 441 | 48 | 100.0 | 11 | 3 | AAH1895 | H35A muta | | 514 | 48 | 100.0 | 12 | 9 | ADZ03810 | Adz03810 | 6His pep |
| 442 | 48 | 100.0 | 11 | 3 | AAH09993 | C. tetani | | 515 | 48 | 100.0 | 12 | 9 | ADT76029 | Adt76029 | PTICAGamm |
| 443 | 48 | 100.0 | 11 | 4 | AAE11753 | Modified | | 516 | 48 | 100.0 | 12 | 9 | ABE79153 | Abe79153 | Additiona |
| 444 | 48 | 100.0 | 11 | 4 | AAH68981 | Fluoresee | | 517 | 48 | 100.0 | 12 | 9 | AAH72792 | Aah72792 | Hexa-hist |
| 445 | 48 | 100.0 | 11 | 5 | AAU96727 | Molecular | | 518 | 48 | 100.0 | 13 | 2 | AAW61548 | Aaw61548 | Endoprote |
| 446 | 48 | 100.0 | 11 | 5 | AAE20416 | His6G14YC | | 519 | 48 | 100.0 | 13 | 2 | AAV05816 | Aav05816 | Non-toxic |
| 447 | 48 | 100.0 | 11 | 5 | AAW50625 | Polyhisti | | 520 | 48 | 100.0 | 13 | 3 | AAV56262 | Aav56262 | Maedi-Vi |
| 448 | 48 | 100.0 | 11 | 5 | ABG31725 | Human PPA | | 521 | 48 | 100.0 | 13 | 3 | AAH10782 | Aah10782 | B. subcil |
| 449 | 48 | 100.0 | 11 | 5 | ABH76132 | Modified | | 522 | 48 | 100.0 | 13 | 4 | AAE13116 | Aae13116 | C-termina |
| 450 | 48 | 100.0 | 11 | 5 | AAU97110 | pAWG21-hu | | 523 | 48 | 100.0 | 13 | 4 | AAH51258 | Aah51258 | pCONGAH H |
| 451 | 48 | 100.0 | 11 | 5 | ABP52434 | Histidine | | 524 | 48 | 100.0 | 13 | 4 | AAE12152 | Aae12152 | Oligopept |
| 452 | 48 | 100.0 | 11 | 5 | ABG70847 | HIS-6 epi | | 525 | 48 | 100.0 | 13 | 4 | AAH72415 | Aah72415 | Synthetic |
| 453 | 48 | 100.0 | 11 | 6 | ABR42764 | Suitable | | 526 | 48 | 100.0 | 13 | 4 | AAH80820 | Aah80820 | HIS tag p |
| 454 | 48 | 100.0 | 11 | 6 | ADA26448 | Suitable | | 527 | 48 | 100.0 | 13 | 4 | AAH80817 | Aah80817 | HIS tag p |
| 455 | 48 | 100.0 | 11 | 7 | ADC42700 | Modified | | 528 | 48 | 100.0 | 13 | 4 | AAU09363 | Aau09363 | N-termi |
| 456 | 48 | 100.0 | 11 | 7 | ADC81600 | Modified | | 529 | 48 | 100.0 | 13 | 4 | AAU09362 | Aau09362 | N-termi |
| 457 | 48 | 100.0 | 11 | 7 | ADC81592 | Modified | | 530 | 48 | 100.0 | 13 | 4 | AAU09364 | Aau09364 | N-termi |
| 458 | 48 | 100.0 | 11 | 7 | ABW00720 | C-termina | | 531 | 48 | 100.0 | 13 | 4 | AAU09365 | Aau09365 | N-termi |
| 459 | 48 | 100.0 | 11 | 7 | ADH85798 | HIS-tag p | | 532 | 48 | 100.0 | 13 | 5 | ABG32366 | Abg32366 | Peptide u |
| 460 | 48 | 100.0 | 11 | 7 | ADJ66025 | Native Hi | | 533 | 48 | 100.0 | 13 | 5 | AAU11045 | Aau11045 | Translate |
| 461 | 48 | 100.0 | 11 | 8 | ADH22663 | Oligohist | | 534 | 48 | 100.0 | 13 | 5 | AAU11796 | Aau11796 | Peptide a |
| 462 | 48 | 100.0 | 11 | 8 | ADT9358 | 6x His ta | | 535 | 48 | 100.0 | 13 | 6 | ABG75997 | Abg75997 | Jellyfish |

| | | | | | | | | | | | | | |
|-----|----|-------|----|---|-----------|------------|-----|----|-------|----|---|-----------|---------------------|
| 536 | 48 | 100.0 | 13 | 6 | ADA45512 | Vector pE | 609 | 48 | 100.0 | 15 | 6 | ABR38536 | Abt38536 Human can |
| 537 | 48 | 100.0 | 13 | 6 | ABP55018 | Hexa-hist | 610 | 48 | 100.0 | 15 | 6 | ABR38508 | Abt38508 Human can |
| 538 | 48 | 100.0 | 13 | 6 | ABP55083 | Hexa-hist | 611 | 48 | 100.0 | 15 | 6 | ABR38402 | Abt38402 Human can |
| 539 | 48 | 100.0 | 13 | 6 | ABU63441 | His-tagge | 612 | 48 | 100.0 | 15 | 6 | ABR38453 | Abt38453 Human can |
| 540 | 48 | 100.0 | 13 | 7 | ADP47860 | Human alp | 613 | 48 | 100.0 | 15 | 6 | ABR38533 | Abt38533 Human can |
| 541 | 48 | 100.0 | 13 | 7 | ADP28728 | Otx1 tran | 614 | 48 | 100.0 | 15 | 6 | ABR64019 | ABR64019 C-termina |
| 542 | 48 | 100.0 | 13 | 7 | ADP28724 | Otx1 tran | 615 | 48 | 100.0 | 15 | 6 | ABR59491 | ABt59491 His tag p |
| 543 | 48 | 100.0 | 13 | 7 | ADP28738 | Otx1 tran | 616 | 48 | 100.0 | 15 | 6 | AAO23103 | AAO23103 C-termina |
| 544 | 48 | 100.0 | 13 | 7 | ADP28725 | Otx1 tran | 617 | 48 | 100.0 | 15 | 6 | ABE37706 | ABe37706 Peptide # |
| 545 | 48 | 100.0 | 13 | 7 | ADP28726 | Otx1 tran | 618 | 48 | 100.0 | 15 | 6 | ABU61520 | ABu61520 Hepatitis |
| 546 | 48 | 100.0 | 13 | 7 | ADP28729 | Otx1 tran | 619 | 48 | 100.0 | 15 | 7 | ADB68861 | ADB68861 Addictiona |
| 547 | 48 | 100.0 | 13 | 7 | ADP28727 | Otx1 tran | 620 | 48 | 100.0 | 15 | 7 | ADC40526 | ADC40526 Peptide t |
| 548 | 48 | 100.0 | 13 | 7 | ADL01702 | GUS beta- | 621 | 48 | 100.0 | 15 | 7 | ADC46940 | ADC46940 Peptide # |
| 549 | 48 | 100.0 | 13 | 8 | ADO21275 | Poly hist | 622 | 48 | 100.0 | 15 | 7 | ADC98709 | ADC98709 His tag-a |
| 550 | 48 | 100.0 | 13 | 8 | ADP84148 | E. coli c | 623 | 48 | 100.0 | 15 | 7 | ADD26197 | Add26197 Hisidline |
| 551 | 48 | 100.0 | 13 | 8 | ADP87521 | Arar C-te | 624 | 48 | 100.0 | 15 | 7 | ADD15437 | Add15437 His tag a |
| 552 | 48 | 100.0 | 13 | 8 | ADU48659 | H. infive | 625 | 48 | 100.0 | 15 | 7 | ADD35403 | Add35403 General m |
| 553 | 48 | 100.0 | 13 | 9 | ADY74754 | Lic aptam | 626 | 48 | 100.0 | 15 | 7 | ADD44367 | Add44367 Cardoxype |
| 554 | 48 | 100.0 | 13 | 9 | ADZ69728 | Toxin sin | 627 | 48 | 100.0 | 15 | 7 | ADD96098 | Add96098 His tag p |
| 555 | 48 | 100.0 | 14 | 2 | AAE60018 | Can fi pe | 628 | 48 | 100.0 | 15 | 7 | ADZ76697 | Adz76697 Recombina |
| 556 | 48 | 100.0 | 14 | 2 | AAV33455 | Chimeric | 629 | 48 | 100.0 | 15 | 7 | ADE49815 | Ade49815 His pepti |
| 557 | 48 | 100.0 | 14 | 3 | AAV51519 | Human TRF | 630 | 48 | 100.0 | 15 | 7 | ADE76495 | Ade76495 APRT reco |
| 558 | 48 | 100.0 | 14 | 3 | AAZ88977 | Peptide # | 631 | 48 | 100.0 | 15 | 7 | ADE86700 | Ade86700 Purifying |
| 559 | 48 | 100.0 | 14 | 3 | AAV90142 | Leader se | 632 | 48 | 100.0 | 15 | 7 | ADP66828 | ADP66828 His tag p |
| 560 | 48 | 100.0 | 14 | 3 | AAV87722 | Feline TR | 633 | 48 | 100.0 | 15 | 7 | ADG36771 | ADg36771 His tag p |
| 561 | 48 | 100.0 | 14 | 3 | AAV98160 | Synthetic | 634 | 48 | 100.0 | 15 | 7 | ADH13051 | ADh13051 Pathogeni |
| 562 | 48 | 100.0 | 14 | 3 | AAH11893 | Cyclo-ICy | 635 | 48 | 100.0 | 15 | 7 | ADG75197 | Adg75197 His tag-r |
| 563 | 48 | 100.0 | 14 | 3 | AAH10559 | Coiled co | 636 | 48 | 100.0 | 15 | 7 | ADH48562 | Adh48562 His tag-r |
| 564 | 48 | 100.0 | 14 | 3 | AAH29044 | Endostati | 637 | 48 | 100.0 | 15 | 7 | ADH48562 | Adh48562 C-termina |
| 565 | 48 | 100.0 | 14 | 4 | AAH82693 | His-tag. | 638 | 48 | 100.0 | 15 | 7 | ADJ66226 | Adj66226 Peptide (|
| 566 | 48 | 100.0 | 14 | 4 | AAE12159 | Human hg- | 639 | 48 | 100.0 | 15 | 7 | ADL46284 | Adl46284 Protein |
| 567 | 48 | 100.0 | 14 | 4 | AAU09361 | N-termina | 640 | 48 | 100.0 | 15 | 8 | ADE71039 | AdE71039 P. aerugi |
| 568 | 48 | 100.0 | 14 | 4 | AAH73439 | C-termina | 641 | 48 | 100.0 | 15 | 8 | ADE18062 | AdE18062 His tag p |
| 569 | 48 | 100.0 | 14 | 4 | AAE10674 | Peptide u | 642 | 48 | 100.0 | 15 | 8 | ADK00359 | AdK00359 His-tag p |
| 570 | 48 | 100.0 | 14 | 5 | ABG67084 | Streptavl | 643 | 48 | 100.0 | 15 | 8 | ADJ74085 | Adj74085 His tag p |
| 571 | 48 | 100.0 | 14 | 5 | AAAG80199 | Human cys | 644 | 48 | 100.0 | 15 | 8 | ADJ62025 | Adj62025 His tag p |
| 572 | 48 | 100.0 | 14 | 5 | ABG31911 | HIS tag p | 645 | 48 | 100.0 | 15 | 8 | ADH96811 | ADh96811 His tag p |
| 573 | 48 | 100.0 | 14 | 5 | ABH08199 | Amino aci | 646 | 48 | 100.0 | 15 | 8 | ADOO5885 | ADOO5885 Rat MOC1- |
| 574 | 48 | 100.0 | 14 | 5 | ABH05986 | Monoclonu | 647 | 48 | 100.0 | 15 | 8 | ADP70101 | ADp70101 Synthetic |
| 575 | 48 | 100.0 | 14 | 6 | ABH99665 | C-terminu | 648 | 48 | 100.0 | 15 | 8 | ADG78337 | ADG78337 Synthetic |
| 576 | 48 | 100.0 | 14 | 6 | ABU57606 | Streptavl | 649 | 48 | 100.0 | 15 | 8 | ADO25327 | ADO25327 Peptide w |
| 577 | 48 | 100.0 | 14 | 6 | ABR62703 | HIS tag u | 650 | 48 | 100.0 | 15 | 8 | ADO59366 | ADO59366 Synthetic |
| 578 | 48 | 100.0 | 14 | 6 | ABU61987 | Synthetic | 651 | 48 | 100.0 | 15 | 8 | ADO80040 | ADO80040 His tag m |
| 579 | 48 | 100.0 | 14 | 7 | ADD11681 | Rat GDNFR | 652 | 48 | 100.0 | 15 | 8 | ADP64426 | ADp64426 Human end |
| 580 | 48 | 100.0 | 14 | 8 | ADJ77664 | N-termina | 653 | 48 | 100.0 | 15 | 8 | ADOO81640 | ADOO81640 Synthetic |
| 581 | 48 | 100.0 | 14 | 8 | ADN00838 | Epitope p | 654 | 48 | 100.0 | 15 | 8 | ADQ58858 | ADq58858 C-termina |
| 582 | 48 | 100.0 | 14 | 8 | ADN00842 | Epitope p | 655 | 48 | 100.0 | 15 | 8 | ADQ48620 | ADQ48620 C-termina |
| 583 | 48 | 100.0 | 14 | 8 | ADO49277 | His tagge | 656 | 48 | 100.0 | 15 | 8 | ADQ48606 | ADq48606 His tag p |
| 584 | 48 | 100.0 | 14 | 8 | ADO59303 | Mutant TC | 657 | 48 | 100.0 | 15 | 8 | ADQ15892 | ADQ15892 Additiona |
| 585 | 48 | 100.0 | 14 | 8 | ADP64434 | Human end | 658 | 48 | 100.0 | 15 | 8 | ADQ94390 | ADQ94390 Aspartate |
| 586 | 48 | 100.0 | 14 | 8 | ADU04614 | CGS5698-0 | 659 | 48 | 100.0 | 15 | 8 | ADR16485 | ADR16485 HCV NS3 p |
| 587 | 48 | 100.0 | 14 | 9 | ADV66856 | Vector jm | 660 | 48 | 100.0 | 15 | 8 | ADR49006 | ADR49006 Caspase r |
| 588 | 48 | 100.0 | 14 | 9 | ADZ66261 | Hexahisti | 661 | 48 | 100.0 | 15 | 8 | ADS51717 | AdS51717 His tag p |
| 589 | 48 | 100.0 | 14 | 9 | ADZ87786 | Novel cop | 662 | 48 | 100.0 | 15 | 8 | ADT08032 | ADt08032 His tag s |
| 590 | 48 | 100.0 | 14 | 9 | AEBS3772 | human glu | 663 | 48 | 100.0 | 15 | 8 | ADU80751 | ADu80751 HMG-CoA r |
| 591 | 48 | 100.0 | 14 | 9 | AEB71104 | Auroara ki | 664 | 48 | 100.0 | 15 | 9 | ADV97506 | ADv97506 S. aureus |
| 592 | 48 | 100.0 | 15 | 2 | AAH60513 | Hexahisti | 665 | 48 | 100.0 | 15 | 9 | ADX85435 | ADx85435 C-termina |
| 593 | 48 | 100.0 | 15 | 3 | AAV96095 | Hexahisti | 666 | 48 | 100.0 | 15 | 9 | ADY39760 | ADy39760 His tag a |
| 594 | 48 | 100.0 | 15 | 3 | AAE13115 | C-termina | 667 | 48 | 100.0 | 15 | 9 | AEC10470 | Aec10470 Hisidline |
| 595 | 48 | 100.0 | 15 | 4 | AAE08870 | Escherich | 668 | 48 | 100.0 | 15 | 9 | AEC13166 | Aec13166 Hisidline |
| 596 | 48 | 100.0 | 15 | 4 | AAAG79094 | Amino aci | 669 | 48 | 100.0 | 16 | 2 | AAH69813 | AAh69813 Cleavage |
| 597 | 48 | 100.0 | 15 | 4 | AAAM5253 | His tag p | 670 | 48 | 100.0 | 16 | 2 | AAV06321 | AAV06321 His-C-myc |
| 598 | 48 | 100.0 | 15 | 4 | AAH67388 | N-termina | 671 | 48 | 100.0 | 16 | 3 | AAV51161 | AAv51161 Modified |
| 599 | 48 | 100.0 | 15 | 4 | AAH66370 | Hepatitis | 672 | 48 | 100.0 | 16 | 4 | AAU27552 | AAu27552 Tag seque |
| 600 | 48 | 100.0 | 15 | 4 | AAAG64156 | Recombina | 673 | 48 | 100.0 | 16 | 4 | AAV72938 | AAv72938 N-termina |
| 601 | 48 | 100.0 | 15 | 5 | ABB05375 | 15 amino | 674 | 48 | 100.0 | 16 | 4 | AAV97659 | AAV97659 Influenta |
| 602 | 48 | 100.0 | 15 | 5 | AAU77664 | His tag p | 675 | 48 | 100.0 | 16 | 4 | AAH66989 | AAh66989 Peptide: |
| 603 | 48 | 100.0 | 15 | 5 | AAV19656 | Arabidops | 676 | 48 | 100.0 | 16 | 5 | AAU98499 | AAu98499 Aminoacyl |
| 604 | 48 | 100.0 | 15 | 5 | ABG32504 | N-termina | 677 | 48 | 100.0 | 16 | 5 | AAE28473 | AAe28473 6His-VSVG |
| 605 | 48 | 100.0 | 15 | 6 | ABR83204 | Membrane | 678 | 48 | 100.0 | 16 | 5 | AAE28475 | AAe28475 6His-RGD |
| 606 | 48 | 100.0 | 15 | 6 | ABR63484 | His tag p | 679 | 48 | 100.0 | 16 | 5 | ABR08039 | ABr08039 Amino aci |
| 607 | 48 | 100.0 | 15 | 6 | ABR38534 | Human can | 680 | 48 | 100.0 | 16 | 5 | AAU77202 | AAu77202 Polyaspar |
| 608 | 48 | 100.0 | 15 | 6 | ABR38535 | Human can | 681 | 48 | 100.0 | 16 | 6 | ABG72595 | ABg72595 N termina |

| | | | | | | | | | | | | | | | |
|-----|-------|-------|----|---|-----------|-----------|-------------|-----|----|-------|----|---|-----------|-----------|-------------|
| 682 | 48 | 100.0 | 16 | 6 | ABU15405 | Abu15405 | Protein e | 755 | 48 | 100.0 | 18 | 7 | ADH61128 | Adh61128 | Mouse son |
| 683 | 48 | 100.0 | 16 | 7 | ADH44349 | Adh44349 | Transfect | 756 | 48 | 100.0 | 18 | 7 | ADH54691 | Adh54691 | Mouse son |
| 684 | 100.0 | | 16 | 7 | ADH44347 | Adh44347 | Transfect | 757 | 48 | 100.0 | 18 | 7 | ADL46283 | Adl46283 | Protein N |
| 685 | 48 | 100.0 | 16 | 7 | ADM34937 | Adm34937 | H1A bindi | 758 | 48 | 100.0 | 18 | 8 | ADO43153 | Ado43153 | Human int |
| 686 | 48 | 100.0 | 16 | 7 | ADM33704 | Adm33704 | H1A bindi | 759 | 48 | 100.0 | 18 | 8 | ADS09421 | Ads09421 | N-termina |
| 687 | 48 | 100.0 | 16 | 8 | ADP12237 | Adp12237 | Transfect | 760 | 48 | 100.0 | 18 | 8 | ADU26453 | Adu26453 | Peptide r |
| 688 | 48 | 100.0 | 16 | 8 | ADP12239 | Adp12239 | Transfect | 761 | 48 | 100.0 | 18 | 8 | ADM38678 | Adm38678 | N-termina |
| 689 | 48 | 100.0 | 16 | 8 | ADM28856 | Adm28856 | Bacterial | 762 | 48 | 100.0 | 18 | 9 | ADM25902 | Adm25902 | N-termina |
| 690 | 48 | 100.0 | 16 | 8 | ADL24430 | Adl24430 | Modified | 763 | 48 | 100.0 | 18 | 9 | ADM21602 | Adm21602 | C-termina |
| 691 | 48 | 100.0 | 16 | 8 | ADL24490 | Adl24490 | Human inc | 764 | 48 | 100.0 | 18 | 9 | ADM38956 | Adm38956 | Plamid p |
| 692 | 48 | 100.0 | 16 | 8 | ADO58594 | Ado58594 | Flag/8Hs | 765 | 48 | 100.0 | 18 | 9 | ADZ76275 | Adz76275 | Mouse son |
| 693 | 48 | 100.0 | 16 | 8 | ADR29318 | Adr29318 | Hirfidine | 766 | 48 | 100.0 | 18 | 9 | AEA04352 | Aea04352 | Small Exp |
| 694 | 48 | 100.0 | 16 | 8 | ADT94020 | Adt94020 | rFel d 1 l | 767 | 48 | 100.0 | 18 | 9 | ADZ76977 | Adz76977 | GH18 prot |
| 695 | 48 | 100.0 | 16 | 8 | ADU04613 | Adu04613 | CGS5698-0 | 768 | 48 | 100.0 | 19 | 2 | AAW00339 | Aaw00339 | Rec2 prot |
| 696 | 48 | 100.0 | 16 | 9 | ADM47934 | Adm47934 | H1s-tag p | 769 | 48 | 100.0 | 19 | 2 | AAW37707 | Aaw37707 | C-termina |
| 697 | 48 | 100.0 | 16 | 9 | ADY53507 | Ady53507 | MUC1 grow | 770 | 48 | 100.0 | 19 | 2 | AAV43533 | Aav43533 | Leishmani |
| 698 | 48 | 100.0 | 16 | 9 | ABE119851 | Abel19851 | PAMG22-Hi | 771 | 48 | 100.0 | 19 | 2 | AAW98067 | Aaw98067 | Streptoco |
| 699 | 48 | 100.0 | 17 | 2 | AAR337708 | Aar337708 | Delta14 S | 772 | 48 | 100.0 | 19 | 3 | AAV90748 | Aav90748 | Protease |
| 700 | 48 | 100.0 | 17 | 2 | AAR68977 | Aar68977 | pGEX-7HPr | 773 | 48 | 100.0 | 19 | 3 | AAH11078 | Aah11078 | S. pyogen |
| 701 | 48 | 100.0 | 17 | 2 | AAW03939 | Aaw03939 | T2 pepid | 774 | 48 | 100.0 | 19 | 4 | ABH49879 | Abh49879 | H1s tag S |
| 702 | 48 | 100.0 | 17 | 2 | ABB08913 | Abb08913 | TNF/hpi f | 775 | 48 | 100.0 | 19 | 5 | ABP56043 | Abp56043 | Negative |
| 703 | 48 | 100.0 | 17 | 2 | AAW95000 | Aaw95000 | N-termina | 776 | 48 | 100.0 | 19 | 5 | AAW79390 | Aaw79390 | H1s tag/E |
| 704 | 48 | 100.0 | 17 | 3 | AAH26262 | Aah26262 | N-termina | 777 | 48 | 100.0 | 19 | 6 | AAE37111 | Aae37111 | Peptide u |
| 705 | 48 | 100.0 | 17 | 5 | AAH99608 | Aah99608 | ERA bindi | 778 | 48 | 100.0 | 19 | 6 | ABR42595 | Abh42595 | Substrate |
| 706 | 48 | 100.0 | 17 | 5 | ABH79628 | Abh79628 | Hexa-hist | 779 | 48 | 100.0 | 19 | 6 | ABE36802 | Abh36802 | His-tagge |
| 707 | 48 | 100.0 | 17 | 6 | ABU63437 | Abu63437 | Thrombin | 780 | 48 | 100.0 | 19 | 6 | ABU673908 | Abu673908 | H1s-tagge |
| 708 | 48 | 100.0 | 17 | 6 | ABE24165 | Abel24165 | Plasmodiu | 781 | 48 | 100.0 | 19 | 6 | ABU61781 | Abu61781 | Synthetic |
| 709 | 48 | 100.0 | 17 | 7 | ADG17892 | Adg17892 | Peptide u | 782 | 48 | 100.0 | 19 | 7 | ADM64739 | Adm64739 | Hepatic tis |
| 710 | 48 | 100.0 | 17 | 8 | ADK51966 | Adk51966 | Repeat pr | 783 | 48 | 100.0 | 19 | 7 | ADM78575 | Adm78575 | PRSET B v |
| 711 | 48 | 100.0 | 17 | 8 | ADK51960 | Adk51960 | Repeat pr | 784 | 48 | 100.0 | 19 | 8 | ADI25167 | Adi25167 | Saxiphilli |
| 712 | 48 | 100.0 | 17 | 8 | ADU50913 | Adu50913 | IFN-beta- | 785 | 48 | 100.0 | 19 | 8 | ADR05296 | Adr05296 | N-termina |
| 713 | 48 | 100.0 | 17 | 8 | ADU04999 | Adu04999 | F. hepari | 786 | 48 | 100.0 | 19 | 9 | ADY53556 | Ady53556 | Truncated |
| 714 | 48 | 100.0 | 17 | 8 | ADS20742 | Ads20742 | TAP N-ter | 787 | 48 | 100.0 | 19 | 9 | ABE110606 | Abel10606 | Polo-like |
| 715 | 48 | 100.0 | 17 | 8 | ADX83549 | Adx83549 | Periphera | 788 | 48 | 100.0 | 19 | 9 | ABE91051 | Abel91051 | Latibibiot |
| 716 | 48 | 100.0 | 17 | 9 | AEA04353 | Aea04353 | Small Exp | 789 | 48 | 100.0 | 20 | 2 | AAH73014 | Aah73014 | N-termina |
| 717 | 48 | 100.0 | 18 | 2 | AAH60253 | Aah60253 | Vector-en | 790 | 48 | 100.0 | 20 | 2 | AAW00869 | Aaw00869 | T-cell re |
| 718 | 48 | 100.0 | 18 | 2 | AAH69814 | Aah69814 | Site reco | 791 | 48 | 100.0 | 20 | 2 | AAW01445 | Aaw01445 | Bioislaeti |
| 719 | 48 | 100.0 | 18 | 2 | AAH78152 | Aah78152 | Synthetic | 792 | 48 | 100.0 | 20 | 2 | AAW08594 | Aaw08594 | Leader se |
| 720 | 48 | 100.0 | 18 | 2 | AAH95870 | Aah95870 | CR2 recep | 793 | 48 | 100.0 | 20 | 2 | AAV33454 | Aav33454 | Chemirc |
| 721 | 48 | 100.0 | 18 | 3 | AAH73374 | Aah73374 | Epitope t | 794 | 48 | 100.0 | 20 | 3 | AAH80347 | Aah80347 | N-termina |
| 722 | 48 | 100.0 | 18 | 3 | AAH11047 | Aah11047 | Staphyloc | 795 | 48 | 100.0 | 20 | 3 | AAH83783 | Aah83783 | Poly (H1s) |
| 723 | 48 | 100.0 | 18 | 3 | AAH23253 | Aah23253 | Hexahisti | 796 | 48 | 100.0 | 20 | 3 | AAV87744 | Aav87744 | Human and |
| 724 | 48 | 100.0 | 18 | 3 | AAH10856 | Aah10856 | pSecretag-V | 797 | 48 | 100.0 | 20 | 3 | AAH28485 | Aah28485 | N-termina |
| 725 | 48 | 100.0 | 18 | 4 | AAH14660 | Aah14660 | Peptide # | 798 | 48 | 100.0 | 20 | 4 | AAE08579 | Aae08579 | D3SD3-FLA |
| 726 | 48 | 100.0 | 18 | 4 | ABH33620 | Abh33620 | Peptide # | 799 | 48 | 100.0 | 20 | 4 | AAH70818 | Aah70818 | MBP/BMP f |
| 727 | 48 | 100.0 | 18 | 4 | AAH27079 | Aah27079 | Peptide # | 800 | 48 | 100.0 | 20 | 4 | AAH82670 | Aah82670 | Recombina |
| 728 | 48 | 100.0 | 18 | 4 | ABH28438 | Abh28438 | Peptide # | 801 | 48 | 100.0 | 20 | 4 | AAH850878 | Aah850878 | Integrin |
| 729 | 48 | 100.0 | 18 | 4 | AAH97657 | Aah97657 | Influenza | 802 | 48 | 100.0 | 20 | 4 | AAH85139 | Aah85139 | Sequence |
| 730 | 48 | 100.0 | 18 | 4 | AAH05390 | Aah05390 | N-termina | 803 | 48 | 100.0 | 20 | 4 | AAH85140 | Aah85140 | Sequence |
| 731 | 48 | 100.0 | 18 | 4 | AAH35459 | Aah35459 | Clostridi | 804 | 48 | 100.0 | 20 | 4 | AAH85142 | Aah85142 | Sequence |
| 732 | 48 | 100.0 | 18 | 4 | ABH19075 | Abh19075 | Protein # | 805 | 48 | 100.0 | 20 | 4 | AAH85141 | Aah85141 | Sequence |
| 733 | 48 | 100.0 | 18 | 4 | AAH66794 | Aah66794 | Human bon | 806 | 48 | 100.0 | 20 | 4 | AAH85143 | Aah85143 | Sequence |
| 734 | 48 | 100.0 | 18 | 4 | AAH85750 | Aah85750 | Mouse son | 807 | 48 | 100.0 | 20 | 4 | AAH59137 | Aah59137 | N-termina |
| 735 | 48 | 100.0 | 18 | 4 | AAH54393 | Aah54393 | Human bra | 808 | 48 | 100.0 | 20 | 4 | AAH73436 | Aah73436 | N-termina |
| 736 | 48 | 100.0 | 18 | 4 | ABG48462 | Abg48462 | Human liv | 809 | 48 | 100.0 | 20 | 5 | ABH94460 | Abh94460 | His tag p |
| 737 | 48 | 100.0 | 18 | 4 | AAH73440 | Aah73440 | C-termina | 810 | 48 | 100.0 | 20 | 5 | ABH76190 | Abh76190 | Modified |
| 738 | 48 | 100.0 | 18 | 4 | AAH02383 | Aah02383 | Peptide # | 811 | 48 | 100.0 | 20 | 5 | AAH021570 | Aah021570 | Murine To |
| 739 | 48 | 100.0 | 18 | 5 | ABG36449 | Abg36449 | Peptide # | 812 | 48 | 100.0 | 20 | 6 | ABP59406 | Abp59406 | Self-abse |
| 740 | 48 | 100.0 | 18 | 5 | ABH79149 | Abh79149 | Human pep | 813 | 48 | 100.0 | 20 | 6 | ABP59407 | Abp59407 | Self-abse |
| 741 | 48 | 100.0 | 18 | 5 | ABH54919 | Abh54919 | Recombina | 814 | 48 | 100.0 | 20 | 6 | ABH83203 | Abh83203 | Membrane |
| 742 | 48 | 100.0 | 18 | 6 | AAH36641 | Aah36641 | Muanolysi | 815 | 48 | 100.0 | 20 | 6 | ABH63483 | Abh63483 | H1s tag p |
| 743 | 48 | 100.0 | 18 | 6 | ABU09400 | Abu09400 | Peptide # | 816 | 48 | 100.0 | 20 | 6 | AAH36646 | Aah36646 | Peptide # |
| 744 | 48 | 100.0 | 18 | 6 | ABU09938 | Abu09938 | Cytochrom | 817 | 48 | 100.0 | 20 | 6 | ABH64018 | Abh64018 | N-termina |
| 745 | 48 | 100.0 | 18 | 6 | ADA26288 | Ada26288 | Hedgehog- | 818 | 48 | 100.0 | 20 | 6 | ABH59490 | Abh59490 | His tag p |
| 746 | 48 | 100.0 | 18 | 6 | ABH81957 | Abh81957 | L. acidop | 819 | 48 | 100.0 | 20 | 6 | AAH023102 | Aah023102 | N-termina |
| 747 | 48 | 100.0 | 18 | 7 | ADD25294 | Add25294 | Hedgehog | 820 | 48 | 100.0 | 20 | 6 | AAH37705 | Aah37705 | Peptide # |
| 748 | 48 | 100.0 | 18 | 7 | ADD25308 | Add25308 | N-termina | 821 | 48 | 100.0 | 20 | 6 | ABH62029 | Abh62029 | Modified |
| 749 | 48 | 100.0 | 18 | 7 | ABW00879 | Abw00879 | Poly (H1s | 822 | 48 | 100.0 | 20 | 7 | ABH68860 | Abh68860 | Additiona |
| 750 | 48 | 100.0 | 18 | 7 | AAH39986 | Aah39986 | Peptide e | 823 | 48 | 100.0 | 20 | 7 | ADC40525 | Adc40525 | Peptide t |
| 751 | 48 | 100.0 | 18 | 7 | ADD71417 | Add71417 | Mouse son | 824 | 48 | 100.0 | 20 | 7 | ADC46939 | Adc46939 | Peptide # |
| 752 | 48 | 100.0 | 18 | 7 | ABW01686 | Abw01686 | PolyH1s 1 | 825 | 48 | 100.0 | 20 | 7 | ADC98708 | Adc98708 | H1s tag-a |
| 753 | 48 | 100.0 | 18 | 7 | ADH02816 | Adh02816 | Plamid p | 826 | 48 | 100.0 | 20 | 7 | ADD26196 | Add26196 | Hirfidine |
| 754 | 48 | 100.0 | 18 | 7 | ADG73574 | Adg73574 | H1s tag-r | 827 | 48 | 100.0 | 20 | 7 | ADD15436 | Add15436 | H1s tag a |

| | | | | | | | | | | | | | | | |
|-----|----|-------|----|---|-----------|-----------|------------|-----|----|-------|----|---|----------|----------|------------|
| 828 | 48 | 100.0 | 20 | 7 | ADD35402 | AdD35402 | General m | 901 | 48 | 100.0 | 21 | 2 | AAV18411 | Aay18411 | Apomilgren |
| 829 | 48 | 100.0 | 20 | 7 | ADBS2550 | AdB2550 | Flis pept | 902 | 48 | 100.0 | 21 | 2 | AAV06793 | Aay06793 | Myc-His p |
| 830 | 48 | 100.0 | 20 | 7 | ADBD6097 | AdB6097 | His tag p | 903 | 48 | 100.0 | 21 | 2 | AAW95646 | Aay95646 | c-myc onc |
| 831 | 48 | 100.0 | 20 | 7 | ADSF6696 | AdF6696 | Recombina | 904 | 48 | 100.0 | 21 | 2 | AAW92557 | Aay92557 | Myc-His-t |
| 832 | 48 | 100.0 | 20 | 7 | ADSF9814 | AdF9814 | His pepti | 905 | 48 | 100.0 | 21 | 2 | AAV07741 | Aay07741 | Human bre |
| 833 | 48 | 100.0 | 20 | 7 | ADSF6494 | AdF6494 | APRT reco | 906 | 48 | 100.0 | 21 | 2 | AAW97132 | Aay97132 | Fusion pe |
| 834 | 48 | 100.0 | 20 | 7 | ADBE6699 | AdE6699 | Purifying | 907 | 48 | 100.0 | 21 | 2 | AAW86030 | Aay86030 | Myc-His p |
| 835 | 48 | 100.0 | 20 | 7 | ADPF6827 | AdF6827 | His tag p | 908 | 48 | 100.0 | 21 | 2 | AAW95563 | Aay95563 | Myc-His t |
| 836 | 48 | 100.0 | 20 | 7 | ADG36770 | AdG36770 | His tag p | 909 | 48 | 100.0 | 21 | 2 | AAW25329 | Aay25329 | Myc-His-t |
| 837 | 48 | 100.0 | 20 | 7 | ADG17903 | AdG17903 | Fusion pr | 910 | 48 | 100.0 | 21 | 2 | AAV13472 | Aay13472 | Myc-His t |
| 838 | 48 | 100.0 | 20 | 7 | ADH13050 | AdH13050 | Pathogeni | 911 | 48 | 100.0 | 21 | 3 | AAE26127 | AAE26127 | Human TGF |
| 839 | 48 | 100.0 | 20 | 7 | ADG75196 | AdG75196 | His tag-r | 912 | 48 | 100.0 | 21 | 3 | AAE26857 | AAE26857 | N-termina |
| 840 | 48 | 100.0 | 20 | 7 | ADH69237 | AdH69237 | D3SD3-FluA | 913 | 48 | 100.0 | 21 | 3 | AAE28465 | AAE28465 | OB gene-r |
| 841 | 48 | 100.0 | 20 | 7 | ADH48561 | AdH48561 | N-termina | 914 | 48 | 100.0 | 21 | 3 | AAE87743 | AAE87743 | Human and |
| 842 | 48 | 100.0 | 20 | 7 | ADL06299 | AdL06299 | Synthetic | 915 | 48 | 100.0 | 21 | 3 | AAE28484 | AAE28484 | OB gene-r |
| 843 | 48 | 100.0 | 20 | 7 | ADJ62225 | AdJ62225 | Peptide (| 916 | 48 | 100.0 | 21 | 3 | AAE29273 | AAE29273 | Human pro |
| 844 | 48 | 100.0 | 20 | 8 | ADSF1038 | AdF1038 | P. aerugi | 917 | 48 | 100.0 | 21 | 3 | AAV90318 | AAV90318 | Human pro |
| 845 | 48 | 100.0 | 20 | 8 | ADFI18061 | AdFI18061 | His tag p | 918 | 48 | 100.0 | 21 | 4 | AAE13185 | AAE13185 | Peptide u |
| 846 | 48 | 100.0 | 20 | 8 | ADJ32488 | AdJ32488 | N-termina | 919 | 48 | 100.0 | 21 | 4 | AAE07326 | AAE07326 | Myc-His t |
| 847 | 48 | 100.0 | 20 | 8 | ADJ83275 | AdJ83275 | PolyHis-e | 920 | 48 | 100.0 | 21 | 4 | AAE08052 | AAE08052 | Myc-His t |
| 848 | 48 | 100.0 | 20 | 8 | ADK00358 | AdK00358 | His-tag p | 921 | 48 | 100.0 | 21 | 4 | AAU04210 | AAU04210 | Myc-His t |
| 849 | 48 | 100.0 | 20 | 8 | ADJ74084 | AdJ74084 | His tag p | 922 | 48 | 100.0 | 21 | 4 | AAO05538 | AAO05538 | Human pol |
| 850 | 48 | 100.0 | 20 | 8 | ADJ62024 | AdJ62024 | His tag p | 923 | 48 | 100.0 | 21 | 5 | AAE21826 | AAE21826 | Myc-His t |
| 851 | 48 | 100.0 | 20 | 8 | ADJ62027 | AdJ62027 | His tag p | 924 | 48 | 100.0 | 21 | 5 | AAO19089 | AAO19089 | Human PS1 |
| 852 | 48 | 100.0 | 20 | 8 | ADH96810 | AdH96810 | His tag p | 925 | 48 | 100.0 | 21 | 5 | AAE22592 | AAE22592 | Peptide # |
| 853 | 48 | 100.0 | 20 | 8 | ADP99715 | AdP99715 | His6 tag | 926 | 48 | 100.0 | 21 | 5 | AAO21842 | AAO21842 | Breast ti |
| 854 | 48 | 100.0 | 20 | 8 | ADP70100 | AdP70100 | Synthetic | 927 | 48 | 100.0 | 21 | 5 | AAO19171 | AAO19171 | Human pro |
| 855 | 48 | 100.0 | 20 | 8 | ADO78336 | AdO78336 | Synthetic | 928 | 48 | 100.0 | 21 | 5 | AAE21835 | AAE21835 | Myc-His t |
| 856 | 48 | 100.0 | 20 | 8 | ADO25326 | AdO25326 | Peptide w | 929 | 48 | 100.0 | 21 | 5 | AAE79563 | AAE79563 | Potato ps |
| 857 | 48 | 100.0 | 20 | 8 | ADO59365 | AdO59365 | Synthetic | 930 | 48 | 100.0 | 21 | 5 | ABE76276 | ABE76276 | Myc-His t |
| 858 | 48 | 100.0 | 20 | 8 | ADO80039 | AdO80039 | His tag m | 931 | 48 | 100.0 | 21 | 5 | ABP53471 | ABP53471 | SELPK re |
| 859 | 48 | 100.0 | 20 | 8 | ADO81639 | AdO81639 | Synthetic | 932 | 48 | 100.0 | 21 | 5 | AAE26119 | AAE26119 | Myc-His t |
| 860 | 48 | 100.0 | 20 | 8 | ADO58857 | AdO58857 | N-termina | 933 | 48 | 100.0 | 21 | 5 | AAE22697 | AAE22697 | Myc-His t |
| 861 | 48 | 100.0 | 20 | 8 | ADQ48619 | AdQ48619 | N-termina | 934 | 48 | 100.0 | 21 | 5 | AAE50815 | AAE50815 | Myc-His p |
| 862 | 48 | 100.0 | 20 | 8 | ADQ48605 | AdQ48605 | His tag p | 935 | 48 | 100.0 | 21 | 5 | AAU80152 | AAU80152 | MyChis ta |
| 863 | 48 | 100.0 | 20 | 8 | ADQ15891 | AdQ15891 | Additiona | 936 | 48 | 100.0 | 21 | 5 | AAE21869 | AAE21869 | Myc-His t |
| 864 | 48 | 100.0 | 20 | 8 | ADQ94389 | AdQ94389 | Aspartate | 937 | 48 | 100.0 | 21 | 5 | ABG68926 | ABG68926 | Laveonia |
| 865 | 48 | 100.0 | 20 | 8 | ADS08306 | AdS08306 | FLAG/His | 938 | 48 | 100.0 | 21 | 5 | AAU75380 | AAU75380 | Immunotox |
| 866 | 48 | 100.0 | 20 | 8 | ADR98706 | AdR98706 | His-tag, | 939 | 48 | 100.0 | 21 | 5 | ABE84133 | ABE84133 | Ob protei |
| 867 | 48 | 100.0 | 20 | 8 | ADS51716 | AdS51716 | His tag p | 940 | 48 | 100.0 | 21 | 6 | ABU12328 | ABU12328 | Myc-His p |
| 868 | 48 | 100.0 | 20 | 8 | ADR90322 | AdR90322 | His tag p | 941 | 48 | 100.0 | 21 | 6 | ABU08632 | ABU08632 | LS147 pol |
| 869 | 48 | 100.0 | 20 | 8 | ADT08031 | AdT08031 | His tag s | 942 | 48 | 100.0 | 21 | 6 | ABG73776 | ABG73776 | Myc-His t |
| 870 | 48 | 100.0 | 20 | 8 | ADT14640 | AdT14640 | Hexahis t | 943 | 48 | 100.0 | 21 | 6 | ABP97471 | ABP97471 | Vector pe |
| 871 | 48 | 100.0 | 20 | 8 | ADU80750 | AdU80750 | HMG-CoA r | 944 | 48 | 100.0 | 21 | 6 | ABU64578 | ABU64578 | Obese (ob |
| 872 | 48 | 100.0 | 20 | 9 | ADY43433 | AdY43433 | 6xHis ext | 945 | 48 | 100.0 | 21 | 6 | ABG99191 | ABG99191 | Guanylate |
| 873 | 48 | 100.0 | 20 | 9 | ADW22621 | AdW22621 | N-termina | 946 | 48 | 100.0 | 21 | 6 | ABU08597 | ABU08597 | Myc-His t |
| 874 | 48 | 100.0 | 20 | 9 | ADW38677 | AdW38677 | N-termina | 947 | 48 | 100.0 | 21 | 6 | ABU92017 | ABU92017 | E. coli p |
| 875 | 48 | 100.0 | 20 | 9 | ADW02460 | AdW02460 | Human int | 948 | 48 | 100.0 | 21 | 6 | ABR62086 | ABR62086 | Anti-vitr |
| 876 | 48 | 100.0 | 20 | 9 | ADV97505 | AdV97505 | S. aureus | 949 | 48 | 100.0 | 21 | 6 | ADA00850 | ADA00850 | Myc-His a |
| 877 | 48 | 100.0 | 20 | 9 | ADX85434 | AdX85434 | N-termina | 950 | 48 | 100.0 | 21 | 6 | ABU62470 | ABU62470 | N-terminu |
| 878 | 48 | 100.0 | 20 | 9 | ADZ11732 | AdZ11732 | His-HIV T | 951 | 48 | 100.0 | 21 | 6 | ABU62469 | ABU62469 | N-terminu |
| 879 | 48 | 100.0 | 20 | 9 | ADZ88431 | AdZ88431 | Modified | 952 | 48 | 100.0 | 21 | 6 | ABU62468 | ABU62468 | N-terminu |
| 880 | 48 | 100.0 | 20 | 9 | AEB00935 | AdE00935 | E. coli e | 953 | 48 | 100.0 | 21 | 6 | ABU62471 | ABU62471 | N-terminu |
| 881 | 48 | 100.0 | 20 | 9 | AEA40240 | AdA40240 | Oct-His t | 954 | 48 | 100.0 | 21 | 6 | ABU62467 | ABU62467 | N-terminu |
| 882 | 48 | 100.0 | 20 | 9 | AEB44158 | AdB44158 | N-terminu | 955 | 48 | 100.0 | 21 | 6 | ABR63854 | ABR63854 | His tag p |
| 883 | 48 | 100.0 | 20 | 9 | AEC10469 | AdC10469 | Histidine | 956 | 48 | 100.0 | 21 | 6 | ADA26386 | ADA26386 | CS198 pur |
| 884 | 48 | 100.0 | 20 | 9 | AEC13165 | AdC13165 | Histidine | 957 | 48 | 100.0 | 21 | 7 | ABU08854 | ABU08854 | Myc-His t |
| 885 | 48 | 100.0 | 21 | 2 | AAE07063 | AAE07063 | Transcrip | 958 | 48 | 100.0 | 21 | 7 | ADB85348 | ADB85348 | Myc-His t |
| 886 | 48 | 100.0 | 21 | 2 | AAE60142 | AAE60142 | pGEX-6Hpr | 959 | 48 | 100.0 | 21 | 7 | AAE39150 | AAE39150 | Myc-His t |
| 887 | 48 | 100.0 | 21 | 2 | AAE87745 | AAE87745 | Hexa-His/ | 960 | 48 | 100.0 | 21 | 7 | ABW00603 | ABW00603 | Myc-His t |
| 888 | 48 | 100.0 | 21 | 2 | AAW23653 | AAW23653 | Recombina | 961 | 48 | 100.0 | 21 | 7 | ADG33993 | ADG33993 | Recombina |
| 889 | 48 | 100.0 | 21 | 2 | AAW08590 | AAW08590 | Leader se | 962 | 48 | 100.0 | 21 | 7 | ADG33984 | ADG33984 | L. intrac |
| 890 | 48 | 100.0 | 21 | 2 | AAW23650 | AAW23650 | Recombina | 963 | 48 | 100.0 | 21 | 7 | ADI35718 | ADI35718 | Tyrosine |
| 891 | 48 | 100.0 | 21 | 2 | AAW23647 | AAW23647 | Recombina | 964 | 48 | 100.0 | 21 | 7 | ADJ66889 | ADJ66889 | Laveonia |
| 892 | 48 | 100.0 | 21 | 2 | AAW5875 | AAW5875 | Myc-His t | 965 | 48 | 100.0 | 21 | 8 | ADP51136 | ADP51136 | Human PS2 |
| 893 | 48 | 100.0 | 21 | 2 | AAW54281 | AAW54281 | Myc-His-t | 966 | 48 | 100.0 | 21 | 8 | ADH41323 | ADH41323 | Recombina |
| 894 | 48 | 100.0 | 21 | 2 | AAW48442 | AAW48442 | Myc-His p | 967 | 48 | 100.0 | 21 | 8 | ADJ32465 | ADJ32465 | Protocate |
| 895 | 48 | 100.0 | 21 | 2 | AAW54435 | AAW54435 | Human PS1 | 968 | 48 | 100.0 | 21 | 8 | ADK51959 | ADK51959 | Repeat pr |
| 896 | 48 | 100.0 | 21 | 2 | AAW79683 | AAW79683 | Human CSI | 969 | 48 | 100.0 | 21 | 8 | ADK51965 | ADK51965 | Repeat pr |
| 897 | 48 | 100.0 | 21 | 2 | AAW97661 | AAW97661 | Myc-His t | 970 | 48 | 100.0 | 21 | 8 | ADN17179 | ADN17179 | Myc-His t |
| 898 | 48 | 100.0 | 21 | 2 | AAV07403 | AAV07403 | Fusion pe | 971 | 48 | 100.0 | 21 | 8 | ADN28580 | ADN28580 | Myc-His p |
| 899 | 48 | 100.0 | 21 | 2 | AAV08480 | AAV08480 | Human B52 | 972 | 48 | 100.0 | 21 | 8 | ADQ96647 | ADQ96647 | Human PS1 |
| 900 | 48 | 100.0 | 21 | 2 | AAV05822 | AAV05822 | GroHEK pe | 973 | 48 | 100.0 | 21 | 8 | ADR46911 | ADR46911 | Myc-His p |

```

974 48 100.0 21 8 ADR88369 Adt88369 pE1158 ve
975 48 100.0 21 8 ADR70601 Adt70601 Histidine
976 48 100.0 21 8 ADR93231 Adt93231 Ob associ
977 48 100.0 21 9 ADV21143 Adv21143 myc-his t
978 48 100.0 21 9 ADM12411 Adm12411 Synthetic
979 48 100.0 21 9 ADM12414 Adm12414 Synthetic
980 48 100.0 21 9 ADM12413 Adm12413 Synthetic
981 48 100.0 21 9 ADM12410 Adm12410 Synthetic
982 48 100.0 21 9 ADM12412 Adm12412 Synthetic
983 48 100.0 21 9 ADM14189 Adm14189 MYC-HIS P
984 48 100.0 21 9 ADM71894 Adm71894 Myc-his t
985 48 100.0 21 9 ADM64710 Adm64710 Novel che
986 48 100.0 21 9 ADM18078 Adm18078 Peptide I
987 48 100.0 21 9 ADX85499 Adx85499 Myc-His t
988 48 100.0 21 9 ADY50197 Ady50197 Vector PE
989 48 100.0 21 9 ADY59600 Ady59600 Myc-His t
990 48 100.0 21 9 ADY74021 Ady74021 Myc-his t
991 48 100.0 21 9 ADZ46753 Adz46753 pE1158 co
992 48 100.0 21 9 ADZ69323 Adz69323 Mycobacte
993 48 100.0 21 9 ADZ67479 Adz67479 Mycobacte
994 48 100.0 21 9 AEA13722 Aea13722 Myc-His t
995 48 100.0 21 9 AEA21291 Aea21291 Nanoparti
996 48 100.0 21 9 AEB28815 Aeb28815 Viral vec
997 48 100.0 21 9 AEB18116 Aeb18116 PER405 L.
998 48 100.0 21 9 AEB55205 Aeb55205 myc-his t
999 48 100.0 21 9 AEB90810 Aeb90810 Human Bcl1
1000 48 100.0 21 9 AEB72742 Aeb72742 polh N-te

```

ALIGNMENTS

RESULT 1

AA49221
ID AAY49221 standard; peptide; 6 AA.

AC AAY49221;

DT 07-FEB-2000 (first entry)

DE Nickel ion binding domain containing 6 His residues.

XX Monoclonal antibody; Mab; 1A7; GD2; Immune response; melanoma;
KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
KW tumor-associated antigen.

XX Synthetic.

XX US5977316-A.

XX 02-NOV-1999.

XX 16-JAN-1996; 96US-00591196.

XX 17-JAN-1995; 95US-00372676.

XX (KENT) UNIV KENTUCKY.

PI Foon KA, Chatterjee SK, Chatterjee M;

XX WPI; 1996-354530/35.

PT Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)
PT - useful to treat or palliate a GD2-associated disease, e.g. melanoma and
PT glioma.

XX Example 7; Col 58; 74pp; English.

CC The invention provides a monoclonal antibody (Mab) designated 1A7, which
CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
CC humans. Mab 1A7 has defined light and heavy chain variable region
CC sequences. The Mab 1A7 and polypeptides can be used for eliciting an anti
CC -GD2 immune response. The polypeptides can also be used for detecting or

CC purifying anti-GD2 antibody. The products can be used for treating GD2 -
CC associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue
CC carcinoma, and small cell carcinoma. They can be used for palliating the
CC disease or for reducing the risk of recurrence

SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
1 HHHHHH 6

DB 1 HHHHHH 6

RESULT 2

AAW19161
ID AAW19161 standard; peptide; 6 AA.

AC AAW19161;

DT 06-AUG-1997 (first entry)

DE Isoelectric point marker peptide 18.

KW Label; fluorescent dye; isoelectric; point; pI; marker; focusing;
KW fluorescence; capillary; stable.

XX Synthetic.

XX EP744614-A2.

XX 27-NOV-1996.

XX 29-MAR-1996; 96EP-00105113.

XX 31-MAR-1995; 95JP-00076873.

XX 19-OCT-1995; 95JP-00271196.

XX (MOLE-) LAB MOLECULAR BIOPHOTONICS.

XX Shimura K, Kasai K, Matsumoto H, Takamoto H;

XX WPI; 1997-001360/01.

PT Isoelectric point markers for isoelectric focusing - comprising
PT fluorescence-labelled oligo-nucleotide(s).

XX Claim 9; Page 21; 29pp; English.

CC The present peptide, when labelled with a fluorescent dye, can be used as
CC an isoelectric point (pI) marker for isoelectric focusing with
CC fluorescence. The dye is linked to the peptide's amino-terminal through
CC an amide, thioamide, sulphonamide, urea, thiourea or urethane bond, and
CC is rhodamine, fluorescein, cyanine, indocyanine, indocarbocyanine,
CC pyronine, lucifer yellow, quinacrine, squarillium, coumarin,
CC fluoranthranil maleimide or anthracene. The marker can be used for
CC capillary isoelectric focusing, and it is possible to construct peptide
CC sets that cover a wide pI range and have good storage stability. The
CC present peptide has respective observed and calculated pI values of 7.16
CC and 7.10

SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
1 HHHHHH 6

DB 1 HHHHHH 6

```

RESULT 3
ID AAM18225 standard; peptide; 6 AA.
XX
AC AAM18225;
XX
DT 26-AUG-1997 (first entry)
XX
DE Purification tag of a TGF-beta fusion protein.
XX
KW Transforming growth factor-beta fusion protein; wound healing;
KW artificial skin; surgery recovery time.
XX
OS Synthetic.
XX
PN WO9639430-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US008973.
XX
PR 06-JUN-1995; 95US-00470837.
XX
PA (HALL/) HALL F L.
PA (NIMNI/) NIMNI M E.
PA (TUAN/) TUAN T.
PA (WU/L/) WU L.
PA (CHEU/) CHEUNG D T.
XX
PI Hall FL, Nimni ME, Tuan T, Wu L, Cheung DT;
XX
DR WPI: 1997-043065/04.
XX
N-PSDB: AAT71737.
XX
PT Prepn. of transforming growth factor-beta fusion protein - useful to
XX
PS reduce surgery recovery time and to prepare artificial skin.
XX
PS Claim 5; Page 40; 59pp; English.
XX
CC A novel transforming growth factor-beta (TGF-beta) fusion protein
CC comprises a purification tag and a TGF active fragment. The present
CC sequence represents a specifically claimed purification tag.
CC Additionally, the fusion protein may comprise proteinase-sensitive linker
CC sites and binding domain so the protein sequence may contain some or all
CC of the following elements: purification tag;proteinase site;ECM binding
CC site;proteinase site;TGF-beta. TGF-beta promotes wound healing, and the
CC fusion protein can be used to reduce surgery recovery time and in the
CC preparation of artificial skin. The inclusion of a purification tag
CC facilitates purification of the fusion protein. The proteinase site is
CC included to permit cleavage and release of the purification tag after
CC purification if desired. The extracellular matrix binding site
CC facilitates delivery of the fusion protein to the desired site of action.
CC Delivery of the TGF-beta to the site to be treated reduces the amount of
CC TGF-beta required to be administered to be effective and reduces the
CC concentration of circulating TGF-beta which may result in undesirable
CC effects
CC
XX
SQ Sequence 6 AA:
XX
Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHHHHH 6
DB 1 HHHHHH 6

```

```

AC AAM63024;
XX
DT 09-NOV-1998 (first entry)
XX
DE Hexa-histidine tag.
XX
KW Dectin-1; dendritic cell; c-type lectin; mouse; immunity; adjuvant;
KW allergy; autoimmune disease; gene therapy; vaccine; diagnosis;
KW drug screening; hexa-histidine tag.
XX
OS Synthetic.
XX
PN WO9828332-A2.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-US023761.
XX
PR 20-DEC-1996; 96US-00772440.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Arizumi K, Takashima A;
XX
DR WPI: 1998-377594/32.
XX
PT Nucleic acid encoding dendritic cell specific peptide(s) dectin-1 and -2
PT - useful, e.g. to regulate immune response, as vaccine adjuvants, for
PT diagnosis and drug screening.
XX
PS Claim 92; Page 157; 200pp; English.
XX
CC This hexa-histidine tag peptide is preferred for use in fusions with
CC murine dectin-1 (see AAM69236) or dectin-2 (see AAM69237) polypeptides of
CC the invention. The dectins are novel murine dendritic cell (DC) specific
CC members of the C-type lectin family that are essential for DC-mediated T
CC cell activation. The His-tagged polypeptides have been expressed in E.
CC coli host cells using recombinant vector pGB30, and used for production
CC of antibodies. The invention provides: dectin-1 and dectin-2 polypeptides
CC and DNA sequences, expression vectors, host cells, probes and primers,
CC antibodies, compounds that modulate dectin-mediated activation of T
CC cells, transgenic animals, and dectin ligands
CC
XX
SQ Sequence 6 AA:
XX
Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHHHHH 6
DB 1 HHHHHH 6

```

RESULT 5

```

ID AAM69961 standard; peptide; 6 AA.
XX
AC AAM69961;
XX
DT 08-OCT-1998 (first entry)
XX
DE Poly-His tag for constructing soluble huRANKL.
XX
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis; TNF; RANKL;
KW RANK ligand; tumour necrosis factor.
XX
OS Synthetic.
XX
PN WO9828426-A2.
XX
PD 02-JUL-1998.

```

```

XX 22-DEC-1997; 97WO-US0233775.
PF 23-DEC-1996; 96US-0059978P.
XX 07-MAR-1997; 97US-00813509.
PR 14-OCT-1997; 97US-0064671P.
XX (IMNV ) IMMUNEX CORP.
PA Anderson DM, Galibert LJ, Maraskovsky E;
PI WPI, 1998-377657/32.
XX New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells.
XX Example 15; Page 67; 80pp; English.
PS
XX This represents a poly-histidine tag used in the construction of a
CC soluble huRANKL (RANK ligand). RANK (receptor activator of necrosis
CC factor-kappaB (NF-kB)) is a member of the tumour necrosis factor (TNF)
CC family. A soluble RANK may be used for inhibiting activation of NF-kB, by
CC contacting a cell expressing membrane-associated RANK with a soluble RANK
CC which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK
CC and can be used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of an
CC inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF-alpha. The products can also be used for detection and drug
CC screening
XX
XX Sequence 6 AA:
SQ
Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
Db 1 HHHHHH 6
RESULT 6
AAW68297 standard; peptide; 6 AA.
XX AAW68297;
XX
XX 08-OCT-1998 (first entry)
XX
XX Poly-His tag for constructing soluble huRANKL.
XX
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis; TNF; RANKL;
KW RANK ligand; tumour necrosis factor.
XX
XX Synthetic.
XX
XX WO9828424-A2.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US023866.
XX

```

```

PR 23-DEC-1996; 96US-0059978P.
PR 07-MAR-1997; 97US-00813509.
XX 14-OCT-1997; 97US-0064671P.
XX (IMNV ) IMMUNEX CORP.
PI Anderson DM, Galibert LJ, Maraskovsky E;
XX WPI, 1998-377655/32.
XX New isolated receptor activator of necrosis factor-kappa B - useful for,
PT e.g. developing products for regulating an immune or inflammatory
PT response, treating toxic shock or sepsis.
XX Example 15; Page 67; 80pp; English.
PS
XX This represents a poly-histidine tag used in the construction of a
CC soluble huRANKL (RANK ligand). RANK (receptor activator of necrosis
CC factor-kappaB (NF-kB)) is a member of the tumour necrosis factor (TNF)
CC family. Host cells transfected or transfected with an expression vector
CC comprising the RANK encoding nucleic acid can be used to produce
CC recombinant RANK protein. The soluble RANK may be used for inhibiting
CC activation of NF-kB, by contacting a cell expressing membrane-associated
CC RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble
CC RANK polypeptide composition may also be used for regulating an immune or
CC inflammatory response. Inhibition of NF-kB by RANK antagonists may be
CC useful in ameliorating negative effects of an inflammatory response that
CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
CC graft-versus-host reactions, or acute inflammatory reactions. They can
CC also be used in adjunct therapy for disease characterised by neoplastic
CC cells that express RANK. The products can also be used for detection and
CC drug screening
XX
XX Sequence 6 AA:
SQ
Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
Db 1 HHHHHH 6
RESULT 7
AAW44011 standard; peptide; 6 AA.
XX AAW44011;
XX
XX 05-JUN-1998 (first entry)
XX
XX Poly-histidine peptide used in an epitope tagged prion protein construct.
XX
XX prion; epitope; FLAG; Strep; poly-histidine; haemagglutinin; recombinant;
KW transgenic animal; scrapie; Creutzfeldt-Jakob disease; CJD;
KW bovine spongiform encephalopathy; BSE.
XX
XX Synthetic.
XX
XX WO9746572-A1.
XX
XX 11-DEC-1997.
XX
XX 29-MAY-1997; 97WO-US009289.
XX
XX 06-JUN-1996; 96US-00660626.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Prusiner SB, Telling GC, Cohen FE, Scott MR;
PI WPI, 1998-042112/04.
XX

```

XX Nucleic acid construct encoding biologically active protein and epitope -
 PT especially epitope-tagged prion protein.
 XX
 PS Claim 4; Page 48; 62pp; English.
 CC This is the sequence of an artificial poly-histidine peptide epitope. It
 CC is used in a recombinant nucleic acid construct encoding an epitope-
 CC tagged prion protein (PrP). The construct comprises a first nucleic acid
 CC sequence encoding an amino acid sequence of a biologically active protein
 CC fragment and a second nucleic acid sequence encoding a heterologous
 CC epitope domain. The heterologous epitope domain is a peptide selected
 CC from a peptide group of FLAG, Strept, poly-histidine, human c-myc peptide
 CC recognised by monoclonal antibody 9B10 and haemagglutinin peptide
 CC recognised by monoclonal antibody 12CA5. The protein is a natural,
 CC synthetic or chimeric PrP molecule. The protein has two different three-
 CC dimensional conformations and the epitope domain is spatially positioned
 CC relative to the protein such that the epitope domain is more exposed in a
 CC first conformation relative to a second conformation. The nucleic acid
 CC construct may be used for the production of transgenic animals or cells
 CC that are useful in a method for distinguishing between different
 CC conformational shapes of a protein. These methods are particularly useful
 CC in studying diseases caused by prion proteins, e.g. Creutzfeldt-Jakob
 CC disease (CJD), scrapie and bovine spongiform encephalopathy (BSE).
 CC
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HHHHHH 6
 Db 1 HHHHHH 6
 RESULT 8
 AAE08742
 ID AAE08742 standard; peptide; 6 AA.
 XX
 AC AAE08742;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Poly-His tag, to generate soluble RANKL.
 XX
 KW Receptor activator of nuclear factor kappaB ligand; RANKL; NF;
 KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KW immune response; inflammatory response; graft-versus-host reaction;
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
 XX
 OS Synthetic.
 XX
 PN US6271349-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 17-DEC-1998; 98US-00215649.
 XX
 PR 23-DEC-1996; 96US-0059978P.
 PR 23-DEC-1996; 96US-00772330.
 PR 07-MAR-1997; 97US-0077181P.
 PR 07-MAR-1997; 97US-00813509.
 PR 14-OCT-1997; 97US-0064671P.
 PR 22-DEC-1997; 97US-00996139.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 PI Dougall WC, Galibert L;
 XX
 DR WPI, 1998-377655/32.
 XX

PT New isolated receptor activator of necrosis factor-kappa B - useful for,
 PT e.g. developing products for regulating an immune or inflammatory
 PT response, treating toxic shock or sepsis.
 XX
 PS Example 15; Col 81; 47pp; English.
 CC The patent discloses novel receptor activator of nuclear factor (NF)-
 CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member of
 CC the tumour necrosis factor (TNF) receptor superfamily and associates with
 CC TNF receptor associated factor (TRAF) 2 and 3 which are important in the
 CC regulation of immune and inflammatory response. The receptors are useful
 CC for regulating immune response and in screening for inhibitors of these
 CC receptors. The cytoplasmic domain of RANK is used in developing assays
 CC for inhibitors of signal transduction, e.g. for screening the molecules
 CC that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3, TRAF5 and
 CC particularly TRAF6. NF-kappaB inhibition by RANK antagonists are useful
 CC in ameliorating the negative effects of an inflammatory response that
 CC result from triggering of RANK, e.g. in treating toxic shock or sepsis,
 CC graft-versus-host reactions, acute inflammatory reactions and the effects
 CC of bone resorption. RANK acts as an anti-apoptotic signal and rescue the
 CC cells that express RANK from apoptosis. Soluble forms of the receptor are
 CC used in vivo or in vitro based screening tests for agonists or
 CC antagonists of RANK activity, as antagonists of RANK-mediated NF-kappa B
 CC activation, or to inhibit transduction of a signal via RANK.
 CC Compositions are used in the development of both agonistic and
 CC antagonistic antibodies, or as an adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. Compounds that
 CC interfere with RANK/TRAF6 interactions are useful for modulating the
 CC formation of osteoclasts from osteoclast precursors and for modulating
 CC osteoclast function and activities. They are used as inhibitors of
 CC diseases associated with excess bone resorption and as immunosuppressants
 CC or anti-inflammatory agents. The RANK DNAs are useful for the expression
 CC of recombinant proteins, as probes for analysis of the presence or
 CC distribution of RANK transcripts, while the proteins are useful in
 CC preparing kits for the detection of soluble RANK, or monitor RANK-related
 CC activity. The present sequence is a poly-His tag which is used in the
 CC exemplification of the invention to generate a soluble, tagged, poly-His
 CC version of human and murine RANKL.
 CC
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HHHHHH 6
 Db 1 HHHHHH 6
 RESULT 9
 ADV42333
 ID ADV42333 standard; peptide; 6 AA.
 XX
 AC ADV42333;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Hexahistidine tag used to facilitate D(II) FGFR1 purification.
 XX
 KW Protein stabilization; protein renaturation; drug screening;
 KW high throughput screening; protein purification; protein folding.
 XX
 OS Synthetic.
 XX
 PN WO9742500-A1.
 XX
 PD 13-NOV-1997.
 XX
 PF 09-MAY-1997; 97WO-US008154.
 XX
 PR 09-MAY-1996; 96US-0017860P.
 XX

PA (THRE-) 3-DIMENSIONAL PHARM INC.
 XX Pantoliano MW, Rhind AW, Salemm FR, Springer BA, Bone RF;
 PI Petrella EC;
 XX WPI; 1998-008452/01.
 DR
 XX Ranking efficiency of molecules and conditions for stabilizing target
 PT molecule - from their effect on thermal denaturation curves, particularly
 PT for identifying agents that favour refolding or crystallisation of
 PT proteins and for assessing affinity for target receptors.
 XX
 PS Example 19; Fig 27; 176pp; English.
 XX
 CC The invention relates to a multi-variable method for ranking the
 CC efficiency of different molecules (e.g., a protein or nucleic acid) which can
 CC stabilizing a target molecule (e.g., a protein or nucleic acid) which can
 CC be denatured by heat. The method comprises: (a) treating a target
 CC molecule, in separate containers, with various different molecules or
 CC biochemical conditions; (b) heating the containers simultaneously and
 CC measuring a physical change associated with denaturation of the target
 CC molecule; (c) generating a thermal denaturation curve for each container;
 CC (d) comparing these curves with each other and with a reference curve
 CC obtained under specified conditions; and (e) ranking efficiency according
 CC to changes in each curve. The invention also relates to a device
 CC comprising many containers in a carrier, each container containing a
 CC different candidate stabilisation molecule plus one molecule from a
 CC combinatorial library; and apparatus that can simultaneously heat many
 CC samples (particularly according to a predetermined temperature profile)
 CC and receive spectral emissions from the samples. The method of the
 CC invention can additionally be adapted to assess molecules and conditions
 CC that facilitate refolding of a denatured protein or crystallization of a
 CC protein; to rank affinity of a molecule for a particular target molecule;
 CC and to rank different molecules or biochemical conditions for optimal
 CC shelf life of proteins. The method of the invention may be specifically
 CC applied to proteins and nucleic acids, particularly where they are
 CC members of combinatorial libraries. In particular, the method can be used
 CC to identify optimum conditions for renaturing recombinantly produced
 CC proteins present in inclusion bodies, or to identify lead compounds from
 CC their high affinity for a selected receptor. The simultaneous heating of
 CC many samples ensures rapid, high throughput screening and the method
 CC provides quantitative information. It can measure binding affinities in
 CC the range 0.1 nM to 0.001 pM in a single well, does not require
 CC radioactive labels, is applicable to any receptor that is a drug target,
 CC and requires only very small (e.g., 5-40 pmole) samples. The new
 CC apparatus provides both heat control and spectral measurements,
 CC eliminating the need for transfers between instruments. The present
 CC sequence represents a hexahistidine tag present in the N-terminus of a
 CC recombinantly produced D(II) domain of fibroblast growth factor receptor
 CC 1 (FGFR1) and used to facilitate purification. The D(II) FGFR1 protein
 CC was used to screen biochemical conditions that facilitate protein folding
 CC in an example of the invention.
 CC
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 DB 1 HHHHHH 6
 RESULT 10
 AAY06469
 ID AAY06469 standard; peptide; 6 AA.
 XX
 AC AAY06469;
 XX
 XX 27-SEP-1999 (first entry)
 DT
 XX Epitope tag.
 DE

XX
 XX Epitope tag; antibody engineering; yeast; surface display;
 KW protein library; peptide library.
 XX
 OS Synthetic.
 XX
 PN WO9336569-A1.
 XX
 XX 22-JUL-1999.
 PD
 XX
 PF 20-JAN-1999; 99WO-US001188.
 XX
 XX 20-JAN-1998; 98US-00009388.
 PR 26-AUG-1998; 98US-00140084.
 XX
 PA (UNIT) UNITV ILLINOIS FOUND.
 XX
 PI Wittrup KD, Kieke MC, Kranz DM, Shuster E, Boder ET;
 XX WPI; 1999-430619/36.
 DR
 XX
 PS This peptide comprises an epitope tag that can be used in methods of the
 PS invention. The invention discloses a powerful new system for engineering
 PS antibody affinity and specificity, by constructing a microbial analogue
 PS of the mammalian system's B cell repertoire. Antibodies are displayed on
 PS the surface of yeast cells by genetic fusion with yeast cell wall
 PS proteins, especially agglutinin proteins. After mutation, variants are
 PS selected on the basis of improved binding characteristics with
 PS fluorescently labeled targets. The selection method also identifies
 PS proteins with enhanced phenotypic characteristics, proteins that are
 PS displayed at higher levels, proteins that are secreted at higher
 PS efficiency and proteins of improved stability
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 DB 1 HHHHHH 6
 RESULT 11
 AAW84203
 ID AAW84203 standard; peptide; 6 AA.
 XX
 AC AAW84203;
 XX
 XX 25-MAR-1999 (first entry)
 DT
 DE Peptide comprising a purification tag.
 XX
 XX Proteinase site; bone morphogenetic fusion protein; bone binding site;
 KW bone morphogenetic protein; transforming growth factor beta;
 KW active fragment; wound healing; bone growth; purification tag.
 XX
 OS Synthetic.
 XX
 PN WO9855137-A1.
 XX
 XX 10-DEC-1998.
 PD
 XX 02-JUN-1998; 98WO-US011189.
 PF
 XX 03-JUN-1997; 97US-00868452.
 PR
 XX

PA (NIMN/) NIMNI M E.
 PA (HALL/) HALL F L.
 PA (WILL/) WU L.
 PA (HAMB/) HAN B.
 PA (SHOR/) SHORS E C.
 PI Nimi ME, Hall FL, Wu L, Han B, Shors EC;
 DR WPI, 1999-059875/05.
 DR N-PSDB: AAV99371.
 XX
 PT New bone morphogenetic fusion proteins - comprising a purification tag
 PT and a bone morphogenetic active fragment, used for enhancing wound
 PT healing or bone growth.
 XX
 PS Claim 5; Page 38; 64pp; English.
 CC The present sequence represents a peptide comprising a purification tag
 CC that was used in the creation of the bone morphogenetic fusion proteins
 CC of the invention. The bone morphogenetic fusion protein may contain some
 CC or all of the following elements: a purification tag, a proteinase site,
 CC an ECM/bone binding site, a second proteinase site, and a bone
 CC morphogenetic protein active fragment. The fusion proteins of the
 CC invention also includes proteins that have transforming growth factor
 CC beta active fragments instead of bone morphogenetic protein active
 CC fragments. The bone morphogenetic fusion proteins can be used for
 CC enhancing wound healing or bone growth
 CC
 SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 1 HHHHHH 6

RESULT 12
 AAY17447
 ID AAY17447 standard; peptide; 6 AA.
 XX
 AC AAY17447;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Major outer membrane protein amino terminal peptide #5.
 XX
 KW Major outer membrane protein; MOMP; Chlamydia trachomatis; antibody;
 KW antigen.
 XX
 OS Synthetic.
 XX
 PN JP1123078-A.
 XX
 PD 11-MAY-1999.
 XX
 PF 22-OCT-1997; 97JP-00289938.
 XX
 PR 22-OCT-1997; 97JP-00289938.
 XX
 PA (ELED) DENKI KAGAKU KOGYO KK.
 XX
 DR WPI, 1999-340514/29.
 XX
 PT New major outer membrane protein of Chlamydia trachomatis - useful for
 PT determination of Chlamydia trachomatis antibody.
 XX
 PS Claim 2; Page 7; 11pp; Japanese.
 CC The present invention describes a major outer membrane protein (MOMP) of
 CC Chlamydia trachomatis in which six amino acid residues are peptide-bound

CC to the amino terminal and which has immunological activity. Also
 CC described are: (1) a method for the preparation of MOMP of Chlamydia
 CC trachomatis in which the gene of the above MOMP of Chlamydia trachomatis
 CC is inserted to an expression vector used to transform E. coli, the
 CC transformant is cultured under conditions where the MOMP of Chlamydia
 CC trachomatis is expressed and the expression product is collected from the
 CC transformant; (2) a method for the determination of the antibody of MOMP
 CC of Chlamydia trachomatis using the above MOMP of Chlamydia trachomatis as
 CC the antigen; and (3) a reagent for the determination of the antibody of
 CC MOMP of Chlamydia trachomatis using the above major MOMP of Chlamydia
 CC trachomatis as the antigen. The method can provide an antigen used for
 CC the determination of Chlamydia trachomatis antibody
 CC
 SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. NO. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 1 HHHHHH 6

RESULT 13
 AAY09544
 ID AAY09544 standard; peptide; 6 AA.
 XX
 AC AAY09544;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE Human TAK1 6xHis peptide.
 XX
 KM Human; TAB1; TAK1; screening; inhibition; TGF-beta;
 KM transforming growth factor beta.
 XX
 OS Homo sapiens.
 XX
 PN WO9921010-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 22-OCT-1998; 98WO-JP004796.
 XX
 PR 22-OCT-1997; 97JP-00290188.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ono K, Ohtomo T, Tsuchiya M;
 XX
 DR WPI, 1999-312645/26.
 XX
 PT Screening for TGF- beta inhibitory substances, which are useful as drugs
 PT for treatment of diseases relating to its disorder.
 XX
 PS Example 1; Page 58; 195pp; Japanese.

CC A method has been developed for screening for substances which inhibit
 CC the binding of TAK1 polypeptide to TAB1 polypeptide. The method
 CC comprises: (a) contacting the polypeptide in the presence of a sample;
 CC and (b) detecting the amount of bound polypeptide, in which the sample
 CC can be pre-mixed with TAK1 or TAB1 polypeptide first. The transforming
 CC growth factor (TGF)-beta inhibitory substances can be used in drugs for
 CC indications e.g. as TGF-beta signal transduction inhibitors or
 CC activators, or extracellular matrix protein production enhancement
 CC inhibitors or activators, or cell proliferation prevention inhibitors or
 CC activators, or monocyte migration inhibitors or activators, or
 CC physiological activity induction inhibitors or activators, or
 CC immunosuppression inhibitors or activators, or amyloid beta protein
 CC precipitation inhibitors or activators, and such substances can also be
 CC inhibitors of the TAK1 polypeptide function, particularly kinase
 CC activity. The present sequence represents a peptide from an example of

CC the present invention
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
1 HHHHHH 6

RESULT 14
AA33592
ID AAY33592 standard; protein; 6 AA.

AC AAY33592;

DT 20-DEC-1999 (first entry)

DE VH-VL domain linker peptide #4.

XX Antigen binding; single chain; variable domain; VH domain; light chain;
XX heavy immunoglobulin chain; VL domain; anticancer; antiviral; tumor;
XX antibacterial; antimetastatic; antiinflammatory; treatment; prevention;
XX diagnosis; vaccine; autoimmune disease; inflammation; blood disorder;
XX transplant rejection; arthritis; nervous system disorder; infection.

OS Synthetic.

PN DE19816141-A1.

PD 14-OCT-1999.

PP 09-APR-1998; 98DE-01016141.

PR 09-APR-1998; 98DE-01016141.

PA (HMKI) HOECHST MARION ROUSSEL DEUT GMBH.

PI Kontermann R, Sedlacek H, Mueller R;

DR WPI; 1999-581511/50.

XX New polypeptide binding agents containing variable heavy and light
XX constructs connected via peptide linker, used for treatment, prevention
XX or diagnosis of e.g. cancer.

PS Example 1; Page 15; 20pp; German.

XX This sequence represents a novel single-chain molecule (I) that binds
XX multiple antigens and comprises two variable domains of heavy
XX immunoglobulin chains (VH), having specificities A and B and two variable
XX domains of light chains (VL), also with specificities A and B. The
XX domains are provided as two VH-VL constructs which are attached via a
XX peptide (P). Any VH and VL may be replaced by their functional fragments.
XX The products of the invention have anticancer, antiviral, antibacterial,
XX antimetastatic and antiinflammatory activity. (I) are used to treat,
XX prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases
XX and inflammation (e.g. transplant rejection and arthritis), blood
XX disorders (e.g. of the coagulation and/or circulatory systems, such as
XX anemia, leucopenia, thrombocytopenia and hypertension), nervous system
XX disorders and/or infections (by viruses or bacteria, or malaria),
XX including, when (I) include a fusogenic peptide, use for gene transfer.
XX (I) are produced simply and in predominantly homogeneous form, in a wide
XX variety of hosts, either in secreted or membrane-bound forms. This
XX sequence represents a VH-VL domain linker peptide which is used to
XX illustrate the method of the invention

SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
1 HHHHHH 6

RESULT 15
AAE1561
ID AAE1561 standard; peptide; 6 AA.

AC AAE1561;

DT 09-APR-2002 (first entry)

DE Epitope tag #5 fused to yeast cell wall protein AGA2.

XX Yeast cell wall protein; AGA2; T cell receptor; multiple sclerosis;
XX cancer; sepsis; autoimmune disease; arthritis; diabetes.

OS Synthetic.

PN US6331391-B1.

PD 18-DEC-2001.

PP 20-JAN-1998; 98US-00009388.

PR 31-MAY-1996; 96US-0018741P.

PR 30-MAY-1997; 97US-00866398.

PA (UNII) UNIV ILLINOIS FOUND.

PI Wiettrup KD, Kranz DM, Kleke M, Boder ET;

DR WPI; 1999-430619/36.

XX Selecting proteins with enhanced phenotypic properties than wild-type
XX proteins, is useful for highly specific cancer diagnosis and therapy.
XX
XX Claim 40; Col 60; 59pp; English.

XX The present invention relates to a method for selecting proteins for
XX displayability on a yeast cell surface. The method comprises transforming
XX yeast cells with a vector that expresses a test protein fused to a yeast
XX cell wall protein (AGA2), contacting the cells with a label that binds to
XX proteins displayed on the cell wall, and isolating label-bound cells,
XX where the test protein is from a variegated population generated by
XX mutagenesis. The invention is also directed to new processes for
XX engineering T cell receptor for improved binding properties. Improved T
XX cell receptor molecules are useful in therapies for cancer, sepsis,
XX autoimmune diseases such as arthritis, diabetes or multiple sclerosis.
XX The methods are useful to select proteins with altered affinity, altered
XX specificity or conditional binding. The present sequence is an epitope
XX tag fused between protein of interest and yeast cell wall protein AGA2

SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
1 HHHHHH 6

RESULT 16
AAY50711
ID AAY50711 standard; peptide; 6 AA.

AC AAY50711;

XX 20-MAR-2003 (revised)
 DT 08-FEB-2000 (first entry)
 XX
 DE Single chain antibody construct polyhistidine tag.
 XX
 KW Immunoglobulin; light chain; VL region; heavy chain; VH region;
 KW single-chain; antigen binding; variable domain; anticancer; treatment;
 KW antiviral; antibacterial; antimalarial; antiinflammatory; diagnosis;
 KW tumor vaccine; autoimmune disease; inflammation; blood disorder;
 KW nervous system; infection.
 XX
 OS Unidentified.
 XX
 PN DE19827239-A1.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1998; 98DE-01027239.
 XX
 PR 09-APR-1998; 98DE-01016141.
 PR 18-JUN-1998; 98DE-01027239.
 XX
 PA (HMRI) HOECHST MARION ROUSSEL DEUT GMBH.
 XX
 PI Kontermann R, Sedlacek H, Mueller R;
 XX
 DR WPI; 1999-591691/51.
 XX
 PT New polyspecific binding agents useful for treatment, prevention and
 PT diagnosis of cancer and autoimmune diseases comprises variable domains of
 PT heavy and light chains of immunoglobulins bound by a peptide.
 XX
 PS Example 1; Page 17; 26pp; German.
 XX
 CC This invention describes a novel single-chain molecule (I) that binds
 CC multiple antigens and comprises two variable domains of heavy
 CC immunoglobulin chains (VH) and two variable domains of light chains (VL).
 CC The domains are provided as two VH-VL constructs which are attached via a
 CC peptide (P). Any VH and VL may be replaced by their functional fragments.
 CC The products of the invention have anticancer, antiviral, antibacterial,
 CC antimalarial, and antiinflammatory activity. (I) are used to treat,
 CC prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases
 CC and inflammation (e.g. transplant rejection and arthritis), blood
 CC disorders (e.g. of the coagulation and/or circulatory systems, such as
 CC anemia, leucopenia, thrombocytopenia and hyperension), nervous system
 CC disorders and/or infections (by viruses or bacteria, or malaria),
 CC including, when (I) include a fusogenic peptide, use for gene transfer.
 CC This sequence represents a polyhistidine tag which is used in the
 CC construction of the single chain construct described in the invention.
 CC NOTE: This specification is a treat as basic for C2-9901215 in Derwent
 CC week 9951. (Updated on 20-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 6 AA;
 XX
 Query Match 100.0%; Score 48; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 |||||
 DB 1 HHHHHH 6
 RESULT 17
 AAY78351
 ID AAY78351 standard; peptide; 6 AA.
 XX
 AC AAY78351;
 XX
 DT 05-MAY-2000 (first entry)
 XX
 DE His-6 peptide SEQ ID NO:2.

XX Caspase; protein array; screening; biomolecular activity; proteomic;
 KW drug development; biosensor; diagnosis.
 KW
 OS Synthetic.
 XX
 PN WO200004382-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 14-JUL-1999; 99WO-US015971.
 XX
 PR 14-JUL-1998; 98US-00115455.
 XX
 PA (ZYOM-) ZYOMTX INC.
 XX
 PI Wagner P, Ault-Riche D, Nock S, Itin C;
 XX
 DR WPI; 2000-171289/15.
 XX
 PT New arrays for analyzing components of a fluid sample, useful for drug
 PT development, functional proteomics, clinical diagnostics and biosensors.
 XX
 PS Example 9; Page 58; 81pp; English.
 XX
 CC The present invention describes an array (I) of proteins comprising a
 CC substrate, at least one organic thinfilm on some or all of the substrate
 CC surface, and patches arranged in discrete, known regions on portions of
 CC the substrate surface covered by organic thinfilm. Each of the patches
 CC comprises a protein immobilised on the underlying organic thinfilm. The
 CC arrays can be used for screening proteins for their ability to interact
 CC with a component of a sample. They can also be used for assaying for
 CC protein-protein binding interactions or analyses. They can be used for
 CC drug development, proteomics, clinical diagnostics and biosensors. The
 CC present sequence represents a peptide used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 6 AA;
 XX
 Query Match 100.0%; Score 48; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 |||||
 DB 1 HHHHHH 6
 RESULT 18
 AAY99641
 ID AAY99641 standard; peptide; 6 AA.
 XX
 AC AAY99641;
 XX
 DT 27-OCT-2000 (first entry)
 XX
 DE His6 tag used to create pDANS D1.3 phagemid.
 KW His6 tag; gene library production.
 KW
 OS Synthetic.
 XX
 PN WO200031246-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 18-NOV-1999; 99WO-EP008856.
 XX
 PR 19-NOV-1998; 98IT-MI002509.
 XX
 PA (SISS-) SISSA SCUOLA INT SUPERIORE DI STUDI AVAN.
 XX
 PI Bradbury ARM, Sblattero D;

```

XX WPI; 2000-400060/34.
XX
XX
XX Preparation of highly diverse nucleic acid and polypeptide libraries
XX useful for the derivation of polypeptides with useful characteristics.
XX
XX Example 2; Page 75; 76pp; English.
XX
XX The present sequence is a His6 tag. It was used in the creation of a
XX phagemid which, when transfected into a bacterial cell, was able to
XX recombine with similar phagemids. This is useful for producing DNA
XX libraries, as previous libraries have contained sequences which it is not
XX possible to recombine further, they contained many contaminating
XX sequences, and did not allow recombination between plasmids. This library
XX overcomes these problems and allows the creation of large and highly
XX diverse libraries
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
   1 HHHHHH 6
Db
RESULT 19
ABB08438
ID ABB08438 standard; peptide; 6 AA.
XX
XX ABB08438;
AC
XX
XX 07-MAY-2002 (first entry)
DT
XX
XX Histidine tag relative to the farnesyltransferase of the invention.
DE
XX
XX Farnesyltransferase; enzyme.
KM
XX
XX Unidentified.
OS
XX
XX KR98075770-A.
PN
XX
XX 16-NOV-1998.
PD
XX
XX 01-APR-1997; 97KR-00012067.
PF
XX
XX 01-APR-1997; 97KR-00012067.
PR
XX
XX 01-APR-1997; 97KR-00012067.
PA
XX
XX (GLDS ) LG CHEM LTD.
PI
XX
XX Moon GD, Kim MJ, Chung HH;
XX
XX WPI; 2000-020309/02.
DR
XX
XX N-PSDB; ABA98900.
DR
XX
XX Farnesyltransferase having histidine tag and process for preparing the
XX same.
PT
XX
XX Disclosure; Page 23; 23pp; Korean.
PS
XX
XX The invention relates to a farnesyltransferase with a histidine tag, and
XX method for preparing it. The current sequence represents a histidine tag
XX relative to the farnesyltransferase of the invention
CC
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
   1 HHHHHH 6
Db

```

```

Db
   |||||
   1 HHHHHH 6
XX
XX
XX RESULT 20
XX AAY78346
XX ID AAY78346 standard; peptide; 6 AA.
XX
XX AAY78346;
AC
XX
XX 05-MAY-2000 (first entry)
DT
XX
XX His-6 peptide SEQ ID NO:2.
DE
XX
XX Immunoglobulin; protein capture; detection; antibody; proteomic;
XX drug screening; diagnosis.
KM
XX
XX Synthetic.
OS
XX
XX WO200004389-A2.
PN
XX
XX 27-JAN-2000.
PD
XX
XX 14-JUL-1999; 99WO-US015968.
PF
XX
XX 14-JUL-1998; 98US-00115455.
PR
XX
XX (ZYOM-) ZYOMYX INC.
PA
XX
XX Wagner P, Nock S, Ault-Riche D, Itin C;
PI
XX
XX WPI; 2000-161175/14.
DR
XX
XX New arrays for assaying proteins, used for analysis of cell expression
XX products, evaluating disease conditions, proteomics, drug screening,
XX diagnostics and measurement of gene activity.
PT
XX
XX Example 6; Page 68; 90pp; English.
PS
XX
XX The present invention describes an array of protein-capture agents (PCA),
XX comprising a substrate, at least one organic thinfilm covering some or
XX all of the surface of the substrate, and patches arranged in discrete,
XX known regions on the portions of the substrate surface covered by organic
XX thinfilm. Each patch comprises PCAs, capable of binding a particular
XX expression product, or a fragment of a cell population, immobilised on
XX the organic thinfilm. The array comprises different PCAs, capable of
XX binding different expression products, or fragments, of the cell
XX population. The arrays can be used for assaying for expression products
XX or fragments of a cell or population of cells. They can be used for
XX evaluating a disease condition in a tissue of an organism. They can be
XX used in proteomics, drug screening, diagnostics, and the measurement of
XX gene activity at the protein level in cells. The present sequence
XX represents a peptide used in an example from the present invention
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
   1 HHHHHH 6
Db
XX
XX
XX RESULT 21
XX AAY77706
XX ID AAY77706 standard; peptide; 6 AA.
XX
XX AAY77706;
AC
XX
XX 12-MAY-2000 (first entry)
DT
XX

```

DE 6-His peptide epitope.
 XX Cell surface receptor; luminescence; protein internalization;
 KM drug discovery; screening assay; epitope.
 XX Synthetic.
 OS
 PN WO200003246-A2.
 XX
 PD 20-JAN-2000.
 XX
 PF 13-JUL-1999; 99WO-US015870.
 XX
 PR 13-JUL-1998; 98US-0092671P.
 XX
 PA (CELL-) CELLOMICS INC.
 XX
 PI Rubin RA, Giuliano KA, Gough A, Dunlay T;
 XX
 DR WPI; 2000-171170/15.
 PT Automated screening method for identifying compounds which induce cell
 PT surface receptor internalization, useful for drug discovery.
 XX
 PS Example 6; Page 67; 148pp; English.
 XX
 CC The invention relates to a method for identifying compounds which inhibit
 CC internalization of cell surface receptors. Provided are an array of
 CC locations, each containing cells with a cell surface receptor protein,
 CC that are treated with a test compound. The protein is luminescently
 CC labeled or contacted with a luminescently labeled cell before or after
 CC test compound treatment. Any luminescence produced is converted into
 CC digital data and automatically analysed to determine if the test compound
 CC induced the protein internalization. The novel method is used to screen
 CC for compounds which modulate cell surface receptor protein
 CC internalization, this can be used in drug discovery, to test compound
 CC efficacy in living biological systems. The assay method is automated and
 CC compact. It has high throughput and uses smaller volumes of reagents and
 CC test compounds. Sequences AAY7704-718 represent examples of peptide
 CC epitope tags used in the course of the invention
 CC
 SQ Sequence 6 AA;
 XX
 QY 1 HHHHHH 6
 DB 1 HHHHHH 6
 XX
 RESULT 22
 AAY96951
 ID AAY96951 standard; peptide; 6 AA.
 XX
 AC AAY96951;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Polylactidone tag for use in rubredoxin fusion protein.
 XX
 KM PRUBEX3; polylactidone; tag; rubredoxin; antigen; vaccine; carrier;
 KM immunogenic; flag tag; fusion.
 XX
 OS Synthetic.
 PN WO2000039310-A1.
 XX
 PD 06-JUL-2000.
 XX
 PF 29-DEC-1999; 99WO-US031176.
 XX

PR 29-DEC-1999; 98US-00114034.
 XX
 XX (UYGE-) UNIV GEORGIA RES FOUND INC.
 PA
 PI Przybyla A, Menon N;
 XX
 DR WPI; 2000-452403/39.
 XX
 PT Nucleic acids encoding fusion peptides comprising rubredoxin, useful as
 PT vaccines.
 XX
 PS Claim 16; Page 61; 67pp; English.
 XX
 CC Fusion proteins comprising rubredoxin and fused antigens and/or haptens
 CC may be used as vaccines to initiate immune responses. In this case, the
 CC rubredoxin acts as a carrier. The fusion protein is capable of binding
 CC iron (Fe-2+) when properly folded, giving it a red color that makes it
 CC easy to identify following or during purification. The C-terminal fused
 CC protein may be insoluble or known to form inclusion bodies in a host
 CC cell. The rubredoxin serves as the carrier molecule to yield immunogenic
 CC fusion products. As rubredoxin is itself only negligibly antigenic, there
 CC is no need to include a cleavage site in the fusion product to allow
 CC cleavage of the N-terminal and C-terminal constituents
 CC
 SQ Sequence 6 AA;
 XX
 QY 1 HHHHHH 6
 DB 1 HHHHHH 6
 XX
 RESULT 23
 AAB10788
 ID AAB10788 standard; peptide; 6 AA.
 XX
 AC AAB10788;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE B. subtilis lumazine synthase protein fragment #15.
 XX
 KM Lumazine synthase; capsid; cytosolic; antiviral; antibacterial; vaccine;
 KM gene therapy; immunotherapy; biosensor; diagnosis.
 XX
 OS Bacillus subtilis.
 PN WO2000053229-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 03-MAR-2000; 2000WO-EP001899.
 XX
 PR 08-MAR-1999; 99DE-01010102.
 XX
 PA (FISC/) FISCHER M.
 PA (BACH/) BACHER A.
 XX
 PI Fischer M, Bacher A;
 XX
 DR WPI; 2000-572230/53.
 XX
 PT Protein conjugate based on lumazine synthase as carrier, useful e.g. for
 PT vaccination and immunotherapy, contains many functional molecules
 PT attached to outside of the carrier.
 XX
 PS Claim 43b; Page 100; 180pp; German.
 XX
 CC This invention describes a novel protein conjugate (1) comprising at
 CC least 1 functional region (FR) at any position in the sequence of a

CC carrier protein (II) to form a capsid three-dimensional structure of the
 CC lumazine synthase (LS) type, such that the outer periphery is covalently
 CC linked to many FR. The invention also describes (1) a hetero-oligomeric
 CC protein conjugate (Ia) comprising either a mixture of at least 2
 CC different (I) or of at least 1 (I) and at least 1 (II) that lacks FR,
 CC with the components optionally covalently linked by chemical treatment;
 CC (2) a method for preparation of (I) and (Ia); (3) a vector for
 CC preparation of (I); (4) a DNA (II) that encodes (I); (5) LS from
 CC *Bacillus subtilis* with Cys 93 and/or Cys139 replaced by Ser; (6) DNA
 CC (IIa) encoding LS from *Aquifex aeolicus* which is codon-optimized for
 CC expression in a recombinant *Escherichia coli* strain; (7) a chimeric
 CC protein (CP) comprising amino acids (aa) 1-60 from LS of *B. subtilis* and
 CC aa 61-154 from LS of *A. aeolicus* for use as (II); and (8) pharmaceutical
 CC compositions and vaccines containing (I) and (Ia). The products of the
 CC invention have cytotoxic, antiviral and antibacterial activity and can
 CC be used in a vaccine or for gene therapy. (I) are used as pharmaceuticals
 CC (e.g. for immunotherapy of human immune deficiency virus infection or
 CC tumors) and in vaccines, including multivalent vaccines, against
 CC bacterial or viral infections, to produce diagnostic or therapeutic
 CC antibodies, for selective detection, purification and characterization of
 CC antibodies, and for preparation of protein libraries. (I) may also be
 CC used as biosensors and for diagnosis, e.g. of tumors. Genes that encode
 CC (I) are useful in DNA vaccines and for preparation of plant-based oral
 CC vaccines. (I) can contain many FR (same or different) at the surface of a
 CC spherical particle (LS comprises 60 subunits that assemble into an
 CC icosahedron). The large number of FR may increase sensitivity in
 CC immunoassays and the efficiency of immunotherapy agents

XX Sequence 6 AA:
 SQ

Query Match 100.0%; Score 48; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHHHHH 6
 1 HHHHHH 6

Db

RESULT 24
 AAB59857
 ID AAB59857 standard; peptide; 6 AA.

XX AAB59857;

XX 30-MAR-2001 (first entry)

XX 6-His peptide epitope.

XX 6-His peptide epitope; macromolecule trafficking; endosomal system;

KW membrane receptor internalisation.

XX Unidentified.

XX WO200079241-A2.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-US040260.

XX 21-JUN-1999; 99US-0140143P.

XX 12-JUL-1999; 99US-00352171.

XX 11-AUG-1999; 99US-0148360P.

XX 13-DEC-1999; 99US-0170313P.

XX (CELL-) CELLONICS INC.

XX Rubin RA, Gough AH, Ghosh RN, Giuliano KA, Dunlay RT;

XX WPI; 2001-091619/10.

XX Identifying compounds modulating macromolecule trafficking through
 PT endosomes, using digital data obtained by converting a luminescent signal

PT from cells contacted with the compound.
 XX
 XX Example 6; Page 53; 113pp; English.

CC The present invention relates to an automated method for identifying
 CC compounds that induce or inhibit macromolecule trafficking through an
 CC endosomal system. The method comprises treating cells which possess a
 CC luminescently-tagged macromolecule, with a test compound, and obtaining
 CC luminescent signals from the cells. The signal is converted into digital
 CC data that is used to determine if the test compound has induced or
 CC inhibited the trafficking. The method can also be used to identify the
 CC extent of internalisation of membrane receptors, by fusing a labelled
 CC peptide epitope to the different domains of the receptor e.g. the
 CC extracellular domain and intracellular domain. The present invention is
 CC on such peptide epitope used in the method of the present invention

XX Sequence 6 AA:
 SQ

Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHHHHH 6
 1 HHHHHH 6

Db

RESULT 25
 AAE12713
 ID AAE12713 standard; peptide; 6 AA.

XX AAE12713;

XX 04-JAN-2002 (first entry)

XX HexHis tag used to construct human blyPH1-IL-2 fusion protein.

XX Tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer; breast;

KW ovary; lung; bladder; cytostatic; therapy; PH1 antibody.

XX Synthetic.

XX WO200175110-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US010589.

XX 30-MAR-2000; 2000US-00538913.

XX (DYAX-) DYAX CORP.

XX Hoogenboom HRJM, Henderikx MPG;

XX WPI; 2001-626437/72.

XX N-PSDB; AAD20743.

XX Novel isolated tumour-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1.
 XX Example 1; Page 36; 126pp; English.

CC The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region, or a
 CC complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film. MUC1-
 CC specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is a polypeptide (hexahis) tag
CC used for constructing human bIVPH1-IL-2 fusion protein which is an
CC immunocytokine MUC1-specific binding member
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
|||||
DB 1 HHHHHH 6

RESULT 26

ID AAE13079 standard; peptide; 6 AA.

XX AAE13079;

DT 28-JAN-2002 (first entry)

DE Epitope tag #7 used in yeast cell surface display of proteins.

KW Phenotypic property; yeast; cell wall protein; epitope tag.

OS Unidentified.

PN USG300065-B1.

PD 09-OCT-2001.

PP 26-AUG-1998; 98US-00140084.

PR 31-MAY-1996; 96US-0018741P.

PR 30-MAY-1997; 97US-00866398.

PR 20-JAN-1998; 98US-00009388.

PA (UNIT1) UNIT1 ILLINOIS FOUNO.

PI Kieke MC, Wiltrop KD, Boder ET, Kranz DM, Shusta E;

DR WPI; 2001-656236/75.

XX Selecting proteins, e.g. antibodies, with enhanced phenotypic properties

PT relative to those of a wild-type comprises transforming yeast cells with

PT a vector expressing a protein to be tested fused to a yeast cell wall

PS protein.

PS Disclosure; Col 5; 64pp; English.

XX The present invention relates to a method for selecting proteins with

CC enhanced phenotypic properties relative to those of a wild-type,

CC comprises transforming yeast cells with a vector expressing a protein to

CC be tested fused to a yeast cell wall protein. The method is particularly

CC useful for selecting antibodies for improved affinity and specificity.

CC The present sequence is an epitope tag which is used in yeast cell

CC surface display of proteins

SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
|||||

DB 1 HHHHHH 6

RESULT 27

ID AAB35439 standard; peptide; 6 AA.

XX AAB35439;

DT 23-MAY-2001 (first entry)

DE Nascent protein detection method related peptide #1.

KW Nascent protein detection; protein analysis; aminoacylated tRNA;

KW BODIPY marker; disease diagnosis.

OS Unidentified.

PN WO200114578-A1.

PD 01-MAR-2001.

PP 23-AUG-2000; 2000WO-US023233.

PR 25-AUG-1999; 99US-00382736.

PR 25-AUG-1999; 99US-00382950.

PA (AMBE-) AMBERGEN INC.

PI Rochschild KJ, Gite S, Olejnik J;

DR WPI; 2001-168972/17.

PT Method for detecting nascent proteins by fluorescence comprises

PT misaminoacylating a tRNA molecule with a marker compound, useful for

PT detecting mutations in proteins, e.g. cancer.

PS Example 22; Page 153; 204pp; English.

CC The present invention describes a method of detecting nascent proteins

CC involving aminoacylating a tRNA molecule with a 4,4-difluoro-4-bora-3a,4a

CC -diaz-a-s-indacene (BODIPY) marker leading to the production of a

CC misaminoacylated tRNA. This enables the detection, isolation and analysis

CC of nascent proteins using UV without the usual accompanying radioactivity

CC problems. It may be used to detect mutations, for example in cancer,

CC Duchenne muscular dystrophy, adenomatous polyposis coli and colon cancer

XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
|||||
DB 1 HHHHHH 6

RESULT 28

ID AAB45989 standard; peptide; 6 AA.

XX AAB45989;

DT 02-APR-2001 (first entry)

DE Transdominant effector peptide associated screening peptide #68.

KW Intracellular transdominant bioactive agent; screening; cell phenotype;

KW effector peptide.

OS Unidentified.

PN US6153380-A.
XX
PD 28-NOV-2000.
XX
PP 23-JAN-1997; 97US-00789333.
XX
PR 23-JAN-1996; 96US-00589108.
PR 23-JAN-1996; 96US-00589911.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PA (RIGE-) RIGEL PHARM INC.
XX
P1 Rothenberg SM, Nolan GP;
XX
DR WPI; 2001-060084/07.
XX
PT Methode for screening intracellular transdominant effector peptides and
PT RNA molecules comprise delivering random oligonucleotides to cells, which
PT are then screened for an altered phenotype.
XX
PS Disclosure; Col 101-102; 57pp; English.
XX
CC This invention describes novel in vitro screening methods (1) for a
CC transdominant intracellular bioactive agent capable of altering the
CC phenotype of a cell. (1) comprises: (a) introducing a molecular library
CC of randomized candidate nucleic acids into several cells; and (b)
CC screening the cells for a cell exhibiting an altered phenotype, where the
CC altered phenotype is due to the presence of a transdominant bioactive
CC agent. The methods are particularly useful for screening intracellular
CC transdominant effector peptides and RNA molecules selected inside living
CC cells from randomized pools. (1) is also useful for introducing random
CC libraries into cells to screen for bioactive compounds. The methods allow
CC rapid and highly efficient screening of large numbers of random
CC oligonucleotides and their corresponding expression products in a single
CC step. In addition, the methods allow screening in the absence of
CC significant prior characterization of the cellular defect
XX
SQ Sequence 6 AA;
XX
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 1 HHHHHH 6
XX
RESULT 29
AAG78043
ID AAG78043 standard; peptide; 6 AA.
XX
AC AAG78043;
XX
DT 20-NOV-2001 (first entry)
XX
DE 6-His epitope tag.
XX
KW abnormal base-pairing; polymorphism; nucleic acid repair enzyme;
KW mutation; infection; cancer; immune system disorder; metabolic disorder;
KW muscle disorder; bone disorder; nervous system disorder;
KW high throughput screening; epitope tag.
XX
OS Synthetic.
XX
PN WO200162968-A2.
XX
PD 30-AUG-2001.
XX
PP 05-JAN-2001; 2001WO-US000452.
XX
PR 25-FEB-2000; 2000US-00514016.
XX

PA (GEAT) GEN ATOMICS.
XX
PI Yuan C;
XX
DR WPI; 2001-536643/59.
XX
PT Detecting abnormal base-pairing, mutation in nucleic acid, or
PT polymorphism in gene locus, comprises contacting nucleic acid with
PT abnormal base-pairing and mutant nucleic acid repair enzyme, and
PT detecting their binding.
XX
PS Disclosure; Page 180; 294pp; English.
XX
CC The invention relates to detecting abnormal base-pairing in a nucleic
CC acid duplex, mutation in a nucleic acid or polymorphism in a gene locus,
CC comprising contacting a nucleic acid duplex having an abnormal base-
CC pairing with a mutant nucleic acid repair enzyme or its complex and
CC detecting the binding between the nucleic acid duplex and mutant enzyme,
CC such that the presence of abnormal base-pairing, mutation or polymorphism
CC is detected. The method is useful for prognosis or diagnosis of the
CC presence or severity of a disease, disorder or infection by a
CC pathological agent associated with the mutation, including cancer, immune
CC system disorders, metabolic disorders, muscle and bone disorders, nervous
CC system disorders, signal disorders and transporter disease or disorder.
CC The method is rapid and accurate and is amenable to high throughput
CC formats. The method requires neither specific probes nor gel
CC electrophoresis and is amenable to automation for simultaneous detection
CC of a large number of nucleic acid mutations. The present sequence is that
CC of an epitope tag, useful to the invention
XX
SQ Sequence 6 AA;
XX
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 1 HHHHHH 6
XX
RESULT 30
AAB97353
ID AAB97353 standard; peptide; 6 AA.
XX
AC AAB97353;
XX
DT 15-AUG-2001 (first entry)
XX
DE 6-His epitope used in dual labelled receptor construction.
XX
KW Automated measurement; cell viability; epitope tag; luminescence;
KW G-protein coupled receptor; high content screen.
XX
OS Synthetic.
XX
PN WO200135072-A2.
XX
PD 17-MAY-2001.
XX
PP 09-NOV-2000; 2000WO-US030896.
XX
PR 09-NOV-1999; 99US-0164353P.
PR 18-JAN-2000; 2000US-0176504P.
XX
PA (CELL-) CELLOMICS INC.
XX
PI Ghosh RN, Debiasio R, Chen Y, Bellutta P, Giuliano K, Pasley JW;
XX
DR WPI; 2001-329169/34.
XX
PT Automated measurement of cell viability, involves contacting cells with
PT luminescent reporter molecule, imaging cells to get signals, converting

PT signals into digital data and using data to measure viable cell.
XX
PS Example 6; Page 52; 155pp; English.
XX
CC This invention relates to a method for the automated measurement of cell
CC viability. The method involves contacting cells with luminescent reporter
CC molecules, imaging cells to get signals, and converting the signals into
CC digital data which can be used as a measurement of cell viability.
CC Included in the invention is a computer readable storage medium
CC comprising a programme which causes the method of the invention to be
CC activated. The method is useful for cell state identification in cells.
CC The method is also useful for drug discovery. An example of the invention
CC relates to the use of inserted sequences and their ligands for high
CC content screens incorporating dual labelled receptors. The present
CC sequence represents an epitope tag used to label one end of a G-protein
CC coupled receptor (GPCR). The intracellular and extracellular domains of
CC the GPCR are distinctly labelled so that using the method of the
CC invention the extent of internalisation of the receptor can be measured
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;
OY 1 HHHHHH 6
DB 1 HHHHHH 6
RESULT 31
AAMS2173
ID AAMS2173 standard; peptide; 6 AA.
AC AAMS2173;
DT 07-FEB-2002 (first entry)
DE Peptide tag 1.
XX
XX Factor VII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW cardiant; hepatocytic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX
OS Synthetic.
XX
XX WO200158935-A2.
XX
XX 16-AUG-2001.
XX
XX 12-FEB-2001; 2001WO-DK000094.
XX
XX 11-FEB-2000; 2000DK-00000218.
XX
XX 18-OCT-2000; 2000DK-00001558.
XX
XX (MAXY-) MAXYGEN APS.
XX
XX Andersen KV, Pedersen AH, Bornaes C;
XX
XX WPI; 2001-581807/65.
XX
XX New conjugate, useful for treating Factor VIIa related diseases or
XX disorders such as hemophilia, liver disease, myocardial infarction and
XX deep-vein thrombosis, comprises non-polypeptide group covalently attached
XX to polypeptide group.
XX
XX Disclosure; Page 42; 89pp; English.
XX
XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX polypeptide conjugates, comprising at least one non-polypeptide group
XX covalently attached to a polypeptide, where the amino acid sequence of
XX polypeptide differs from that of the wildtype FVIIa (AAMS2171) in that at
XX least one amino acid residue containing an attachment group for the non-

CC polypeptide group has been introduced or removed. The FVIIa conjugates
CC have haemostatic, thrombolytic, cardiant, hepatocytic and
CC cerebroprotective activity and are useful for treating FVIIa/TF-related
CC diseases or disorders such as haemophilia, liver disease, myocardial
CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC have increased functional in vivo half life and/or increased plasma half
CC life, increased bioavailability and/or reduced sensitivity to proteolytic
CC degradation. Consequently medical treatment using the conjugates has a
CC number of advantages over currently available such as longer duration
CC between injections. The present sequence is that of a peptide tag, useful
CC to the invention
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;
OY 1 HHHHHH 6
DB 1 HHHHHH 6
RESULT 32
ABB76820
ID ABB76820 standard; peptide; 6 AA.
AC ABB76820;
DT 16-JUL-2002 (first entry)
DE His tag.
XX
XX Angiopoietin-Y2; His tag.
XX
XX Unidentified.
XX
XX KR2000059883-A.
XX
XX 16-OCT-2000.
XX
XX 09-MAR-1999; 99KR-00007779.
XX
XX 09-MAR-1999; 99KR-00007779.
XX
XX (KOHG/) KOH G Y.
XX
XX (KIMT/) KIM I J.
XX
XX Kwak HJ, Ahn JB, Koh GN, Kim SY;
XX
XX WPI; 2001-254061/26.
XX
XX Novel angiopoietin-Y2 gene and recombinant protein.
XX
XX Example 1; Page 4; 10pp; Korean.
XX
XX The present invention relates to a novel angiopoietin-Y2 gene and
XX recombinant protein. The present sequence is a His tag used in an example
XX from the invention
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;
OY 1 HHHHHH 6
DB 1 HHHHHH 6
RESULT 33
AAB66801

ID AAB66801 standard; peptide; 6 AA.
 XX
 AC AAB66801;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE 6-His epitope.
 DE
 KW Analyte-binding enzyme; analyte analysis; epitope.
 XX
 OS unidentified.
 XX
 PN WO200102600-A2.
 PD
 PD 11-JAN-2001.
 XX
 PE 30-JUN-2000; 2000WO-US018057.
 XX
 PR 06-JUL-1999; 99US-00347878.
 PR 06-DEC-1999; 99US-00457205.
 XX
 PA (GEAT) GEN ATOMICS.
 XX
 PI Yuan C;
 XX
 DR WPI; 2001-071583/08.
 XX
 PT Assaying method, useful for prognosis and diagnosis of disease, comprises
 PT contacting sample with a mutant analyte-binding enzyme and detecting
 PT binding.
 XX
 PS Disclosure; Page 104; 187pp; English.
 XX
 CC The present invention relates to a method for assaying an analyte in a
 CC sample comprising: contacting the sample with a mutant analyte-binding
 CC enzyme which has binding affinity for the analyte or an immediate analyte
 CC enzymatic conversion product but has attenuated catalytic activity; and
 CC detecting resulting binding. The method is useful in monitoring
 CC biological systems/processes, or prognosis/diagnosis of disease caused by
 CC imbalances of the analytes. The present sequence is an epitope used in
 CC the present invention
 CC
 XX
 SQ Sequence 6 AA;
 XX
 Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHHHHH 6
 |||||
 DB 1 HHHHHH 6
 |||||
 RESULT 34
 AAE01997
 ID AAE01997 standard; peptide; 6 AA.
 XX
 AC AAE01997;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Poly-His tag used to prepare poly-His version of huRANKL.
 XX
 KW Receptor activator of NF-kappaB; RANK; nuclear factor-kappaB; NF-kappaB;
 KW tumour necrosis factor; TNF; type I transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 KW early onset Paget's disease of bone; BP; cytostatic; poly-his tag.
 XX
 OS Synthetic.
 XX
 PN WO200136637-A1.
 XX

XX
 PD 25-MAY-2001.
 XX
 PF 14-NOV-2000; 2000WO-US011459.
 XX
 PR 17-NOV-1999; 99US-00442029.
 XX
 PA (IMNV) IMMUNEX CORP.
 XX
 PI Anderson DM, Hughes AE;
 XX
 DR WPI; 2001-329222/34.
 XX
 PT New DNA encoding a receptor activator of NF-kappaB polypeptide for the
 PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO).
 XX
 PS Example 15; Page 82; 96pp; English.
 XX
 CC The present invention relates to a novel receptor, referred to as RANK
 CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
 CC (tumour necrosis factor) receptor superfamily. RANK is a Type I
 CC transmembrane protein that interacts with TNF receptor-associated factors
 CC (TRAFs). Triggering of RANK by overexpression or co-expression of RANK
 CC and membrane bound RANK ligand (RANKL) results in upregulation of the
 CC transcription factor NF-kappaB, a ubiquitous transcription factor that is
 CC most extensively utilized in cells of the immune system. Inhibition of NF
 CC -kappaB by RANK antagonists is useful in ameliorating negative effects of
 CC inflammatory reactions, and the effects of excess bone resorption. The
 CC RANK DNAs, proteins and their analogues are useful for the preparation of
 CC pharmaceutical compositions, for infecting target cells for use in gene
 CC therapy applications in diagnosing diseases associated with RANK, and as
 CC targets for use in screening assays. They may be used in the treatment or
 CC diagnosis of immune system dysfunction. The present invention also
 CC encompasses gene therapy methods to correct gene-activating mutations,
 CC associated with e.g. familial expansile osteolysis (FEO) and early onset
 CC Paget's disease of bone (BP). The present sequence is a synthetic poly-
 CC his tag used to prepare soluble, tagged, poly-his version of human RANKL
 CC protein
 CC
 XX
 SQ Sequence 6 AA;
 XX
 Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHHHHH 6
 |||||
 DB 1 HHHHHH 6
 |||||
 RESULT 35
 AAG65669
 ID AAG65669 standard; peptide; 6 AA.
 XX
 AC AAG65669;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE His tag used for recombinant expression of FGF-like polypeptide.
 XX
 KW Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic;
 KW fat deposition; vulnerability; antidiabetic; dermatological; anorectic;
 KW antidiabetic; antiinflammatory; cytostatic; hepatic; virucide;
 KW neuroprotectant; pulmonary; gene therapy; vaccine; human.
 XX
 OS Synthetic.
 XX
 PN WO200172957-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 02-APR-2001; 2001WO-1B000664.
 XX

PR 31-MAR-2000; 2000US-00540118.
 XX (ITOH/) ITOH N.
 XX
 XX Itoh N;
 PI
 XX WPI; 2001-611623/70.
 DR
 XX New human nucleic acid encoding fibroblast growth factor-like peptide,
 PT useful for treatment and diagnosis of e.g. wounds and inflammatory bowel
 PT disease.
 XX
 XX Example 3; Page 117; 172pp; English.
 XX
 CC The invention provides human nucleic acids encoding fibroblast growth
 CC factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by
 CC standard recombinant methodology and are mitogenic for a wide range of
 CC cells, inducing differentiation and proliferation, and inhibiting
 CC deposition of fat. The FGF-like polypeptides, polynucleotides and
 CC specific antibodies and modulators are useful for treating a very wide
 CC range of diseases and conditions, e.g. wounds, ulcers, skin aging, viral
 CC obesity, diabetes, alopecia, inflammatory bowel disease, emphysema, viral
 CC hepatitis, multiple sclerosis, respiratory distress syndrome, tumors of
 CC the eye, etc., also for maintaining organs before transplant and
 CC supporting culture of primary cells and tissues. Sequences AAG6568-69
 CC represent amino acid sequences of protein tags used for recombinant
 CC expression of FGF-like polypeptide
 XX
 SO Sequence 6 AA;
 QY
 Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 HHHHHH 6
 1 HHHHHH 6
 RESULT 36
 AAU00163
 ID AAU00163 standard; peptide; 6 AA.
 XX
 AC AAU00163;
 XX
 DT 16-MAY-2001 (first entry)
 XX
 DE His Tag for purification of interferon beta fusion proteins.
 XX
 KW Human; interferon beta; antibody; multiple sclerosis; gene therapy;
 KW viral infection; viral hepatitis; cancer; breast cancer; inflammation;
 KW Crohn's disease; acute myeloid leukaemia; Hodgkin's disease;
 KW ulcerative colitis; immunomodulation; His tag.
 XX
 OS Synthetic.
 XX
 PN WO200115736-A2.
 PD 08-MAR-2001.
 XX
 PF 25-AUG-2000; 2000WO-DK000471.
 XX
 PR 27-AUG-1999; 99DK-00001197.
 PR 21-OCT-1999; 99US-0160782P.
 PR 26-NOV-1999; 99DK-00001691.
 PR 07-FEB-2000; 2000DK-00000194.
 PR 07-MAR-2000; 2000DK-00000363.
 PR 14-APR-2000; 2000DK-00000642.
 XX
 XX (MAXY-) MAXYGEN APS.
 PA
 XX Pedersen AH, Schambye HT, Andersen KV, Bornaes C, Rasmussen PB;
 XX

DR WPI; 2001-218488/22.
 XX
 XX A conjugate exhibiting interferon beta activity useful for treating
 PT multiple sclerosis comprises a non-polypeptide group covalently attached
 PT to an interferon beta polypeptide.
 XX
 XX Disclosure; Page 40; 108pp; English.
 PS
 XX The sequence is a His tag suitable for purification of Human interferon
 CC beta fusion proteins and to facilitate conjugation to a non-polypeptide
 CC moiety. Conjugates of the invention exhibiting interferon beta activity
 CC comprise at least one first non-polypeptide group covalently attached to
 CC an interferon beta polypeptide, the amino acid sequence of which differs
 CC from wild-type human interferon beta in at least one introduced and at
 CC least one removed amino acid residue comprising an attachment group for
 CC the first non-polypeptide group. The invention also concerns reducing the
 CC immunogenicity and/or increasing functional in vivo half-life and/or
 CC serum half-life of an interferon beta polypeptide comprising introducing
 CC an amino acid residue constituting an attachment group for a first non-
 CC polypeptide group into a position exposed at the surface of the protein
 CC that does not contain such a group and removing an amino acid residue
 CC constituting an attachment group for a first non-polypeptide group and
 CC subjecting the modified peptide to conjugation with the non-polypeptide
 CC group. The conjugate and a cell culture expressing the mutated
 CC polypeptides are useful in the treatment of disease, especially multiple
 CC sclerosis, and for treating mammals having circulating antibodies against
 CC interferon beta 1a or 1b. DNA encoding the mutated proteins may be used
 CC for gene therapy. The DNA and proteins can also be used to treat viral
 CC infections (e.g. viral hepatitis), cancer (e.g. breast cancer),
 CC inflammation, Crohn's disease, acute myeloid leukaemia, Hodgkin's disease
 CC and ulcerative colitis and for immunomodulation
 XX
 SO Sequence 6 AA;
 QY
 Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 HHHHHH 6
 1 HHHHHH 6
 RESULT 37
 AAG62605
 ID AAG62605 standard; peptide; 6 AA.
 XX
 AC AAG62605;
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE Metal capturing protein related peptide #2.
 XX
 KW Metal capturing protein; metal capture; secretory signal;
 KW waste treatment.
 XX
 OS Synthetic.
 XX
 PN WO200138517-A1.
 PD 31-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-JP007518.
 XX
 PR 19-NOV-1999; 99JP-00330226.
 XX
 PA (TOYT) TOYOTA JIDOSHA KK.
 XX
 PI Tanaka A, Ueda M;
 XX
 XX WPI; 2001-355927/37.
 DR N-PSDB; AAH45709.
 XX

PT Fused gene with DNA expressing polypeptide capable of capturing metal,
PT for recombinant vectors and transformants applicable in purifying
PT environment and recovering metal efficiently, including waste treatment.
XX
PS Claim 4; Page 32; 45pp; Japanese.
XX
CC The present invention relates to a fused gene containing DNAs encoding a
CC secretory signal peptide, a protein capable of capturing a metal and a
CC protein localised on the cell surface. The gene can be used to express
CC the metal capturing protein, which can then be used in purifying and
CC recovering metal for example in waste treatment. The present sequence is
CC a peptide described in the exemplification of the invention
XX
SQ Sequence 6 AA;
XX
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 1 HHHHHH 6
XX
RESULT 38
AAB62662
ID AAB62662 standard; peptide; 6 AA.
XX
AC AAB62662;
XX
DT 23-JUN-2001 (first entry)
XX
DE C-terminal His tag.
XX
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; antiaesthetic; antiatherosclerotic;
KW immunosuppressive; chromosome 6q24.1-25.2; human.
XX
OS Synthetic.
XX
PN WO200140467-A1.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032703.
XX
PR 03-DEC-1999; 99US-0169049P.
PR 13-SEP-2000; 2000US-0232219P.
PR 31-OCT-2000; 2000US-0244610P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
DR WPI; 2001-356158/37.
XX
PT New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions.
XX
PS Example 1; Page 193; 210pp; English.
XX
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cells (progenitors); reducing IL-
CC TIF induced or IL-9 induced inflammation; and suppressing an inflammatory
CC response in a mammal with inflammation. Heteromeric/ multimeric receptor
CC polypeptides such as soluble zcytor 16/CRP2-4 can be used to reduce
CC progression and symptoms of cancer. zcytor16 polypeptides can also be
CC used to detect IL-TIF levels which is indicative of pathological
CC conditions including inflammatory states (e.g. rheumatoid arthritis) and
CC cancer. Antibodies that bind zcytor16 polypeptides and the polypeptides

CC themselves are useful for the treatment of inflammation, inflammatory
CC diseases (e.g. infection, asthma, inflammatory bowel disease, rheumatoid
CC arthritis and atherosclerosis) and autoimmune diseases. The antibodies
CC and zcytor16 polynucleotides are also useful for detecting cancer. The
CC present sequence represents a C-terminal His tag, used in the
CC construction of a zcytor16 mammalian expression vector
XX
SQ Sequence 6 AA;
XX
Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 1 HHHHHH 6
XX
RESULT 39
AAU02090
ID AAU02090 standard; peptide; 6 AA.
XX
AC AAU02090;
XX
DT 07-SEP-2001 (first entry)
XX
DE His-tag peptide.
XX
KW Fibroblast growth factor 20; FGF-20; Parkinson's disease;
KW substantia nigra; dopaminergic neuron; cochlea-associated disease;
KW otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW diabetes-associated hearing loss; congenital malformations;
KW autoimmune disease-related hearing loss; age-related hearing loss;
KW deafness; ischaemia-related hearing disturbance; immunogen; antibody;
KW neuro-degenerative disease; tendonitis; wound healing; stroke; ischaemia;
KW His-tag.
XX
OS Synthetic.
XX
PN WO200131008-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US029237.
XX
PR 22-OCT-1999; 99US-0161162P.
PR 08-MAR-2000; 2000US-0187856P.
XX
PA (CHIR) CHIRON CORP.
XX
PI (KYOU) UNITIV KYOTO.
XX
PI Itoh N, Kavanagh WM;
XX
DR WPI; 2001-308642/32.
XX
PT New human and rat fibroblast Growth Factor (FGF) polypeptides for
PT providing trophic support for cells used in Parkinson patients, and
PT alleviating brain and cochlea conditions.
XX
PS Example 6; Page 44; 73pp; English.
XX
CC The sequence an His-tag which can be incorporated into a fusion protein
CC (to allow purification of the fusion protein) with Human or rat
CC fibroblast growth factor 20, FGF-20. The FGF polypeptides and nucleic
CC acids encoding them are useful for providing trophic support for cells in
CC a patient, especially a patient with Parkinson's disease, and FGF-20 is
CC additionally used to treat patients with conditions of the substantia
CC nigra. The polypeptides and nucleic acids are useful for alleviating
CC human brain conditions by slowing degeneration, restoring function of,
CC increasing the number of, dopaminergic neurons. The polypeptides and
CC nucleic acids are also useful for alleviating cochlea-associated disease
CC by slowing degeneration of or restoring or maintaining normal function of
CC the structure of cochlea, where the disease is otosclerosis, Cogan's

CC syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated
CC hearing loss, congenital malformations, autoimmune disease-related
CC hearing loss, age-related hearing loss, deafness associated with lack of
CC FGF receptor and ischaemia-related hearing disturbance. Other diseases
CC thought to be amenable to FGF therapeutic activity include neuro-
CC degenerative diseases, tendonitis, wound healing, stroke and ischaemia.
CC The polypeptides can be used to screen for agonists and antagonists.
CC Epitope bearing fragments of the FGF-20 polypeptides can be used to raise
CC anti-FGF-20 antibodies

XX Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 40

AAB85699 standard; peptide; 6 AA.

AC AAB85699;

DT 29-OCT-2001 (first entry)

DE Amino acid sequence of six-histidine epitope tag.

KW Multivalent protein; immune response; Plasmodium vivax; parasite;
KW protozoacide; vaccine; malaria; recombinant; VIVac1; VIVac2.

OS Synthetic.

PN WO200155181-A2.

PD 02-AUG-2001.

PF 29-JAN-2001; 2001WO-US002937.

PR 31-JAN-2000; 2000US-0179213P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lal AA, Xiao L, Zhou Z;

DR WPI; 2001-514557/56.

PT New recombinant multivalent protein comprising antigenic determinants
PT derived from more than one stage in a life cycle of Plasmodium vivax,
PT useful as a vaccine for treating, preventing and reducing malarial
PT infection.

PS Example 1; Page 25; 59pp; English.

XX The invention relates to recombinant multivalent proteins (I) that
CC stimulate an immune response to Plasmodium vivax. (I) comprises antigenic
CC determinants, fragments or conservative substitutions, derived from more
CC than one stage in a life cycle of a Plasmodium vivax parasite. (I) is
CC useful as a vaccine for stimulating an immune response, specifically a
CC protective immune response that confers increased resistance to infection
CC by Plasmodium parasites, such as P. vivax. (I) is especially useful in
CC the treatment, prevention and reduction of malarial infection, as
CC research or diagnostic reagents for the detection of Plasmodium species
CC in a biological sample, and for conferring immunity against multiple
CC stages of the malarial parasite. The antibodies produced are useful for
CC the detection or measurement of antigenic epitopes derived from one or
CC more stages in a life cycle of a parasite, particularly P. vivax. The
CC vaccine comprising the recombinant proteins, is cost-effective, health-
CC promoting intervention for controlling, preventing or treating the
CC incidence of malaria. The present sequence represents the amino acid

CC sequence of a six-histidine epitope tag, a component of the multivalent
CC and multistage proteins VIVacip and VIVac2p

XX Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 41

ABR00924 standard; peptide; 6 AA.

AC ABR00924;

DT 03-APR-2003 (first entry)

DE Hexahistidine peptide tag SEQ ID NO 32.

KW Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;
KW antiinflammatory; gastrointestinal; gene therapy; vaccine; asthma;
KW obesity; inflammatory bowel disease.

OS Synthetic.

PN WO200178894-A2.

PD 25-OCT-2001.

PF 13-APR-2001; 2001WO-US012245.

PR 13-APR-2000; 2000US-00548797.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Keith T;

DR WPI; 2001-639428/73.

PT Isolated genes (Gene 216) from human chromosome 20p13-p12 and the
PT proteins they encode, useful for the prevention, diagnosis and treatment
PT of asthma, obesity and inflammatory bowel disease.

PS Disclosure; Page 45; 520pp; English.

XX The invention relates to isolated genes (Gene 216) from human chromosome
CC 20p13-p12 and the proteins they encode. The nucleic acids and proteins
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate Gene 216 expression. For example, the
CC nucleic acids (or vectors) and proteins may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of gene 216 by expressing
CC inactive proteins or to supplement the patient's own production of Gene
CC 216 proteins. Additionally, the nucleic acids may be used to produce the
CC secreted gene 216 protein, by inserting the nucleic acids into a host
CC cell and culturing the cell to express the protein. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acid
CC sequences in samples and therefore which patients may be in need of
CC restorative therapy. The Gene 216 protein may also be used as antigens in
CC the production of antibodies against Gene 216 and in assays to identify
CC modulators of Gene 216 expression and activity. The anti-Gene 216
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. The anti-Gene 216 antibodies may also be used as diagnostic
CC agents for detecting the presence of Gene 216 proteins in samples (e.g.
CC by enzyme linked immunosorbent assay or ELISA). Disorders that may be
CC prevented, diagnosed and/or treated by the above methods include, for
CC example asthma, obesity and inflammatory bowel disease. The present

CC sequence is that of a peptide tag used in analysis of the Gene 216
 CC encoded protein
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 1 HHHHHH 6

RESULT 42
 AAE08006
 ID AAE08006 standard; peptide; 6 AA.

AC AAE08006;
 DT 01-NOV-2001 (first entry)

XX His tag useful as antibody recognition sequences.

KW Neuropeptide Y; NPY receptor; G-protein-coupled transmembrane protein;
 KW transmembrane; TM domain; therapy; obesity; blood pressure; epilepsy;
 KW Huntington's disorder; Parkinson's disorder; eating disorder; seizure;
 KW locomotor; anxiety disorder; limbic seizure; tranquilizer; his tag.

XX Unidentified.

XX WO200155103-A2.

XX 02-AUG-2001.

XX 29-JAN-2001; 2001WO-US002804.

XX 28-JAN-2000; 2000US-0178652P.

XX (NEUR-) NEUROGEN CORP.

XX Bennett M, Brodbeck R, Krause J;

XX WPI; 2001-514543/56.

PT New chemist receptor proteins comprising a single polypeptide chain of
 PT amino acids, useful as targets for drug actions, and as basis for drug
 PT discovery and development.

XX Disclosure; Page 54; 72pp; English.

CC The present invention relates to chimeric neuropeptide Y (NPY) receptors.
 CC The NPY receptors are G-protein-coupled transmembrane proteins with seven
 CC membrane spanning transmembrane (TM) domains. The compounds that modulate
 CC the activity of a NPY receptor is useful in the preparation of a
 CC medicament for treating conditions including obesity, high/low blood
 CC pressure, epilepsy, Huntington's and Parkinson's disorder and eating,
 CC seizure, locomotor and anxiety disorders. They can also be used as
 CC targets for drug actions, and as basis for drug discovery and
 CC development. The NPYs receptor may have an anti-epileptic activity in the
 CC control of limbic seizures. The present sequence is a hexa-histidine (His
 CC -6x) tag which is used as antibody recognition sequences in the
 CC exemplification of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 1 HHHHHH 6

RESULT 43
 AAM51720
 ID AAM51720 standard; peptide; 6 AA.

AC AAM51720;

DT 29-JAN-2002 (first entry)

DE FSH alpha or beta tagging peptide 1.

KW Human; FSH alpha; FSH beta; follicle stimulating hormone; glycosylation;
 KW antiinfertility.

XX Synthetic.

XX WO200156493-A1.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-DK000090.

XX 11-FEB-2000; 2000DK-00000220.

XX 14-JUL-2000; 2000DK-00001092.

XX (MAXY-) MAXYGEN APS.

PI Schambye HT, Andersen KV, Van Den Hazel B, Christiansen J;

PI Jeppesen CB;

XX WPI; 2001-607186/69.

PT New polypeptide conjugate with follicle stimulating hormone (FSH)
 PT activity, used to treat infertility, comprises polypeptide having
 PT modified FSH alpha and beta subunits with attachment group for non-
 PT polypeptide moiety.

XX Disclosure; Page 37; 88pp; English.

CC The invention relates to new polypeptides and polypeptide conjugates
 CC exhibiting follicle stimulating hormone (FSH) activity. FSH is a dimeric
 CC hormone comprising of an alpha (AAM51709) and beta (AAM51711) subunit.
 CC The invention relates to a heterodimeric FSH conjugate comprising, a
 CC dimeric polypeptide having FSH alpha (AAM51733-AAM51800, AAM51442-
 CC AAM51449) and beta (AAM52001-AAM52104) subunits, where at least one
 CC subunit differs from corresponding wild-type subunit in that an amino
 CC acid residue containing an attachment group for a non-polypeptide
 CC molecule has been introduced or removed, especially where at least one of
 CC the FSH-alpha and FSH-beta subunits comprises at least one introduced N-
 CC or O-glycosylation site at its N-terminal and the glycosylation site
 CC being glycosylated. The polypeptides have antiinfertility activity. The
 CC polypeptides have increased functional in vivo half life and/or serum
 CC half life as compared to human FSH, replenishing insufficient endogenous
 CC FSH production in a patient. The present sequence is that of a peptide
 CC tag for protein purification

XX Sequence 6 AA;

Query Match 100.0%; Score 48; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 1 HHHHHH 6

RESULT 44
 AAE26107
 ID AAE26107 standard; peptide; 6 AA.

AC AAE26107;

XX 14-NOV-2002 (first entry)
 XX His tag peptide used to generate soluble human RANKL protein.
 DE
 XX
 KW RANK; receptor activator of nuclear factor-kappaB; NF-kB; sepsis;
 KW immune response; toxic shock; graft-versus-host reaction; therapy; TRAF;
 KW tumour necrosis factor receptor-associated factor; immunosuppressive;
 KW antibacterial; antiinflammatory.
 XX
 OS Synthetic.
 XX
 PN US2002086827-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 30-MAY-2001; 2001US-00871291.
 XX
 PR 23-DEC-1996; 96US-0059978P.
 PR 07-MAR-1997; 97US-0077181P.
 PR 14-OCT-1997; 97US-0064671P.
 PR 22-DEC-1997; 97US-0099613P.
 PR 17-DEC-1999; 99US-0046496.
 PR 24-MAY-2000; 2000US-00577800.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Anderson DM;
 XX
 DR WPI; 2002-642254/69.
 XX
 PT A novel RANK (receptor activator of nuclear factor-kappaB (NF-kB))
 PT polypeptide, useful for inhibiting activation of NF-kB and for regulating
 PT an immune or inflammatory response in an individual.
 XX
 PS Example 15; Page 40; 49pp; English.
 XX
 CC The invention relates to novel RANK (receptor activator of nuclear factor
 CC -kappaB (NF-kB)) proteins and polynucleotides encoding them. Sequences of
 CC the invention are useful for inhibiting activation of NF-kappaB. They are
 CC useful for regulating an immune or inflammatory response in an individual
 CC at risk for an immune or inflammatory response. Inhibition of NF-kappaB
 CC by RANK antagonists is useful in ameliorating negative effects of an
 CC inflammatory response that results from triggering of RANK, for e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions or acute
 CC inflammatory reactions. Soluble RANK is useful as an adjunct therapy for
 CC diseases characterised by neoplastic cells that express RANK. Soluble
 CC forms of the receptor are useful in vitro to screen for agonists or
 CC antagonists of RANK activity. The cytoplasmic domain of RANK is useful in
 CC developing assays for inhibitors of signal transduction, to screen for
 CC molecules that inhibit interaction of RANK with tumour necrosis factor
 CC receptor-associated factor (TRAF) 2 or TRAF3. The present sequence is a
 CC His tag peptide used to generate a soluble, tagged, poly-His version of
 CC human RANK ligand (RANKL) protein. This peptide is used in the
 CC exemplification of the invention
 XX
 SQ Sequence 6 AA;
 XX
 QY Query Match 100.0%; Score 48; DB 5; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 Db Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 HHHHHH 6
 XX |||||
 XX 1 HHHHHH 6
 XX
 RESULT 45
 ID AAE28476 standard; peptide; 6 AA.
 XX
 AC AAE28476;
 XX

DT 27-DEC-2002 (first entry)
 XX
 DE 6HTS peptide used for transfection enhancement.
 XX
 KW Tat region; nucleic acid-binding group; cell transfection system; cancer;
 KW gene therapy.
 XX
 OS Unidentified.
 XX
 PN US6376248-B1.
 XX
 PD 23-APR-2002.
 XX
 PF 16-MAR-1998; 98US-00039780.
 XX
 PR 14-MAR-1997; 97US-00818200.
 XX
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX
 PI Hawley-Nelson P, Lan J, Shih P, Jesse JA, Schifferli KP;
 PI Gebeyehu G, Ciccarone VC, Evans KL;
 DR WPI; 2002-680647/73.
 XX
 PT New peptide comprising Tat sequence linked to nucleic acid-binding group,
 PT useful, e.g. in gene therapy, for improving cell-transfection efficiency.
 XX
 PS Example 1; Col 171-172; 108pp; English.
 XX
 CC The invention relates to a peptide comprising Tat sequence linked to
 CC nucleic acid-binding group. Peptides of the invention are used as
 CC components of a cell transfection system particularly for gene therapy
 CC (especially of cancer). The present sequence is a chimeric peptide useful
 CC for transfection enhancement. This peptide contains a His tail and a RGD
 CC peptide. This sequence is used in the exemplification of the invention
 XX
 SQ Sequence 6 AA;
 XX
 QY Query Match 100.0%; Score 48; DB 5; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 2e+06;
 Db Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 HHHHHH 6
 XX |||||
 XX 1 HHHHHH 6
 XX
 RESULT 46
 ID AAM49702 standard; peptide; 6 AA.
 AC AAM49702;
 XX
 DT 28-MAY-2002 (first entry)
 XX
 DE KpnI/SalI His-tag region.
 XX
 KW US6 gene; immunodominant; glycoprotein D; antigen; serological testing.
 XX
 OS Unidentified.
 XX
 PN RU2178806-C2.
 XX
 PD 27-JAN-2002.
 XX
 PF 21-JAN-2000; 2000RU-00101648.
 XX
 PR 21-JAN-2000; 2000RU-00101648.
 XX
 PA (VECT-) VECTOR VIROLOGY & BIOTECHN RES CENTRE.
 XX
 PI Susloparov MA, Susloparov IM, Plyasunov IV;
 XX

DR WPI; 2002-194324/25.
DR N-PSDB; ABA93644.
XX
PT Recombinant plasmid DNA phavd1 determining expression of gene US6
PT fragment of herpes simplex type-1 virus encoding immunodominant group of
PT glycoprotein d(gd)hsv-1 in bacterium Escherichia coli cells.
XX
PS Disclosure; Col 7; 9pp; Russian.
XX This invention describes a novel recombinant plasmid DNA constructed in
CC vitro and containing the herpes simplex type-1 virus (HSV-1) US6 gene
CC fragment which encodes an immunodominant group of glycoprotein D (gd).
CC This polypeptide shows the antigenic properties of herpes simplex virus
CC type-1. Purified recombinant protein can be used as HSV-1 antigen for the
CC serological testing of HSV-1 in clinical practice. This sequence
CC represents a His-tag sequence useful to the invention
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
Db 1 HHHHHH 6
RESULT 47
AAU10567
ID AAU10567 standard; peptide; 6 AA.
XX
AC AAU10567;
XX
DT 14-FEB-2002 (first entry)
XX
DE Purification peptide tag.
XX
KW Compound library screening; signal transduction; peptide tether;
KW cellular receptor; reporter molecule.
XX
OS Synthetic.
XX
PN US6109842-B1.
XX
PD 30-OCT-2001.
XX
PF 24-NOV-1997; 97US-00977378.
XX
PR 03-DEC-1996; 96US-00758307.
XX
PA (GLAX) GLAXO WELLCOME INC.
XX
PI Dower WJ, Gates CM, Heinkei GL, Lalonde G, Matheakis LC;
PI Paddon CJ, Schatz PJ;
XX
DR WPI; 2002-048370/06.
XX
PT Screening compounds having capacity to transduce signal through cellular
PT receptor by contacting complexes having test compound and tether
PT susceptible to modification with cell having receptor and reporter
PT molecule.
XX
PS Disclosure; Fig 6; 50pp; English.
XX
CC The invention relates to screening compounds for the capacity to
CC transduce a signal through a cellular receptor, by contacting complexes
CC having a test compound, a tag recording a step in synthesis of the
CC screened compound and a tether susceptible to modification by a reporter
CC molecule with cells having a receptor and a DNA fragment encoding the
CC reporter. Modification of the tether indicates that the complex contains
CC the compound. Supports must be provided, each bearing multiple copies of
CC a test compound and a tether, and are contacted with cells in order to

CC free a portion of the multiple copies of each of the compounds under test
CC from the support. At least one compound transduces a signal through the
CC receptor of a cell causing expression of the reporter molecule, and
CC isolating the support having the modified tether, which support bears the
CC compound transducing the signal. An array of compounds can also be
CC provided on a membrane, which is contacted with a cell, where at least
CC one compound transduces a signal through the cell receptor, causing
CC expression of the reporter molecule, which is released from the cell, and
CC modifies the membrane at a position proximate to the compound transducing
CC the signal. The modification of the membrane allows identification and
CC isolation of the compound transducing the signal. The methods are useful
CC for the identification of compounds with desired properties, allowing the
CC isolation of novel pharmaceuticals. This sequence represents a
CC purification peptide tag of the invention
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 48; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
Db 1 HHHHHH 6
RESULT 48
ABG32021
ID ABG32021 standard; peptide; 6 AA.
XX
AC ABG32021;
XX
DT 15-NOV-2002 (first entry)
XX
DE Synthetic protein tag, #1.
XX
XX Tag; single-chain multimeric polypeptide; polyethylene glycol; PEG;
XX granulocyte colony stimulating factor; G-CSF; hematopoietic disorder;
XX radiation therapy; chemotherapy; bone marrow transplantation;
XX acquired immunodeficiency syndrome; AIDS; immunodeficiency disease;
XX leukopenia; acute myeloid leukemia; half-life; clearance;
XX immunogenicity; bioavailability; single chain G-CSF dimer; HIV;
XX antihuman immunodeficiency virus; haemostatic.
XX
OS Synthetic.
XX
PN WO200236626-A1.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-DK000724.
XX
PR 02-NOV-2000; 2000DK-00001647.
XX
PA (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX
PI Nissen TL, Jensen AD;
PI WPI; 2002-618972/66.
XX
DR WPI; 2002-618972/66.
XX
PT Single chain multimeric polypeptide conjugate for treating hematopoietic
PT disorders, has two units of monomeric polypeptides linked via peptide
PT bond/linker and polymer group bound to attachment group of polypeptide.
XX
PS Disclosure; Page 43; 108pp; English.
XX
XX The invention discloses a single-chain multimeric polypeptide conjugate
XX comprising at least two units of a monomeric polypeptide linked via a
XX peptide bond or a peptide linker, where the monomeric polypeptide is
XX biologically active in its monomeric form and has at least one polymer
XX group covalently bound to an attachment group of the polypeptide e.g.
XX polyethylene glycol (PEG). The polypeptide is preferably a single-chain

CC multimeric granulocyte colony stimulating factor (G-CSF) polypeptide
 CC comprising at least two G-CSF polypeptide monomers, linked via a peptide
 CC bond or a peptide linker, where at least one of the monomers is a variant
 CC of wild-type human G-CSF comprising at least one amino acid residue
 CC modification. The monomeric and multimeric polypeptides are useful in
 CC therapy and for manufacture of a medicament for treatment of general
 CC hematopoietic disorders, including disorders arising from radiation
 CC therapy, chemotherapy or bone marrow transplantations, acquired
 CC immunodeficiency syndrome (AIDS) or other immunodeficiency diseases,
 CC leukopenia and acute myeloid leukemia. The conjugate has one or more
 CC important properties as compared to the native polypeptide, including
 CC increased functional in vivo half-life, increased serum half-life,
 CC reduced clearance, reduced immunogenicity and/or increased
 CC bioavailability. Consequently, medical treatment with a conjugate offers
 CC advantages including longer duration between injections and fewer side
 CC effects. The sequence presented is the synthetic protein tag, #1, which
 CC can be used for purification of the single chain G-CSF dimer or aid
 CC conjugation with a non-polypeptide moiety

CC Sequence 6 AA;

Query Match 100.0%; Score 48; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||

Db 1 HHHHHH 6

RESULT 49
 AAE23795
 ID AAE23795 standard; peptide; 6 AA.

AC AAE23795;

DT 10-SEP-2002 (first entry)

XX H1e6 tag used in the invention.

XX Human, interleukin-17 related protein; inflammation mediated disorder;
 KW LP-48; asthma; allergic conjunctivitis; allergic rhinitis; cirrhosis;
 KW allograft rejection; Alzheimer's disease; chronic bronchitis; ARDS;
 KW gastritis; adult respiratory distress syndrome; contact dermatitis;
 KW Crohn's disease; glomerulonephritis; graft versus host disease; GVHD;
 KW hepatitis; hypertension; irritable bowel syndrome; myasthenia gravis;
 KW myeloma; osteoarthritis; pancreatitis; rheumatoid arthritis; sepsis;
 KW septic shock; Sjogren's syndrome; systemic lupus erythematosus; burn;
 KW SLE; acne; ulcerative colitis; uveitis; autoimmune disorder; psoriasis;
 KW insulin-dependent diabetes mellitus; cancer; multiple sclerosis; AIDS;
 KW transplant rejection; anaemia; medical disorder; atherosclerosis; HIV;
 KW T-cell mediated condition; human immunodeficiency virus; lymphoma.

XX Synthetic.

OS WO20023083-A2.

PN 25-APR-2002.

XX 28-SEP-2001; 2001WO-US027737.

XX 13-OCT-2000; 2000US-0240177P.

PR 03-AUG-2001; 2001US-030936P.

XX (EHLI) LILLY & CO EHI.

XX Glasebrook AL, Liu L, Newton CM, Tetreault JW;

XX WPI, 2002-444244/47.

PT Treating or preventing an inflammation mediated disorder or autoimmune
 disorder, or a T cell or Th2 cell mediated condition in a mammal,
 PT comprises administering interleukin-17 related polypeptide, LP-48 or its

PT antagonist.
 XX Disclosure, Page 17; 112pp; English.

CC The present invention relates to a method for treating or preventing
 CC inflammation mediated or autoimmune disorder, disorder associated with
 CC endothelial cell apoptosis and T or Th2 cell mediated condition. The
 CC method involves administering human interleukin-17 related polypeptide,
 CC LP-48 or its analogue/homologue or antagonist to a mammal. The method is
 CC useful for treating or preventing inflammation mediated disorders such as
 CC acne, allergic conjunctivitis, allergic rhinitis, allograft rejection,
 CC Alzheimer's disease, adult respiratory distress syndrome (ARDS), asthma,
 CC burns, chronic bronchitis, cirrhosis, contact dermatitis, Crohn's
 CC disease, gastritis, glomerulonephritis, graft-versus-host disease
 CC (GVHD), hepatitis, hypertension, irritable bowel syndrome, migraine,
 CC myasthenia gravis, osteoarthritis, pancreatitis, rheumatoid arthritis,
 CC sepsis, septic shock, Sjogren's syndrome, systemic lupus erythematosus
 CC (SLE), ulcerative colitis, uveitis and chronic inflammation), autoimmune
 CC disorders such as psoriasis, insulin-dependent diabetes mellitus, cancer,
 CC multiple sclerosis, transplant rejection, fulminant viral hepatitis B,
 CC and aplastic anaemia), medical disorders associated with endothelial cell
 CC apoptosis (e.g. atherosclerosis), and T-cell mediated condition (such as
 CC human immunodeficiency virus (HIV)-induced lymphoma or AIDS). The
 CC present sequence is h1e6 tag used in the invention

CC Sequence 6 AA;

Query Match 100.0%; Score 48; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||

Db 1 HHHHHH 6

RESULT 50
 AAE28606
 ID AAE28606 standard; peptide; 6 AA.

AC AAE28606;

DT 27-DEC-2002 (first entry)

XX His peptide tag.

XX Cytokine receptor; Zcytoric; IL-11F; autoimmune disease; dermatological;
 KW inflammatory disease; inflammatory bowel disease; rheumatoid arthritis;
 KW asthma; systemic lupus erythematosus; myasthenia gravis; pancreatitis;
 KW diabetes; atherosclerosis; glomerulonephritis; gene therapy; cystostatic;
 KW immunosuppressive; nephrotropic; allergy; placental health; abortion;
 KW cancer.

XX Synthetic.

OS WO200270655-A2.

PN 12-SEP-2002.

XX 04-MAR-2002; 2002WO-US006267.

XX 02-MAR-2001; 2001US-0273035P.

PR 27-MAR-2001; 2001US-0279232P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Xu W, Kindsvogel W, Chen Z;

XX WPI, 2002-698750/75.

PT New Zcytoric polypeptide useful for treating autoimmune or inflammatory
 diseases, e.g. inflammatory bowel disease, rheumatoid arthritis, asthma,
 PT atherosclerosis, cancer or diabetes, or in assessing therapeutic aspects

PT of IL-TIF.

XX
PS Example 1; Page 195; 221pp; English.

XX
CC The invention relates to cytokine receptor designated as mouse Zcytor16
CC which can bind and antagonise the IL-TIF. The Zcytor16 polypeptide is
CC useful in modulating the immune system by binding Zcytor16 ligand, and
CC thus, preventing the binding of the ligand with endogenous Zcytor16
CC receptor. It is useful for studying human inflammation or immune
CC function, or for treating autoimmune or inflammatory diseases such as
CC inflammatory bowel disease, rheumatoid arthritis, asthma, systemic lupus
CC erythematosus, myasthenia gravis or allergy, atherosclerosis, cancer,
CC diabetes, glomerulonephritis or pancreatitis, or in assessing therapeutic
CC aspects of IL-TIF, chemical therapeutics, anti-IL-TIF antibodies, anti-
CC Zcytor16 antibodies or Zcytor16 soluble receptors. Zcytor16 DNA and the
CC anti-mouse Zcytor16 antibody are useful as probes in detecting gene
CC expression and gene structure, such as in the diagnosis and/or prevention
CC of spontaneous abortions or in monitoring placental health and function.
CC It is also used in gene therapy. The present sequence is a peptide tag
CC used to construct Zcytor16 mammalian expression vector
XX

SO Sequence 6 Aa;

Query Match 100.0%; Score 48; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
|||
1 HHHHHH 6

Search completed: March 21, 2006, 11:04:21
Job time : 226 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:04:41 ; Search time 39 Seconds
(without alignments)
14.803 Million cell updates/sec

Title: US-10-719-523-5
Perfect score: 48
Sequence: 1 HHHHHH 6

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 48 | 100.0 | 16 | 1 LFRCH | his operon leader |
| 2 | 48 | 100.0 | 16 | 2 C90981 | his operon leader |
| 3 | 48 | 100.0 | 16 | 2 A85827 | his operon leader |
| 4 | 48 | 100.0 | 16 | 2 H64698 | histidine and glut |
| 5 | 48 | 100.0 | 60 | 2 C64698 | probable histidine |
| 6 | 48 | 100.0 | 64 | 2 S57787 | hypothetical prote |
| 7 | 48 | 100.0 | 77 | 2 D71821 | probable histidine |
| 8 | 48 | 100.0 | 77 | 2 T16436 | hypothetical prote |
| 9 | 48 | 100.0 | 83 | 2 T16435 | hypothetical prote |
| 10 | 48 | 100.0 | 92 | 2 T34146 | hypothetical prote |
| 11 | 48 | 100.0 | 101 | 2 B44971 | hypothetical prote |
| 12 | 48 | 100.0 | 102 | 2 T30119 | hypothetical prote |
| 13 | 48 | 100.0 | 114 | 2 S37150 | asr2 protein - tom |
| 14 | 48 | 100.0 | 115 | 2 H72583 | hypothetical prote |
| 15 | 48 | 100.0 | 122 | 2 T01558 | auxin-induced prot |
| 16 | 48 | 100.0 | 130 | 2 S14983 | extensin class I (|
| 17 | 48 | 100.0 | 132 | 2 I31913 | gene HOXA1 protein |
| 18 | 48 | 100.0 | 133 | 2 B10242 | stem cell protein |
| 19 | 48 | 100.0 | 136 | 2 T23959 | hypothetical prote |
| 20 | 48 | 100.0 | 139 | 2 T33968 | hypothetical prote |
| 21 | 48 | 100.0 | 140 | 2 T06554 | probable profilin |
| 22 | 48 | 100.0 | 140 | 2 A54523 | histidine-rich pro |
| 23 | 48 | 100.0 | 140 | 2 T19083 | hypothetical prote |
| 24 | 48 | 100.0 | 141 | 2 T06553 | probable profilin |
| 25 | 48 | 100.0 | 143 | 1 B64421 | conserved hypothet |
| 26 | 48 | 100.0 | 172 | 2 T51065 | hypothetical prote |
| 27 | 48 | 100.0 | 176 | 2 T48265 | hypothetical prote |
| 28 | 48 | 100.0 | 180 | 2 E84774 | probable RING zinc |
| 29 | 48 | 100.0 | 192 | 2 T39367 | hypothetical prote |

| | | | | | |
|-----|----|-------|-----|----------|---------------------|
| 30 | 48 | 100.0 | 206 | 2 T25384 | hypothetical prote |
| 31 | 48 | 100.0 | 208 | 2 T24446 | hypothetical prote |
| 32 | 48 | 100.0 | 216 | 2 T53100 | ethAND - mouse |
| 33 | 48 | 100.0 | 219 | 2 T32443 | hypothetical prote |
| 34 | 48 | 100.0 | 222 | 2 T39192 | gene HOXA1 protein |
| 35 | 48 | 100.0 | 230 | 2 T47866 | regulatory protein |
| 36 | 48 | 100.0 | 235 | 2 D89101 | protein F25E5.8 (1 |
| 37 | 48 | 100.0 | 236 | 2 S41512 | Brn-3b protein - m |
| 38 | 48 | 100.0 | 239 | 2 B66346 | PI6F4.1 protein - |
| 39 | 48 | 100.0 | 255 | 2 S41511 | Brn-3a protein - m |
| 40 | 48 | 100.0 | 259 | 2 T51679 | myb-related trans |
| 41 | 48 | 100.0 | 259 | 2 A70359 | hydrogenase expres |
| 42 | 48 | 100.0 | 259 | 2 B66300 | protein F309.30 (1 |
| 43 | 48 | 100.0 | 268 | 2 A56446 | Ig heavy chain V r |
| 44 | 48 | 100.0 | 269 | 2 P96506 | hypothetical prote |
| 45 | 48 | 100.0 | 270 | 2 A26480 | knob protein - mal |
| 46 | 48 | 100.0 | 275 | 2 T02334 | probable urease ac |
| 47 | 48 | 100.0 | 285 | 2 B84766 | probable At-hook D |
| 48 | 48 | 100.0 | 290 | 2 T21868 | hypothetical prote |
| 49 | 48 | 100.0 | 292 | 2 T51171 | transcription fact |
| 50 | 48 | 100.0 | 294 | 2 B69759 | hypothetical prote |
| 51 | 48 | 100.0 | 295 | 2 B84747 | hypothetical prote |
| 52 | 48 | 100.0 | 297 | 2 S23737 | proline-rich prote |
| 53 | 48 | 100.0 | 298 | 2 S41469 | homeotic protein M |
| 54 | 48 | 100.0 | 302 | 2 A56641 | homeotic protein G |
| 55 | 48 | 100.0 | 303 | 2 B49122 | homeobox protein M |
| 56 | 48 | 100.0 | 303 | 2 A56837 | homeotic protein M |
| 57 | 48 | 100.0 | 303 | 2 A48130 | growth arrest-spec |
| 58 | 48 | 100.0 | 305 | 2 A56534 | transcription fact |
| 59 | 48 | 100.0 | 305 | 2 I57039 | genomic screen hom |
| 60 | 48 | 100.0 | 306 | 2 T09067 | extensin-like prot |
| 61 | 48 | 100.0 | 307 | 2 S38152 | hypothetical prote |
| 62 | 48 | 100.0 | 307 | 2 A45581 | distal-less homeob |
| 63 | 48 | 100.0 | 308 | 2 E70392 | cation efflux syst |
| 64 | 48 | 100.0 | 308 | 2 H89839 | hypothetical prote |
| 65 | 48 | 100.0 | 309 | 2 T29293 | hypothetical prote |
| 66 | 48 | 100.0 | 311 | 2 A56235 | transcription acti |
| 67 | 48 | 100.0 | 314 | 2 P96527 | protein F27J15.20 |
| 68 | 48 | 100.0 | 315 | 2 J67572 | sonite Maf1 protei |
| 69 | 48 | 100.0 | 320 | 2 G83839 | hypothetical prote |
| 70 | 48 | 100.0 | 321 | 2 T02987 | myb-related protei |
| 71 | 48 | 100.0 | 323 | 2 I49529 | transcription fact |
| 72 | 48 | 100.0 | 323 | 2 T48160 | transcription fact |
| 73 | 48 | 100.0 | 323 | 2 T51751 | homeotic protein o |
| 74 | 48 | 100.0 | 324 | 2 B85064 | MYB-like protein (|
| 75 | 48 | 100.0 | 326 | 2 D83483 | probable metal tra |
| 76 | 48 | 100.0 | 328 | 2 S45998 | hypothetical prote |
| 77 | 48 | 100.0 | 328 | 2 G02469 | homeotic protein D |
| 78 | 48 | 100.0 | 331 | 2 S78452 | POU-domain protein |
| 79 | 48 | 100.0 | 331 | 2 A30242 | homeotic protein E |
| 80 | 48 | 100.0 | 332 | 2 JH0465 | homeotic protein T |
| 81 | 48 | 100.0 | 333 | 2 T52594 | squamosa promoter |
| 82 | 48 | 100.0 | 335 | 2 G01448 | homeobox protein H |
| 83 | 48 | 100.0 | 348 | 2 T04618 | heat shock protein |
| 84 | 48 | 100.0 | 349 | 2 E95858 | conserved hypothet |
| 85 | 48 | 100.0 | 349 | 2 AH2382 | hypothetical prote |
| 86 | 48 | 100.0 | 350 | 2 A30046 | homeotic protein r |
| 87 | 48 | 100.0 | 351 | 1 K5ZQHL | histidine-rich gly |
| 88 | 48 | 100.0 | 351 | 2 T02070 | hypothetical prote |
| 89 | 48 | 100.0 | 354 | 2 S39406 | homeotic protein o |
| 90 | 48 | 100.0 | 355 | 2 S35345 | oxk1 protein - mou |
| 91 | 48 | 100.0 | 355 | 2 T56547 | homeodomain protei |
| 92 | 48 | 100.0 | 356 | 2 T48354 | hypothetical prote |
| 93 | 48 | 100.0 | 359 | 2 T21705 | hypothetical prote |
| 94 | 48 | 100.0 | 359 | 2 S14283 | transcription fact |
| 95 | 48 | 100.0 | 365 | 2 H87288 | conserved hypothet |
| 96 | 48 | 100.0 | 368 | 2 H96712 | probable DNA-bindi |
| 97 | 48 | 100.0 | 369 | 1 TVFVAR | transforming protei |
| 98 | 48 | 100.0 | 370 | 2 T57555 | c-Maf protein - mo |
| 99 | 48 | 100.0 | 373 | 2 T52182 | probable transcrip |
| 100 | 48 | 100.0 | 374 | 2 H88503 | protein B0361.4 (1 |
| 101 | 48 | 100.0 | 375 | 2 A46390 | cAMP receptor subu |
| 102 | 48 | 100.0 | 376 | 2 A49077 | transcription init |

| | | | | | | |
|-----|----|-------|------|---|--------|---------------------|
| 103 | 48 | 100.0 | 379 | 2 | S42543 | hypothetical prote |
| 104 | 48 | 100.0 | 380 | 2 | S14188 | carbonate dehydrat |
| 105 | 48 | 100.0 | 385 | 1 | OMRTP | seleoprotein P pr |
| 106 | 48 | 100.0 | 385 | 2 | A84696 | probable zinc tran |
| 107 | 48 | 100.0 | 385 | 2 | T19201 | hypothetical prote |
| 108 | 48 | 100.0 | 387 | 2 | A47446 | HNF-3/for head fa |
| 109 | 48 | 100.0 | 390 | 1 | A38565 | polycomb (Pc) prot |
| 110 | 48 | 100.0 | 390 | 1 | TVMVCB | transferring prote |
| 111 | 48 | 100.0 | 391 | 2 | A49645 | transcription fact |
| 112 | 48 | 100.0 | 391 | 2 | H66187 | hypothetical prote |
| 113 | 48 | 100.0 | 391 | 2 | H96572 | protein F12M6.13 |
| 114 | 48 | 100.0 | 392 | 2 | S11998 | finger protein odd |
| 115 | 48 | 100.0 | 401 | 2 | S53405 | probable membrane |
| 116 | 48 | 100.0 | 404 | 2 | D86321 | hypothetical prote |
| 117 | 48 | 100.0 | 404 | 2 | T02396 | hypothetical prote |
| 118 | 48 | 100.0 | 407 | 2 | G84783 | probable pectinest |
| 119 | 48 | 100.0 | 409 | 2 | S60988 | hypothetical prote |
| 120 | 48 | 100.0 | 410 | 2 | I38502 | gene Bm-3b protei |
| 121 | 48 | 100.0 | 411 | 2 | I58156 | Bm-3.2 - mouse |
| 122 | 48 | 100.0 | 414 | 2 | A40350 | transcription repr |
| 123 | 48 | 100.0 | 414 | 2 | A48273 | delta/Y1/NF-E1/UC |
| 124 | 48 | 100.0 | 420 | 2 | T39712 | hypothetical prote |
| 125 | 48 | 100.0 | 420 | 2 | I59234 | octamer binding tr |
| 126 | 48 | 100.0 | 420 | 2 | A48642 | transcription fact |
| 127 | 48 | 100.0 | 425 | 1 | JH0710 | transcription fact |
| 128 | 48 | 100.0 | 427 | 2 | T42516 | neuron-derived rec |
| 129 | 48 | 100.0 | 430 | 2 | S66671 | hypothetical prote |
| 130 | 48 | 100.0 | 434 | 2 | I51436 | HNF-3beta - Africa |
| 131 | 48 | 100.0 | 439 | 2 | T46375 | hypothetical protei |
| 132 | 48 | 100.0 | 444 | 2 | T09474 | forhead protein F |
| 133 | 48 | 100.0 | 448 | 1 | A56018 | transcription fact |
| 134 | 48 | 100.0 | 449 | 1 | S30205 | transcription fact |
| 135 | 48 | 100.0 | 451 | 1 | A40168 | transcription fact |
| 136 | 48 | 100.0 | 451 | 2 | A55909 | transforming prote |
| 137 | 48 | 100.0 | 467 | 2 | G84545 | BHLH transcription |
| 138 | 48 | 100.0 | 467 | 2 | T47773 | hypothetical prote |
| 139 | 48 | 100.0 | 469 | 2 | I37451 | HBf-G2 (HRK-2) pr |
| 140 | 48 | 100.0 | 470 | 2 | T20851 | hypothetical prote |
| 141 | 48 | 100.0 | 471 | 2 | T33997 | hypothetical prote |
| 142 | 48 | 100.0 | 473 | 2 | A54494 | knob-associated hi |
| 143 | 48 | 100.0 | 474 | 2 | A40721 | neuroblast prolif |
| 144 | 48 | 100.0 | 476 | 2 | S57963 | methyl CpG bindi |
| 145 | 48 | 100.0 | 476 | 2 | A54743 | transcription fact |
| 146 | 48 | 100.0 | 477 | 2 | T47753 | hypothetical prote |
| 147 | 48 | 100.0 | 480 | 2 | JH0672 | brain factor 1 pro |
| 148 | 48 | 100.0 | 480 | 2 | S52830 | HMS1 protein - yea |
| 149 | 48 | 100.0 | 492 | 2 | A41907 | methyl-CpG-binding |
| 150 | 48 | 100.0 | 495 | 1 | S31223 | transcription fact |
| 151 | 48 | 100.0 | 496 | 2 | S33791 | ARS-binding protei |
| 152 | 48 | 100.0 | 498 | 2 | T13434 | hypothetical prote |
| 153 | 48 | 100.0 | 499 | 2 | S09880 | hypothetical prote |
| 154 | 48 | 100.0 | 504 | 2 | T33485 | hypothetical prote |
| 155 | 48 | 100.0 | 508 | 2 | S59870 | fork head domain p |
| 156 | 48 | 100.0 | 510 | 2 | T20850 | hypothetical prote |
| 157 | 48 | 100.0 | 525 | 2 | F85227 | hyc-Like protein |
| 158 | 48 | 100.0 | 529 | 2 | T00677 | hypothetical prote |
| 159 | 48 | 100.0 | 533 | 2 | H86282 | protein F10B6.34 [|
| 160 | 48 | 100.0 | 549 | 1 | S19095 | transcription fact |
| 161 | 48 | 100.0 | 550 | 2 | T23760 | hypothetical prote |
| 162 | 48 | 100.0 | 550 | 2 | S63641 | hypothetical prote |
| 163 | 48 | 100.0 | 559 | 2 | T26141 | hypothetical prote |
| 164 | 48 | 100.0 | 564 | 2 | T21983 | hypothetical prote |
| 165 | 48 | 100.0 | 568 | 2 | S15008 | gene disco protein |
| 166 | 48 | 100.0 | 576 | 2 | S69214 | deformed epidermal |
| 167 | 48 | 100.0 | 580 | 2 | T46024 | hypothetical prote |
| 168 | 48 | 100.0 | 601 | 1 | B56564 | transcription fact |
| 169 | 48 | 100.0 | 604 | 2 | T00119 | probable transcrip |
| 170 | 48 | 100.0 | 604 | 2 | S56027 | hypothetical prote |
| 171 | 48 | 100.0 | 604 | 2 | A33369 | homeotic protein B |
| 172 | 48 | 100.0 | 606 | 2 | S13367 | Om(1D) protein - f |
| 173 | 48 | 100.0 | 609 | 2 | A49839 | odd-paired - fruit |
| 174 | 48 | 100.0 | 610 | 2 | A57632 | homeotic protein B |
| 175 | 48 | 100.0 | 620 | 2 | S52494 | protein kinase hom |
| 176 | 48 | 100.0 | 622 | 2 | S71342 | calnexin precursor |
| 177 | 48 | 100.0 | 623 | 1 | S33167 | gene pointed prote |
| 178 | 48 | 100.0 | 625 | 2 | S71930 | neuron-derived rec |
| 179 | 48 | 100.0 | 628 | 2 | JC2493 | neuron derived crp |
| 180 | 48 | 100.0 | 633 | 1 | A26030 | serine/threonine-s |
| 181 | 48 | 100.0 | 633 | 2 | A28412 | histidine-rich pro |
| 182 | 48 | 100.0 | 634 | 2 | A54495 | knob protein precu |
| 183 | 48 | 100.0 | 638 | 2 | D85435 | BEI1-like homeobox |
| 184 | 48 | 100.0 | 654 | 2 | B71623 | knob-associated Hi |
| 185 | 48 | 100.0 | 657 | 2 | A29454 | knob-associated hi |
| 186 | 48 | 100.0 | 661 | 2 | T46364 | hypothetical prote |
| 187 | 48 | 100.0 | 665 | 2 | S02358 | lamin A - African |
| 188 | 48 | 100.0 | 669 | 2 | T07865 | receptor-like prot |
| 189 | 48 | 100.0 | 682 | 2 | A44493 | serum-inducible ki |
| 190 | 48 | 100.0 | 688 | 2 | T23108 | hypothetical prote |
| 191 | 48 | 100.0 | 717 | 2 | S38177 | SSV7 protein homol |
| 192 | 48 | 100.0 | 735 | 2 | T45059 | hypothetical prote |
| 193 | 48 | 100.0 | 754 | 2 | JC4898 | Down-syndrome-crit |
| 194 | 48 | 100.0 | 758 | 2 | A29253 | finger protein hun |
| 195 | 48 | 100.0 | 766 | 2 | T02702 | hypothetical prote |
| 196 | 48 | 100.0 | 776 | 2 | S57702 | hypothetical prote |
| 197 | 48 | 100.0 | 791 | 2 | T41573 | hypothetical prote |
| 198 | 48 | 100.0 | 794 | 2 | T39171 | probable peroxisom |
| 199 | 48 | 100.0 | 802 | 2 | T33295 | hypothetical prote |
| 200 | 48 | 100.0 | 816 | 2 | S05548 | gap protein hunchb |
| 201 | 48 | 100.0 | 819 | 2 | D85440 | Cu2+-transporting |
| 202 | 48 | 100.0 | 820 | 1 | TWCTPR | protein-tyrosine k |
| 203 | 48 | 100.0 | 820 | 2 | I48347 | protein-tyrosine k |
| 204 | 48 | 100.0 | 828 | 2 | T08423 | Axin homolog Ax11 |
| 205 | 48 | 100.0 | 832 | 2 | T17291 | hypothetical prote |
| 206 | 48 | 100.0 | 845 | 2 | T46347 | hypothetical prote |
| 207 | 48 | 100.0 | 860 | 2 | T23296 | hypothetical prote |
| 208 | 48 | 100.0 | 895 | 2 | JC7089 | zinc finger bindi |
| 209 | 48 | 100.0 | 896 | 2 | T51891 | hypothetical prote |
| 210 | 48 | 100.0 | 896 | 2 | B43817 | transforming prote |
| 211 | 48 | 100.0 | 906 | 2 | A43817 | transforming prote |
| 212 | 48 | 100.0 | 946 | 2 | S48255 | probable membrane |
| 213 | 48 | 100.0 | 950 | 2 | S27473 | URSL1 protein - sm |
| 214 | 48 | 100.0 | 972 | 2 | S35521 | DNA topoisomerase |
| 215 | 48 | 100.0 | 991 | 2 | C96764 | hypothetical prote |
| 216 | 48 | 100.0 | 1001 | 2 | T28897 | hypothetical prote |
| 217 | 48 | 100.0 | 1019 | 2 | T00117 | dve protein - fruit |
| 218 | 48 | 100.0 | 1057 | 2 | T04874 | hypothetical prote |
| 219 | 48 | 100.0 | 1113 | 2 | T26954 | hypothetical prote |
| 220 | 48 | 100.0 | 1116 | 2 | S57382 | hypothetical prote |
| 221 | 48 | 100.0 | 1145 | 2 | T33606 | hypothetical prote |
| 222 | 48 | 100.0 | 1166 | 2 | T13958 | synGAP-b1 protein |
| 223 | 48 | 100.0 | 1172 | 2 | F84572 | probable cadmium-t |
| 224 | 48 | 100.0 | 1172 | 2 | T00065 | hypothetical prote |
| 225 | 48 | 100.0 | 1180 | 2 | S69205 | ectipe a/b protein |
| 226 | 48 | 100.0 | 1196 | 2 | T14108 | SH3-containing pro |
| 227 | 48 | 100.0 | 1212 | 2 | T13804 | she protein - fruit |
| 228 | 48 | 100.0 | 1225 | 2 | T16346 | hypothetical prote |
| 229 | 48 | 100.0 | 1245 | 2 | T49815 | related to multi fu |
| 230 | 48 | 100.0 | 1249 | 2 | T14270 | Rae-GTPase activat |
| 231 | 48 | 100.0 | 1252 | 2 | S36016 | oocyst wall protei |
| 232 | 48 | 100.0 | 1273 | 2 | T00338 | hypothetical prote |
| 233 | 48 | 100.0 | 1291 | 2 | T13389 | hypothetical prote |
| 234 | 48 | 100.0 | 1293 | 2 | T14259 | ras GTPase-activat |
| 235 | 48 | 100.0 | 1305 | 2 | A40879 | phospholipase C (E |
| 236 | 48 | 100.0 | 1312 | 1 | B40879 | phospholipase C (E |
| 237 | 48 | 100.0 | 1336 | 2 | T18287 | protein-Lysozyme K |
| 238 | 48 | 100.0 | 1358 | 2 | S51389 | ROM2 protein - yea |
| 239 | 48 | 100.0 | 1370 | 2 | T19188 | hypothetical prote |
| 240 | 48 | 100.0 | 1398 | 2 | T13741 | hypothetical prote |
| 241 | 48 | 100.0 | 1441 | 2 | T33717 | CRAG protein - fru |
| 242 | 48 | 100.0 | 1465 | 2 | T23056 | chromodomain helic |
| 243 | 48 | 100.0 | 1557 | 2 | T23160 | protein CNK - fruit |
| 244 | 48 | 100.0 | 1560 | 2 | T00080 | hypothetical prote |
| 245 | 48 | 100.0 | 1585 | 2 | T31611 | hypothetical prote |
| 246 | 48 | 100.0 | 1597 | 1 | BVFESL | sol protein, large |
| 247 | 48 | 100.0 | 1597 | 2 | T08428 | gene small optic l |
| 248 | 48 | 100.0 | 1664 | 2 | T18216 | integrin-like pro |

| | | | | | | | | | | | | | |
|-----|----|-------|------|---|--------|---------------------|-----|----|------|------|---|--------|---------------------|
| 249 | 48 | 100.0 | 1753 | 2 | S30855 | hypothetical prote | 322 | 41 | 85.4 | 1214 | 2 | UC2069 | zinc-finger protei |
| 250 | 48 | 100.0 | 1785 | 2 | T21558 | hypothetical prote | 323 | 41 | 85.4 | 1611 | 2 | T38236 | hypothetical prote |
| 251 | 48 | 100.0 | 1820 | 2 | T19430 | hypothetical prote | 324 | 40 | 83.3 | 82 | 2 | A29653 | histidine-rich pro |
| 252 | 48 | 100.0 | 1887 | 2 | C66478 | protein F1504.13 l | 325 | 40 | 83.3 | 102 | 2 | AB2009 | hypothetical prote |
| 253 | 48 | 100.0 | 1929 | 2 | T21559 | hypothetical prote | 326 | 40 | 83.3 | 107 | 2 | A29995 | probatine p2 precu |
| 254 | 48 | 100.0 | 1958 | 2 | B40505 | hypothetical prote | 327 | 40 | 83.3 | 113 | 2 | S66936 | probable membrane |
| 255 | 48 | 100.0 | 2212 | 2 | A41098 | calcium channel pr | 328 | 40 | 83.3 | 115 | 2 | T06588 | abscisic stress ri |
| 256 | 48 | 100.0 | 2248 | 1 | D42088 | adenylate cyclase | 329 | 40 | 83.3 | 117 | 2 | T28394 | hypothetical prote |
| 257 | 48 | 100.0 | 2254 | 2 | T09053 | low voltage-activa | 330 | 40 | 83.3 | 124 | 2 | C72205 | conserved hypothet |
| 258 | 48 | 100.0 | 2273 | 2 | I46477 | calcium channel B | 331 | 40 | 83.3 | 128 | 1 | H69052 | conserved hypothet |
| 259 | 48 | 100.0 | 2326 | 2 | B47447 | calcium channel pr | 332 | 40 | 83.3 | 130 | 2 | F70585 | probable fuib prot |
| 260 | 48 | 100.0 | 2396 | 2 | T13714 | kakapo gene protei | 333 | 40 | 83.3 | 131 | 2 | B53024 | Leydig insulin-lik |
| 261 | 48 | 100.0 | 2416 | 2 | T13825 | adenomatous polyp | 334 | 40 | 83.3 | 133 | 2 | T45733 | transcription regu |
| 262 | 48 | 100.0 | 2424 | 2 | I46480 | calcium channel B | 335 | 40 | 83.3 | 138 | 2 | D83824 | transcription regu |
| 263 | 48 | 100.0 | 2494 | 2 | T51023 | hypothetical prote | 336 | 40 | 83.3 | 138 | 2 | T21299 | hypothetical prote |
| 264 | 48 | 100.0 | 3345 | 2 | T13423 | hypothetical prote | 337 | 40 | 83.3 | 141 | 2 | AE1255 | transcription regu |
| 265 | 42 | 87.5 | 207 | 2 | T30118 | hypothetical prote | 338 | 40 | 83.3 | 141 | 2 | T46654 | transcription regu |
| 266 | 42 | 87.5 | 209 | 2 | F84563 | hypothetical prote | 339 | 40 | 83.3 | 141 | 2 | AB1618 | transcription regu |
| 267 | 42 | 87.5 | 244 | 2 | A84687 | probable homeodoma | 340 | 40 | 83.3 | 145 | 2 | H69954 | transcription regu |
| 268 | 42 | 87.5 | 271 | 2 | JC6553 | transcription fact | 341 | 40 | 83.3 | 145 | 2 | AE3531 | zinc uptake regula |
| 269 | 42 | 87.5 | 280 | 2 | E96589 | hypothetical prote | 342 | 40 | 83.3 | 146 | 2 | A95254 | adc operon repres |
| 270 | 42 | 87.5 | 309 | 2 | G96782 | hypothetical prote | 343 | 40 | 83.3 | 146 | 2 | T46753 | repressor protein |
| 271 | 42 | 87.5 | 319 | 2 | T40156 | sun family protein | 344 | 40 | 83.3 | 147 | 2 | T01039 | hypothetical prote |
| 272 | 42 | 87.5 | 370 | 2 | T23553 | hypothetical prote | 345 | 40 | 83.3 | 148 | 2 | G83681 | urease accessory p |
| 273 | 42 | 87.5 | 391 | 2 | T18604 | hypothetical prote | 346 | 40 | 83.3 | 149 | 2 | A54530 | eggshell protein - |
| 274 | 42 | 87.5 | 433 | 2 | S51773 | transcription fact | 347 | 40 | 83.3 | 151 | 2 | AE2017 | cell wall-binding |
| 275 | 42 | 87.5 | 507 | 2 | T49519 | hypothetical prote | 348 | 40 | 83.3 | 152 | 2 | T51796 | hypothetical prote |
| 276 | 42 | 87.5 | 511 | 2 | T26124 | hypothetical prote | 349 | 40 | 83.3 | 161 | 2 | B43719 | ureB protein - pro |
| 277 | 42 | 87.5 | 638 | 2 | E84799 | similar to axl 1 p | 350 | 40 | 83.3 | 165 | 2 | S76947 | hypothetical prote |
| 278 | 42 | 87.5 | 661 | 2 | T27016 | hypothetical prote | 351 | 40 | 83.3 | 166 | 2 | G98118 | hypothetical prote |
| 279 | 42 | 87.5 | 680 | 2 | T10656 | Probable ABC-type | 352 | 40 | 83.3 | 169 | 2 | T02081 | ABA- and ripening- |
| 280 | 42 | 87.5 | 723 | 2 | I39066 | N-methyl-D-asparta | 353 | 40 | 83.3 | 188 | 2 | H82933 | hypothetical prote |
| 281 | 42 | 87.5 | 824 | 2 | I50618 | C-fps proto onco | 354 | 40 | 83.3 | 196 | 2 | G85435 | TINY-like protein |
| 282 | 42 | 87.5 | 873 | 1 | TYRPF | protein-tyrosine k | 355 | 40 | 83.3 | 207 | 2 | H85070 | hypothetical prote |
| 283 | 42 | 87.5 | 1482 | 2 | I49704 | glutamate receptor | 356 | 40 | 83.3 | 217 | 2 | T06455 | Myo26 protein - ga |
| 284 | 42 | 87.5 | 1484 | 2 | B43274 | N-methyl-D-asparta | 357 | 40 | 83.3 | 220 | 2 | UC2337 | T-cell receptor al |
| 285 | 42 | 87.5 | 1484 | 2 | S52086 | N-methyl-D-asparta | 358 | 40 | 83.3 | 222 | 2 | C84866 | probable PRG1-lik |
| 286 | 42 | 87.5 | 1557 | 2 | T02859 | probable serine/th | 359 | 40 | 83.3 | 235 | 2 | S55883 | CCHH finger protei |
| 287 | 42 | 87.5 | 1839 | 1 | OYBYK | adenylate cyclase | 360 | 40 | 83.3 | 240 | 2 | T45727 | hypothetical prote |
| 288 | 42 | 87.5 | 1941 | 2 | T23979 | hypothetical prote | 361 | 40 | 83.3 | 245 | 2 | T23153 | hypothetical prote |
| 289 | 42 | 87.5 | 1943 | 2 | T23986 | hypothetical prote | 362 | 40 | 83.3 | 251 | 2 | T06387 | knotted I class ho |
| 290 | 41 | 85.4 | 66 | 2 | T06697 | hypothetical prote | 363 | 40 | 83.3 | 259 | 2 | T52619 | TINY-like protein |
| 291 | 41 | 85.4 | 134 | 2 | S71249 | embryonic protein | 364 | 40 | 83.3 | 262 | 2 | B82120 | zinc ABC transport |
| 292 | 41 | 85.4 | 136 | 2 | A89936 | hypothetical prote | 365 | 40 | 83.3 | 264 | 2 | T52104 | GATrA-binding trans |
| 293 | 41 | 85.4 | 140 | 2 | T27059 | hypothetical prote | 366 | 40 | 83.3 | 265 | 2 | T49008 | hypothetical prote |
| 294 | 41 | 85.4 | 143 | 2 | S66340 | phloem-specific pr | 367 | 40 | 83.3 | 270 | 2 | S74993 | hypothetical prote |
| 295 | 41 | 85.4 | 197 | 2 | AE1154 | methyltransferase | 368 | 40 | 83.3 | 274 | 2 | T29574 | hypothetical prote |
| 296 | 41 | 85.4 | 199 | 2 | A11512 | weakly methyltrans | 369 | 40 | 83.3 | 274 | 2 | A64978 | hypothetical prote |
| 297 | 41 | 85.4 | 268 | 2 | B64066 | probable ABC trans | 370 | 40 | 83.3 | 276 | 2 | T29894 | hypothetical prote |
| 298 | 41 | 85.4 | 281 | 2 | AB1894 | hydrogenase expres | 371 | 40 | 83.3 | 279 | 2 | S54157 | extensin-like prot |
| 299 | 41 | 85.4 | 306 | 2 | S59540 | heat shock transcr | 372 | 40 | 83.3 | 279 | 2 | H80992 | hypothetical prote |
| 300 | 41 | 85.4 | 329 | 2 | T45972 | hypothetical prote | 373 | 40 | 83.3 | 283 | 2 | C65838 | hypothetical prote |
| 301 | 41 | 85.4 | 335 | 2 | T34086 | hypothetical prote | 374 | 40 | 83.3 | 285 | 2 | S75853 | hypothetical prote |
| 302 | 41 | 85.4 | 356 | 2 | T06756 | hypothetical prote | 375 | 40 | 83.3 | 292 | 2 | T00829 | muschel protein - |
| 303 | 41 | 85.4 | 367 | 2 | S46727 | hypothetical prote | 376 | 40 | 83.3 | 293 | 2 | T05153 | hypothetical prote |
| 304 | 41 | 85.4 | 368 | 2 | G88635 | protein W09G12.7 l | 377 | 40 | 83.3 | 293 | 2 | D84558 | probable homeodoma |
| 305 | 41 | 85.4 | 370 | 2 | S59539 | heat shock transcr | 378 | 40 | 83.3 | 298 | 2 | H84785 | probable MYB famli |
| 306 | 41 | 85.4 | 371 | 2 | F85434 | geranylgeranyl pyr | 379 | 40 | 83.3 | 298 | 2 | AE3531 | high-affinity zinc |
| 307 | 41 | 85.4 | 386 | 2 | T09598 | cyclin 4, D-type - | 380 | 40 | 83.3 | 302 | 2 | AE7369 | copper-binding pro |
| 308 | 41 | 85.4 | 551 | 2 | T49922 | pectin methyl ester | 381 | 40 | 83.3 | 303 | 2 | H97212 | co/Zn/Cd efflux sy |
| 309 | 41 | 85.4 | 590 | 2 | T01237 | hypothetical prote | 382 | 40 | 83.3 | 303 | 2 | S23440 | hypothetical prote |
| 310 | 41 | 85.4 | 632 | 2 | T32454 | hypothetical prote | 383 | 40 | 83.3 | 306 | 2 | T44684 | hypothetical prote |
| 311 | 41 | 85.4 | 658 | 2 | T04219 | hypothetical prote | 384 | 40 | 83.3 | 306 | 2 | A88040 | protein F47F6.1 li |
| 312 | 41 | 85.4 | 669 | 2 | S14535 | asparagine-rich pr | 385 | 40 | 83.3 | 312 | 2 | A10138 | probable cation tr |
| 313 | 41 | 85.4 | 762 | 2 | C96653 | hypothetical prote | 386 | 40 | 83.3 | 315 | 2 | T50561 | SINA1 protein (lmp |
| 314 | 41 | 85.4 | 884 | 2 | C98402 | protein H05C05.1 l | 387 | 40 | 83.3 | 317 | 2 | AH0351 | hypothetical prote |
| 315 | 41 | 85.4 | 887 | 1 | IUCHCL | E-cadherin precurs | 388 | 40 | 83.3 | 324 | 2 | T22580 | hypothetical prote |
| 316 | 41 | 85.4 | 1028 | 2 | A56038 | DNA-binding protei | 389 | 40 | 83.3 | 326 | 2 | B84812 | hypothetical prote |
| 317 | 41 | 85.4 | 1036 | 1 | A34755 | nitrogen regulator | 390 | 40 | 83.3 | 328 | 2 | AH3531 | high-affinity zinc |
| 318 | 41 | 85.4 | 1046 | 2 | S67786 | hypothetical prote | 391 | 40 | 83.3 | 329 | 2 | D82449 | conserved hypothet |
| 319 | 41 | 85.4 | 1087 | 2 | T49496 | hypothetical prote | 392 | 40 | 83.3 | 330 | 2 | T05717 | probable extensin |
| 320 | 41 | 85.4 | 1198 | 2 | T42223 | ladder protein - C | 393 | 40 | 83.3 | 331 | 1 | S69190 | myd-related protei |
| 321 | 41 | 85.4 | 1213 | 2 | S16356 | ovo protein - fru1 | 394 | 40 | 83.3 | 334 | 2 | H96791 | unknown protein Fl |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|------|---|--------|---------------------|
| 395 | 40 | 83.3 | 341 | 2 | E83340 | hypothetical prote | 468 | 40 | 83.3 | 822 | 1 | TVHUF | protein-tyrosine k |
| 396 | 40 | 83.3 | 341 | 2 | T51957 | metalloproteinase | 469 | 40 | 83.3 | 839 | 1 | TQZMC | probable transposa |
| 397 | 40 | 83.3 | 342 | 2 | G84885 | probable metallopr | 470 | 40 | 83.3 | 841 | 1 | S2462 | probable 3',5'-cyc |
| 398 | 40 | 83.3 | 343 | 2 | T29547 | hypothetical prote | 471 | 40 | 83.3 | 880 | 2 | S56828 | finger protein yJL |
| 399 | 40 | 83.3 | 353 | 2 | AB2396 | hypothetical prote | 472 | 40 | 83.3 | 884 | 1 | ITMSCR | E-cadherin precurs |
| 400 | 40 | 83.3 | 360 | 2 | T04535 | hypothetical prote | 473 | 40 | 83.3 | 884 | 2 | S34438 | uvomoulin - mouse |
| 401 | 40 | 83.3 | 361 | 2 | B84716 | hypothetical prote | 474 | 40 | 83.3 | 918 | 2 | D8854 | protein R08D7.6 [1 |
| 402 | 40 | 83.3 | 361 | 2 | JQ2379 | homeobox 1 protein | 475 | 40 | 83.3 | 960 | 2 | G84652 | probable receptor- |
| 403 | 40 | 83.3 | 364 | 2 | T02801 | hypothetical prote | 476 | 40 | 83.3 | 963 | 2 | T48707 | related to regulat |
| 404 | 40 | 83.3 | 374 | 2 | AB1943 | probable membrane | 477 | 40 | 83.3 | 971 | 2 | T24866 | hypothetical prote |
| 405 | 40 | 83.3 | 377 | 2 | A35795 | hypothetical prote | 478 | 40 | 83.3 | 1014 | 2 | T13476 | hypothetical prote |
| 406 | 40 | 83.3 | 380 | 2 | T10442 | carbonate dehydrat | 479 | 40 | 83.3 | 1040 | 2 | T29092 | TSC-22 protein hom |
| 407 | 40 | 83.3 | 380 | 2 | H83994 | seleoprotein P pr | 480 | 40 | 83.3 | 1057 | 2 | T25396 | hypothetical prote |
| 408 | 40 | 83.3 | 381 | 1 | A47327 | seleoprotein P pr | 481 | 40 | 83.3 | 1090 | 2 | A41696 | regulatory protein |
| 409 | 40 | 83.3 | 383 | 1 | S76964 | hypothetical prote | 482 | 40 | 83.3 | 1184 | 2 | S50832 | atrophin-1 - human |
| 410 | 40 | 83.3 | 388 | 2 | AG3256 | cobw protein limpo | 483 | 40 | 83.3 | 1184 | 2 | G01763 | atrophin-1 - human |
| 411 | 40 | 83.3 | 395 | 2 | S43344 | sex-determining pr | 484 | 40 | 83.3 | 1201 | 2 | G86441 | unknown protein [1 |
| 412 | 40 | 83.3 | 395 | 2 | S35565 | sex-determining pr | 485 | 40 | 83.3 | 1246 | 2 | T51085 | related to protein |
| 413 | 40 | 83.3 | 398 | 2 | T02681 | probable zinc tran | 486 | 40 | 83.3 | 1299 | 1 | S66119 | membrane protein p |
| 414 | 40 | 83.3 | 402 | 2 | A72312 | conserved hypotet | 487 | 40 | 83.3 | 1307 | 2 | G36711 | unknown protein, 9 |
| 415 | 40 | 83.3 | 408 | 2 | P85023 | probable potassium | 488 | 40 | 83.3 | 1398 | 2 | S56814 | microtubule-intera |
| 416 | 40 | 83.3 | 411 | 2 | AG3003 | conserved hypotet | 489 | 40 | 83.3 | 1541 | 2 | T02831 | AAA protein L4171. |
| 417 | 40 | 83.3 | 411 | 2 | B98280 | hypothetical prote | 490 | 40 | 83.3 | 1557 | 2 | T18412 | lipid-binding prot |
| 418 | 40 | 83.3 | 415 | 2 | B84858 | hypothetical prote | 491 | 40 | 83.3 | 2163 | 2 | T15276 | hypothetical prote |
| 419 | 40 | 83.3 | 416 | 2 | T31486 | hypothetical prote | 492 | 40 | 83.3 | 2237 | 2 | T45115 | N-type calcium cha |
| 420 | 40 | 83.3 | 419 | 1 | WJFFH2 | homeotic protein H | 493 | 40 | 83.3 | 2288 | 2 | S41080 | calcium channel al |
| 421 | 40 | 83.3 | 426 | 2 | AH1831 | hypothetical prote | 494 | 40 | 83.3 | 2336 | 2 | A45386 | omega-conotoxin-se |
| 422 | 40 | 83.3 | 426 | 2 | A26330 | hypothetical prote | 495 | 40 | 83.3 | 2339 | 2 | A42566 | omega-conotoxin-se |
| 423 | 40 | 83.3 | 427 | 2 | A32372 | female-specific do | 496 | 40 | 83.3 | 2342 | 2 | T13412 | hypothetical prote |
| 424 | 40 | 83.3 | 427 | 2 | T04869 | transforming prote | 497 | 40 | 81.2 | 143 | 2 | A86819 | hypothetical prote |
| 425 | 40 | 83.3 | 430 | 2 | T04678 | hypothetical prote | 498 | 40 | 81.2 | 167 | 2 | B3034 | urase accessory p |
| 426 | 40 | 83.3 | 439 | 2 | P86592 | probable zinc fing | 499 | 39 | 81.2 | 191 | 2 | A02871 | urase accessory p |
| 427 | 40 | 83.3 | 461 | 2 | S34472 | Mpf-1 protein - mo | 500 | 40 | 81.2 | 196 | 2 | T26943 | hypothetical prote |
| 428 | 40 | 83.3 | 462 | 2 | C84473 | probable protein k | 501 | 39 | 81.2 | 198 | 2 | E86261 | FltK23.6 protein - |
| 429 | 40 | 83.3 | 466 | 2 | A88868 | protein T2385.3 [i | 502 | 39 | 81.2 | 201 | 2 | AH3332 | urase accessory p |
| 430 | 40 | 83.3 | 471 | 2 | S41768 | splicing factor ho | 503 | 39 | 81.2 | 222 | 2 | P97647 | urase accessory p |
| 431 | 40 | 83.3 | 471 | 2 | G01211 | 54 kDa protein - h | 504 | 39 | 81.2 | 247 | 2 | P81410 | hydrogenase isoenz |
| 432 | 40 | 83.3 | 472 | 2 | A26357 | homeotic protein C | 505 | 39 | 81.2 | 248 | 2 | D56535 | RING-H2 finger pro |
| 433 | 40 | 83.3 | 473 | 2 | T04225 | hypothetical prote | 506 | 39 | 81.2 | 251 | 2 | P64745 | probable hydroxyc |
| 434 | 40 | 83.3 | 473 | 2 | A54691 | occamer-binding pr | 507 | 40 | 81.2 | 251 | 2 | H90654 | probable hydroxyc |
| 435 | 40 | 83.3 | 490 | 2 | T25147 | hypothetical prote | 508 | 39 | 81.2 | 251 | 2 | H85505 | probable hydroxyc |
| 436 | 40 | 83.3 | 491 | 2 | H84840 | hypothetical prote | 509 | 39 | 81.2 | 252 | 2 | A82102 | probable hydroxyc |
| 437 | 40 | 83.3 | 491 | 2 | C86390 | hypothetical prote | 510 | 39 | 81.2 | 258 | 2 | G83417 | probable hydroxyc |
| 438 | 40 | 83.3 | 493 | 2 | S52421 | amino acid transpo | 511 | 39 | 81.2 | 269 | 2 | B82959 | zinc transport pro |
| 439 | 40 | 83.3 | 496 | 2 | T33496 | hypothetical prote | 512 | 39 | 81.2 | 275 | 2 | T52333 | urase accessory p |
| 440 | 40 | 83.3 | 506 | 2 | A86169 | hypothetical prote | 513 | 39 | 81.2 | 305 | 2 | JN0647 | hydrogenase expres |
| 441 | 40 | 83.3 | 507 | 2 | C71412 | probable hydroxypr | 514 | 39 | 81.2 | 310 | 2 | T00609 | hypothetical prote |
| 442 | 40 | 83.3 | 510 | 2 | A33380 | nuclear protein tk | 515 | 39 | 81.2 | 311 | 2 | B85577 | probable transport |
| 443 | 40 | 83.3 | 513 | 2 | S69181 | protein disulfide- | 516 | 39 | 81.2 | 312 | 2 | A86279 | Fla117.21 protein |
| 444 | 40 | 83.3 | 515 | 1 | T38946 | phosphoprotein pho | 517 | 39 | 81.2 | 313 | 1 | H64810 | yBgr protein - Bac |
| 445 | 40 | 83.3 | 516 | 2 | T01419 | cellulase (BC 3.2. | 518 | 40 | 81.2 | 313 | 2 | D90726 | probable transport |
| 446 | 40 | 83.3 | 529 | 2 | H81650 | conserved hypotet | 519 | 39 | 81.2 | 332 | 2 | C36882 | hypothetical prote |
| 447 | 40 | 83.3 | 531 | 2 | H72040 | conserved hypotet | 520 | 39 | 81.2 | 355 | 2 | T47235 | sex determining pr |
| 448 | 40 | 83.3 | 531 | 2 | G86583 | CT632 Hypothetical | 521 | 39 | 81.2 | 356 | 2 | T43145 | hypothetical prote |
| 449 | 40 | 83.3 | 532 | 2 | T07903 | tubulin delta chai | 522 | 39 | 81.2 | 372 | 2 | AC3548 | low affinity zinc |
| 450 | 40 | 83.3 | 549 | 2 | B32372 | male-specific doub | 523 | 39 | 81.2 | 374 | 2 | A96798 | hypothetical prote |
| 451 | 40 | 83.3 | 571 | 2 | T01511 | hypothetical prote | 524 | 39 | 81.2 | 375 | 2 | AB3110 | conserved hypotet |
| 452 | 40 | 83.3 | 571 | 2 | D96516 | Fl6b3.14 [imported | 525 | 39 | 81.2 | 375 | 2 | B98177 | hypothetical prote |
| 453 | 40 | 83.3 | 576 | 2 | A26628 | homeotic protein I | 526 | 39 | 81.2 | 434 | 2 | C96515 | hypothetical prote |
| 454 | 40 | 83.3 | 586 | 2 | T04716 | hypothetical prote | 527 | 39 | 81.2 | 444 | 2 | P96836 | hypothetical prote |
| 455 | 40 | 83.3 | 602 | 2 | P84432 | probable C2H2-type | 528 | 39 | 81.2 | 458 | 2 | B39535 | transcription fact |
| 456 | 40 | 83.3 | 612 | 2 | A54282 | reversed polarity | 529 | 39 | 81.2 | 459 | 1 | B54258 | transcription fact |
| 457 | 40 | 83.3 | 624 | 2 | T05090 | hypothetical prote | 530 | 39 | 81.2 | 466 | 2 | S19365 | hypothetical prote |
| 458 | 40 | 83.3 | 640 | 2 | A41726 | homeotic protein B | 531 | 39 | 81.2 | 477 | 2 | T29592 | hypothetical prote |
| 459 | 40 | 83.3 | 642 | 2 | S27806 | homeotic protein B | 532 | 39 | 81.2 | 509 | 2 | A53741 | transcription fact |
| 460 | 40 | 83.3 | 654 | 2 | T08600 | hypothetical prote | 533 | 39 | 81.2 | 537 | 2 | JH0415 | synapogaminin o-p65 |
| 461 | 40 | 83.3 | 657 | 2 | S05517 | lamn - chicken | 534 | 39 | 81.2 | 617 | 2 | A90644 | probable membrane |
| 462 | 40 | 83.3 | 661 | 2 | P83342 | probable cation-cr | 535 | 39 | 81.2 | 617 | 2 | A85495 | probable membrane |
| 463 | 40 | 83.3 | 699 | 2 | A54660 | histidine rich cal | 536 | 39 | 81.2 | 617 | 2 | E64734 | yach protein - Bac |
| 464 | 40 | 83.3 | 719 | 2 | C88216 | protein B0495.2 [i | 537 | 39 | 81.2 | 617 | 2 | T23197 | hypothetical prote |
| 465 | 40 | 83.3 | 752 | 2 | G03273 | LIV-1 protein - hu | 538 | 39 | 81.2 | 623 | 2 | T28958 | hypothetical prote |
| 466 | 40 | 83.3 | 759 | 2 | S67164 | probable membrane | 539 | 39 | 81.2 | 642 | 2 | T45904 | protein kinase-1lk |
| 467 | 40 | 83.3 | 808 | 2 | T51232 | scarecrow-like pro | 540 | 39 | 81.2 | 642 | 2 | T47896 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|------|------|------|---|--------|---------------------|
| 541 | 39 | 81.2 | 1016 | 1 | A46079 | protein kinase C (| 614 | 37 | 77.1 | 315 | 2 | T04624 | hypothetical prote |
| 542 | 39 | 81.2 | 2026 | 1 | OVBX | adenylate cyclase | 615 | 37 | 77.1 | 356 | 2 | G84904 | probable DOF zinc |
| 543 | 39 | 81.2 | 2167 | 2 | S50658 | bud emergence proc | 616 | 37 | 77.1 | 389 | 2 | C96830 | unknown protein P1 |
| 544 | 39 | 81.2 | 3119 | 2 | T18414 | protein g377 - mal | 617 | 37 | 77.1 | 429 | 2 | S01919 | knirps protein - f |
| 545 | 38 | 79.2 | 86 | 2 | T16437 | hypothetical prote | 618 | 37 | 77.1 | 431 | 2 | T51266 | hypothetical prote |
| 546 | 38 | 79.2 | 99 | 2 | JH0238 | hypothetical 11.6K | 619 | 37 | 77.1 | 432 | 2 | B96515 | hypothetical prote |
| 547 | 38 | 79.2 | 116 | 2 | T46320 | hypothetical prote | 620 | 37 | 77.1 | 433 | 2 | C97682 | probable intracell |
| 548 | 38 | 79.2 | 147 | 2 | T16440 | hypothetical prote | 621 | 37 | 77.1 | 443 | 2 | B84449 | hypothetical prote |
| 549 | 38 | 79.2 | 158 | 2 | D16138 | urea protein - xle | 622 | 37 | 77.1 | 477 | 2 | T45722 | hypothetical prote |
| 550 | 38 | 79.2 | 160 | 2 | A81075 | PKB-type peptidyl | 623 | 37 | 77.1 | 523 | 2 | S67271 | hypothetical prote |
| 551 | 38 | 79.2 | 199 | 2 | T48099 | hypothetical prote | 624 | 37 | 77.1 | 529 | 2 | T08684 | hypothetical prote |
| 552 | 38 | 79.2 | 273 | 2 | T49442 | hypothetical prote | 625 | 37 | 77.1 | 537 | 2 | T23961 | hypothetical prote |
| 553 | 38 | 79.2 | 290 | 2 | T49631 | probable Ni-bindin | 626 | 37 | 77.1 | 637 | 2 | S66953 | hypothetical prote |
| 554 | 38 | 79.2 | 295 | 2 | A48013 | proline-rich prote | 627 | 37 | 77.1 | 643 | 2 | T27429 | hypothetical prote |
| 555 | 38 | 79.2 | 297 | 2 | A35874 | myogenic factor 1 | 628 | 37 | 77.1 | 798 | 2 | S20881 | hypothetical prote |
| 556 | 38 | 79.2 | 299 | 2 | S32874 | hyde protein - Rhi | 629 | 37 | 77.1 | 832 | 2 | T08422 | hypothetical prote |
| 557 | 38 | 79.2 | 303 | 2 | AG1396 | cation transport p | 630 | 37 | 77.1 | 834 | 2 | UC7993 | ary1 hydrocarbon r |
| 558 | 38 | 79.2 | 303 | 2 | AB1772 | cation transport p | 631 | 37 | 77.1 | 883 | 2 | T33656 | hypothetical prote |
| 559 | 38 | 79.2 | 311 | 2 | A53808 | homeotic protein c | 632 | 37 | 77.1 | 901 | 2 | JC6093 | dead ringier nuclea |
| 560 | 38 | 79.2 | 313 | 2 | A46233 | Flat element-bindi | 633 | 37 | 77.1 | 982 | 2 | T19526 | hypothetical prote |
| 561 | 38 | 79.2 | 325 | 2 | T44365 | cation-efflux svet | 634 | 37 | 77.1 | 1733 | 1 | B45344 | probable nuclear a |
| 562 | 38 | 79.2 | 325 | 2 | G90008 | hypothetical prote | 635 | 37 | 77.1 | 1762 | 2 | T03222 | probable polykeid |
| 563 | 38 | 79.2 | 335 | 2 | T52249 | probable basic hel | 636 | 37 | 77.1 | 2101 | 2 | S57245 | insulin receptor (|
| 564 | 38 | 79.2 | 336 | 1 | S75947 | hypothetical prote | 637 | 37 | 77.1 | 2148 | 1 | A56081 | insulin receptor - |
| 565 | 38 | 79.2 | 338 | 2 | T36785 | hypothetical prote | 638 | 37 | 76.0 | 237 | 2 | T09848 | H+-exporting ATPas |
| 566 | 38 | 79.2 | 346 | 2 | AH1189 | B. subtilis ycgr p | 639 | 36.5 | 76.0 | 346 | 2 | T32585 | hypothetical prote |
| 567 | 38 | 79.2 | 346 | 2 | AT1547 | B. subtilis ycgr p | 640 | 36.5 | 76.0 | 368 | 2 | T32587 | hypothetical prote |
| 568 | 38 | 79.2 | 349 | 2 | A63365 | silk gland factor- | 641 | 36.5 | 76.0 | 482 | 2 | S22654 | AB8-binding factor |
| 569 | 38 | 79.2 | 359 | 2 | B86409 | F3H9.6 protein - A | 642 | 36.5 | 76.0 | 540 | 2 | AD0522 | probable exported |
| 570 | 38 | 79.2 | 361 | 2 | F87286 | cation efflux faml | 643 | 36.5 | 76.0 | 813 | 2 | AH3258 | cation-transportin |
| 571 | 38 | 79.2 | 380 | 2 | JQ2338 | omega-3 fatty acid | 644 | 36.5 | 76.0 | 828 | 2 | T06133 | hypothetical prote |
| 572 | 38 | 79.2 | 405 | 2 | T21188 | hypothetical prote | 645 | 36.5 | 76.0 | 974 | 1 | A40213 | optic lobe develop |
| 573 | 38 | 79.2 | 410 | 2 | T25757 | hypothetical prote | 646 | 36.5 | 76.0 | 1429 | 2 | T13720 | gene expanded prot |
| 574 | 38 | 79.2 | 470 | 2 | S33639 | finger protein esc | 647 | 36 | 75.0 | 173 | 2 | T51469 | glycine/proline-ri |
| 575 | 38 | 79.2 | 482 | 2 | E84680 | probable glucosylt | 648 | 36 | 75.0 | 240 | 2 | T45724 | hypothetical prote |
| 576 | 38 | 79.2 | 491 | 2 | A32584 | Abd-B protein - fr | 649 | 36 | 75.0 | 261 | 2 | T18320 | hypothetical prote |
| 577 | 38 | 79.2 | 493 | 2 | A34220 | homeotic protein A | 650 | 36 | 75.0 | 271 | 2 | B83027 | thiosulfate sulfur |
| 578 | 38 | 79.2 | 572 | 2 | T34658 | hypothetical prote | 651 | 36 | 75.0 | 415 | 2 | T13651 | hypothetical prote |
| 579 | 38 | 79.2 | 577 | 2 | T16333 | hypothetical prote | 652 | 36 | 75.0 | 430 | 2 | C63346 | hypothetical prote |
| 580 | 38 | 79.2 | 594 | 2 | UC5146 | ary1phorin gene-sp | 653 | 36 | 75.0 | 1819 | 2 | T32008 | hypothetical prote |
| 581 | 38 | 79.2 | 629 | 2 | A30168 | homeotic protein L | 654 | 35.5 | 74.0 | 118 | 1 | A31429 | hihaecophilin [val |
| 582 | 38 | 79.2 | 632 | 2 | S44917 | ZK688.2 protein - | 655 | 35.5 | 74.0 | 184 | 2 | S35751 | lox10 protein - 1e |
| 583 | 38 | 79.2 | 635 | 2 | S01164 | homeotic protein L | 656 | 35.5 | 74.0 | 1851 | 2 | T19964 | hypothetical prote |
| 584 | 38 | 79.2 | 670 | 1 | S50591 | myb-related protei | 657 | 35 | 72.9 | 144 | 2 | F71446 | hypothetical prote |
| 585 | 38 | 79.2 | 688 | 2 | T03941 | transcription fact | 658 | 35 | 72.9 | 161 | 2 | T25483 | hypothetical prote |
| 586 | 38 | 79.2 | 731 | 1 | UC2464 | probable copper-ct | 659 | 35 | 72.9 | 224 | 2 | T14474 | MADS box protein a |
| 587 | 38 | 79.2 | 732 | 1 | T08420 | 1-phosphatidylinos | 660 | 35 | 72.9 | 224 | 2 | T14473 | MADS box protein 2 |
| 588 | 38 | 79.2 | 743 | 2 | T02828 | conserved hypochet | 661 | 35 | 72.9 | 268 | 2 | C90056 | conserved hypochet |
| 589 | 38 | 79.2 | 894 | 2 | F84870 | hypothetical prote | 662 | 35 | 72.9 | 316 | 2 | T19435 | hypothetical prote |
| 590 | 38 | 79.2 | 943 | 2 | T03306 | SEC14 protein homo | 663 | 35 | 72.9 | 445 | 2 | S23055 | slp2 protein - fru |
| 591 | 38 | 79.2 | 1008 | 2 | T41244 | PSD-95/SAP90-associ | 664 | 35 | 72.9 | 445 | 2 | S23056 | slp2 protein - fru |
| 592 | 38 | 79.2 | 1241 | 2 | S01827 | period clock prote | 665 | 35 | 72.9 | 459 | 2 | D86315 | hypothetical prote |
| 593 | 38 | 79.2 | 1257 | 2 | S28764 | neurocan precursor | 666 | 35 | 72.9 | 546 | 2 | H86239 | hypothetical prote |
| 594 | 38 | 79.2 | 1268 | 2 | S52781 | neurocan - mouse | 667 | 35 | 72.9 | 542 | 2 | S29522 | hypothetical prote |
| 595 | 38 | 79.2 | 1355 | 2 | S40022 | spalt protein - fr | 668 | 35 | 72.9 | 553 | 2 | T27245 | casein kinase I ho |
| 596 | 38 | 79.2 | 1375 | 1 | S03170 | homeotic protein c | 669 | 35 | 72.9 | 568 | 2 | H88904 | hypothetical prote |
| 597 | 37.5 | 78.1 | 320 | 2 | A96570 | NAM-like protein. | 670 | 35 | 72.9 | 624 | 2 | T26148 | hypothetical prote |
| 598 | 37.5 | 78.1 | 324 | 2 | F96588 | hypothetical prote | 671 | 35 | 72.9 | 659 | 2 | T27246 | hypothetical prote |
| 599 | 37.5 | 78.1 | 694 | 2 | S71786 | wingless receptor | 672 | 35 | 72.9 | 1615 | 2 | B49502 | protein-tyrosine-p |
| 600 | 37.5 | 78.1 | 2559 | 2 | T09144 | probable guanine n | 673 | 35 | 72.9 | 1767 | 2 | A49502 | protein-tyrosine-p |
| 601 | 37 | 77.1 | 47 | 2 | E81833 | hypothetical prote | 674 | 34.5 | 71.9 | 1969 | 2 | T08875 | histidine kinase h |
| 602 | 37 | 77.1 | 126 | 2 | T09789 | abecisic acid- and | 675 | 34 | 70.8 | 87 | 2 | C84494 | hypothetical prote |
| 603 | 37 | 77.1 | 126 | 2 | T15993 | abecisic acid- and | 676 | 34 | 70.8 | 90 | 2 | D71568 | hypothetical prote |
| 604 | 37 | 77.1 | 138 | 2 | T02663 | abecisic acid- and | 677 | 34 | 70.8 | 98 | 2 | G82826 | hypothetical prote |
| 605 | 37 | 77.1 | 143 | 2 | T12245 | ABA stress ripenin | 678 | 34 | 70.8 | 107 | 2 | H82365 | gene msg2 protein |
| 606 | 37 | 77.1 | 153 | 2 | T09832 | water-stress-induc | 679 | 34 | 70.8 | 150 | 2 | I48670 | hypothetical prote |
| 607 | 37 | 77.1 | 170 | 2 | A22937 | transforming prote | 680 | 34 | 70.8 | 158 | 2 | T46139 | hypothetical prote |
| 608 | 37 | 77.1 | 195 | 2 | H66586 | hypothetical prote | 681 | 34 | 70.8 | 176 | 2 | C90271 | conserved hypochet |
| 609 | 37 | 77.1 | 228 | 2 | T07066 | MADS-box protein h | 682 | 34 | 70.8 | 179 | 2 | G96001 | conserved hypochet |
| 610 | 37 | 77.1 | 228 | 2 | T07410 | MADS box protein h | 683 | 34 | 70.8 | 185 | 2 | H84601 | probable dehydrin |
| 611 | 37 | 77.1 | 231 | 2 | S31693 | MADS box protein h | 684 | 34 | 70.8 | 196 | 2 | G89907 | hypothetical prote |
| 612 | 37 | 77.1 | 278 | 2 | E87704 | hypothetical prote | 685 | 34 | 70.8 | 199 | 2 | C96681 | hypothetical prote |
| 613 | 37 | 77.1 | 285 | 2 | I51412 | hypothetical trans | 686 | 34 | 70.8 | 208 | 2 | T52368 | homeobox protein H |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|------|------|------|---|--------|--------------------|
| 687 | 34 | 70.8 | 217 | 2 | T02548 | hypothetical prote | 760 | 34 | 70.8 | 790 | 2 | T12203 | transcription fact |
| 688 | 34 | 70.8 | 217 | 2 | T48642 | hypothetical prote | 761 | 34 | 70.8 | 857 | 2 | T04208 | probable anthranil |
| 689 | 34 | 70.8 | 228 | 2 | S55888 | CCHH finger protei | 762 | 34 | 70.8 | 873 | 1 | TWVFS | protein-tyrosine k |
| 690 | 34 | 70.8 | 235 | 2 | B84967 | hypothetical prote | 763 | 34 | 70.8 | 952 | 2 | D86179 | hypothetical prote |
| 691 | 34 | 70.8 | 245 | 2 | T07139 | cytosine proteins | 764 | 34 | 70.8 | 1032 | 2 | F65071 | hypothetical prote |
| 692 | 34 | 70.8 | 249 | 2 | T21920 | hypothetical prote | 765 | 34 | 70.8 | 1032 | 2 | C85943 | probable oxidoredu |
| 693 | 34 | 70.8 | 257 | 2 | A84848 | probable C2H2-type | 766 | 34 | 70.8 | 1032 | 2 | G91097 | probable oxidoredu |
| 694 | 34 | 70.8 | 265 | 2 | T47898 | hypothetical prote | 767 | 34 | 70.8 | 1048 | 2 | C96669 | protein FIN19.15 f |
| 695 | 34 | 70.8 | 280 | 2 | A39484 | androgen-wilthdrwa | 768 | 34 | 70.8 | 1129 | 2 | T19779 | hypothetical prote |
| 696 | 34 | 70.8 | 280 | 2 | T24454 | hypothetical prote | 769 | 34 | 70.8 | 1146 | 2 | S46837 | hypothetical prote |
| 697 | 34 | 70.8 | 283 | 2 | JC4256 | hypothetical 32.0k | 770 | 34 | 70.8 | 1240 | 2 | S52734 | hypothetical prote |
| 698 | 34 | 70.8 | 291 | 2 | S33209 | extensin-like prot | 771 | 34 | 70.8 | 1256 | 2 | S14556 | asparagine-rich pr |
| 699 | 34 | 70.8 | 292 | 2 | H96811 | protein F3F9.20 [l | 772 | 34 | 70.8 | 1325 | 2 | T25753 | hypothetical prote |
| 700 | 34 | 70.8 | 304 | 2 | D81182 | adhesin, probable | 773 | 34 | 70.8 | 1407 | 2 | B42239 | adenylate cyclase |
| 701 | 34 | 70.8 | 307 | 2 | S37252 | homeotic protein H | 774 | 34 | 70.8 | 1671 | 2 | S71628 | sensory transducti |
| 702 | 34 | 70.8 | 308 | 2 | T06218 | catalase (EC 1.11. | 775 | 34 | 70.8 | 1966 | 2 | T32552 | hypothetical prote |
| 703 | 34 | 70.8 | 314 | 2 | D71410 | hypothetical prote | 776 | 34 | 70.8 | 2161 | 2 | JH0564 | calcium channel al |
| 704 | 34 | 70.8 | 315 | 2 | C96666 | protein F22C12.4 [| 777 | 34 | 70.8 | 2181 | 2 | A38198 | calcium channel al |
| 705 | 34 | 70.8 | 316 | 2 | E84636 | NAM (no apical mer | 778 | 34 | 70.8 | 2203 | 2 | T12742 | voltage-dependent |
| 706 | 34 | 70.8 | 322 | 2 | S23053 | slippy paired prot | 779 | 34 | 70.8 | 2848 | 2 | T32550 | hypothetical prote |
| 707 | 34 | 70.8 | 348 | 2 | T06385 | probable Fe(II) tr | 780 | 33.5 | 69.8 | 183 | 2 | C85439 | probable cytoskele |
| 708 | 34 | 70.8 | 349 | 2 | S61414 | DNA-binding protei | 781 | 33.5 | 69.8 | 438 | 2 | B84922 | hypothetical prote |
| 709 | 34 | 70.8 | 351 | 2 | T03946 | kn1 like-homoe box | 782 | 33.5 | 69.8 | 992 | 1 | GNMVR3 | structural polypor |
| 710 | 34 | 70.8 | 352 | 2 | T23464 | hypothetical prote | 783 | 33.5 | 69.8 | 1063 | 1 | GNMVR7 | structural polypor |
| 711 | 34 | 70.8 | 362 | 2 | T48564 | probable serine ri | 784 | 33.5 | 69.8 | 1063 | 1 | GNMVR4 | structural polypor |
| 712 | 34 | 70.8 | 398 | 2 | C84780 | hypothetical prote | 785 | 33.5 | 69.8 | 1063 | 1 | GNMVR4 | structural polypor |
| 713 | 34 | 70.8 | 400 | 2 | T25889 | hypothetical prote | 786 | 33.5 | 69.8 | 1291 | 2 | T00019 | period protein hom |
| 714 | 34 | 70.8 | 401 | 2 | T48495 | hypothetical prote | 787 | 33 | 68.8 | 84 | 2 | AD2158 | hypothetical prote |
| 715 | 34 | 70.8 | 407 | 2 | T08965 | hypothetical prote | 788 | 33 | 68.8 | 96 | 2 | T46181 | hypothetical prote |
| 716 | 34 | 70.8 | 439 | 2 | A84431 | probable C2H2-type | 789 | 33 | 68.8 | 121 | 2 | A84906 | probable auxin-reg |
| 717 | 34 | 70.8 | 441 | 2 | S50112 | nuclear factor 1-X | 790 | 33 | 68.8 | 122 | 2 | C53234 | globulin-I0 - maiz |
| 718 | 34 | 70.8 | 441 | 2 | B31256 | transcription fact | 791 | 33 | 68.8 | 136 | 2 | AD2898 | ATP synthase eps11 |
| 719 | 34 | 70.8 | 442 | 2 | E71523 | hypothetical prote | 792 | 33 | 68.8 | 136 | 2 | E97673 | ATP synthase eps11 |
| 720 | 34 | 70.8 | 446 | 2 | B82975 | conserved hypotbet | 793 | 33 | 68.8 | 140 | 2 | T16574 | hypothetical prote |
| 721 | 34 | 70.8 | 465 | 2 | T18793 | hypothetical prote | 794 | 33 | 68.8 | 150 | 2 | A84488 | hypothetical prote |
| 722 | 34 | 70.8 | 471 | 2 | A81680 | conserved hypotbet | 795 | 33 | 68.8 | 152 | 2 | D75485 | conserved hypotbet |
| 723 | 34 | 70.8 | 472 | 2 | T18801 | hypothetical prote | 796 | 33 | 68.8 | 152 | 2 | F84642 | hypothetical prote |
| 724 | 34 | 70.8 | 488 | 2 | A55180 | homeotic protein H | 797 | 33 | 68.8 | 158 | 2 | AE2476 | hypothetical prote |
| 725 | 34 | 70.8 | 490 | 2 | A46391 | CAMP receptor subc | 798 | 33 | 68.8 | 176 | 2 | A86441 | hypothetical prote |
| 726 | 34 | 70.8 | 492 | 1 | CS8Y | catalase (EC 1.11. | 799 | 33 | 68.8 | 179 | 2 | T49508 | hypothetical prote |
| 727 | 34 | 70.8 | 492 | 2 | S71112 | catalase (EC 1.11. | 800 | 33 | 68.8 | 180 | 2 | B97242 | hypothetical prote |
| 728 | 34 | 70.8 | 492 | 2 | T15969 | catalase (EC 1.11. | 801 | 33 | 68.8 | 184 | 2 | S32095 | embryonic abundant |
| 729 | 34 | 70.8 | 492 | 2 | S62696 | catalase (EC 1.11. | 802 | 33 | 68.8 | 184 | 2 | A85036 | hypothetical prote |
| 730 | 34 | 70.8 | 492 | 2 | S48124 | catalase (EC 1.11. | 803 | 33 | 68.8 | 187 | 2 | T50832 | superoxide dismuta |
| 731 | 34 | 70.8 | 492 | 2 | S10770 | catalase (EC 1.11. | 804 | 33 | 68.8 | 190 | 2 | D64087 | probable peptidylp |
| 732 | 34 | 70.8 | 492 | 2 | S17493 | catalase (EC 1.11. | 805 | 33 | 68.8 | 205 | 2 | T18811 | probable chloride |
| 733 | 34 | 70.8 | 492 | 2 | S10395 | catalase (EC 1.11. | 806 | 33 | 68.8 | 207 | 2 | B71446 | hypothetical prote |
| 734 | 34 | 70.8 | 492 | 2 | T08754 | catalase (EC 1.11. | 807 | 33 | 68.8 | 215 | 2 | S28062 | homeotic protein g |
| 735 | 34 | 70.8 | 492 | 2 | T09756 | catalase (EC 1.11. | 808 | 33 | 68.8 | 219 | 2 | H84584 | hypothetical prote |
| 736 | 34 | 70.8 | 492 | 2 | T05779 | catalase (EC 1.11. | 809 | 33 | 68.8 | 224 | 2 | T49923 | hypothetical prote |
| 737 | 34 | 70.8 | 492 | 2 | S46297 | catalase (EC 1.11. | 810 | 33 | 68.8 | 228 | 2 | S03639 | superoxide dismuta |
| 738 | 34 | 70.8 | 492 | 2 | T10902 | catalase (EC 1.11. | 811 | 33 | 68.8 | 228 | 2 | T50828 | superoxide dismuta |
| 739 | 34 | 70.8 | 493 | 2 | T07911 | catalase (EC 1.11. | 812 | 33 | 68.8 | 229 | 2 | AC0698 | probable pathogeni |
| 740 | 34 | 70.8 | 494 | 1 | CS8M | catalase (EC 1.11. | 813 | 33 | 68.8 | 232 | 2 | A42095 | floral homeotic pr |
| 741 | 34 | 70.8 | 507 | 2 | B96590 | hypothetical prote | 814 | 33 | 68.8 | 236 | 2 | T01662 | globulin-1 - maize |
| 742 | 34 | 70.8 | 518 | 1 | NIBCRT | nitrogenase (EC 1. | 815 | 33 | 68.8 | 240 | 2 | A37004 | outer membrane cla |
| 743 | 34 | 70.8 | 521 | 2 | S27475 | nitrogenase (EC 1. | 816 | 33 | 68.8 | 242 | 2 | A81782 | outer membrane pro |
| 744 | 34 | 70.8 | 529 | 2 | D71489 | hypothetical prote | 817 | 33 | 68.8 | 242 | 2 | C81205 | outer membrane pro |
| 745 | 34 | 70.8 | 531 | 2 | T04722 | hypothetical prote | 818 | 33 | 68.8 | 244 | 2 | F68830 | conserved hypotbet |
| 746 | 34 | 70.8 | 537 | 2 | T34380 | hypothetical prote | 819 | 33 | 68.8 | 251 | 2 | AC0534 | probable hydroxyc |
| 747 | 34 | 70.8 | 566 | 2 | S54629 | hypothetical prote | 820 | 33 | 68.8 | 251 | 2 | T52370 | homeobox protein H |
| 748 | 34 | 70.8 | 575 | 2 | T01552 | hypothetical prote | 821 | 33 | 68.8 | 251 | 2 | T49950 | homeobox ABC trans |
| 749 | 34 | 70.8 | 587 | 2 | A56015 | finger protein SIG | 822 | 33 | 68.8 | 251 | 2 | H90949 | probable ABC trans |
| 750 | 34 | 70.8 | 615 | 2 | T06108 | hypothetical prote | 823 | 33 | 68.8 | 251 | 2 | D85798 | hypothetical prote |
| 751 | 34 | 70.8 | 627 | 2 | T00600 | hypothetical prote | 824 | 33 | 68.8 | 251 | 2 | B64948 | hypothetical prote |
| 752 | 34 | 70.8 | 633 | 2 | T14612 | hypothetical prote | 825 | 33 | 68.8 | 251 | 2 | AH0742 | asparagine-rich pr |
| 753 | 34 | 70.8 | 650 | 2 | T02536 | CER1-like protein | 826 | 33 | 68.8 | 256 | 2 | T39108 | hypothetical prote |
| 754 | 34 | 70.8 | 655 | 2 | S44806 | Om(2D) protein - f | 827 | 33 | 68.8 | 260 | 2 | T26496 | adenylate cyclase |
| 755 | 34 | 70.8 | 671 | 2 | S51599 | GI cyclin C1N1 - f | 828 | 33 | 68.8 | 274 | 2 | S70130 | hypothetical prote |
| 756 | 34 | 70.8 | 698 | 2 | S49206 | malate synthase BH | 829 | 33 | 68.8 | 281 | 2 | T15980 | hypothetical prote |
| 757 | 34 | 70.8 | 727 | 2 | B83916 | DNA-binding protei | 830 | 33 | 68.8 | 285 | 2 | S62179 | hypothetical prote |
| 758 | 34 | 70.8 | 731 | 2 | S2870 | probable GCN4-comp | 831 | 33 | 68.8 | 300 | 2 | T38986 | hypothetical prote |
| 759 | 34 | 70.8 | 776 | 2 | A96634 | | 832 | 33 | 68.8 | 303 | 2 | G85062 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|--------------------|-----|----|------|-----|---|--------|------------------------|
| 833 | 33 | 66.8 | 313 | 2 | T01587 | hypothetical prote | 906 | 32 | 66.7 | 102 | 2 | AE1795 | PTS cellobiose-spe |
| 834 | 33 | 66.8 | 318 | 2 | T06322 | anexin, isoform P | 907 | 32 | 66.7 | 102 | 2 | S09828 | hypothetical prote |
| 835 | 33 | 66.8 | 315 | 2 | AE0251 | exported high-affi | 908 | 32 | 66.7 | 104 | 2 | S57666 | protamine 2 - rat |
| 836 | 33 | 66.8 | 323 | 2 | T45601 | hypothetical prote | 909 | 32 | 66.7 | 106 | 2 | T17663 | hypothetical prote |
| 837 | 33 | 66.8 | 324 | 2 | F84719 | probable glyoxalas | 910 | 32 | 66.7 | 106 | 2 | C70794 | hypothetical prote |
| 838 | 33 | 66.8 | 325 | 2 | T04677 | hypothetical prote | 911 | 32 | 66.7 | 107 | 2 | A69547 | conserved hypotet |
| 839 | 33 | 66.8 | 325 | 2 | G96718 | unknown protein, 5 | 912 | 32 | 66.7 | 111 | 2 | C35826 | hypothetical 13K p |
| 840 | 33 | 66.8 | 336 | 2 | F85021 | probable transcrip | 913 | 32 | 66.7 | 112 | 2 | T34857 | hypothetical prote |
| 841 | 33 | 66.8 | 347 | 2 | S43771 | phosphatidylcholin | 914 | 32 | 66.7 | 115 | 2 | A23925 | proline-rich phosp |
| 842 | 33 | 66.8 | 348 | 2 | T02006 | transcription fact | 915 | 32 | 66.7 | 126 | 2 | T52525 | tyrosinase co-fact |
| 843 | 33 | 66.8 | 350 | 2 | S43772 | phosphatidylcholin | 916 | 32 | 66.7 | 131 | 2 | B87012 | probable ferric up |
| 844 | 33 | 66.8 | 350 | 2 | AH2005 | phosphatidylcholin | 917 | 32 | 66.7 | 131 | 2 | A53024 | Leydig insulin-lik |
| 845 | 33 | 66.8 | 352 | 2 | T15981 | hypothetical prote | 918 | 32 | 66.7 | 132 | 2 | G75466 | hypothetical ferric up |
| 846 | 33 | 66.8 | 357 | 2 | F70193 | hypothetical prote | 919 | 32 | 66.7 | 133 | 2 | AB0990 | nickel responsive |
| 847 | 33 | 66.8 | 364 | 2 | T24996 | hypothetical prote | 920 | 32 | 66.7 | 133 | 2 | B86018 | nickel responsive |
| 848 | 33 | 66.8 | 367 | 2 | T25093 | hypothetical prote | 921 | 32 | 66.7 | 133 | 2 | D91172 | nickel-responsive |
| 849 | 33 | 66.8 | 367 | 2 | D97096 | probable permease, | 922 | 32 | 66.7 | 134 | 2 | S47700 | nickel-responsive |
| 850 | 33 | 66.8 | 369 | 2 | T48612 | hypothetical prote | 923 | 32 | 66.7 | 134 | 2 | A26986 | hypothetical prote |
| 851 | 33 | 66.8 | 376 | 1 | QDBEW2 | UL53 protein - hum | 924 | 32 | 66.7 | 139 | 2 | B33910 | sal homeotic prote |
| 852 | 33 | 66.8 | 381 | 2 | T24290 | hypothetical prote | 925 | 32 | 66.7 | 139 | 2 | T20162 | hypothetical prote |
| 853 | 33 | 66.8 | 383 | 2 | T06753 | hypothetical prote | 926 | 32 | 66.7 | 142 | 2 | S00262 | sal homeotic prote |
| 854 | 33 | 66.8 | 397 | 2 | S54018 | DBP2 protein-inter | 927 | 32 | 66.7 | 142 | 2 | C33910 | sal homeotic prote |
| 855 | 33 | 66.8 | 398 | 2 | D85080 | KNAT1 homeobox-11k | 928 | 32 | 66.7 | 146 | 2 | H37788 | hypothetical prote |
| 856 | 33 | 66.8 | 405 | 2 | D96709 | probable B-box zin | 929 | 32 | 66.7 | 146 | 2 | C36708 | hypothetical prote |
| 857 | 33 | 66.8 | 407 | 2 | T02258 | globulin1 - maize | 930 | 32 | 66.7 | 147 | 2 | T52015 | hypothetical prote |
| 858 | 33 | 66.8 | 413 | 2 | H81659 | branched-chain ami | 931 | 32 | 66.7 | 149 | 2 | B82894 | hypothetical prote |
| 859 | 33 | 66.8 | 424 | 2 | JC5891 | omega 6 desaturase | 932 | 32 | 66.7 | 150 | 2 | C71706 | hypothetical prote |
| 860 | 33 | 66.8 | 445 | 2 | A60488 | histidine-rich gly | 933 | 32 | 66.7 | 151 | 2 | A53570 | nickel-responsive |
| 861 | 33 | 66.8 | 457 | 2 | T21063 | hypothetical prote | 934 | 32 | 66.7 | 151 | 2 | B37107 | ferric uptake regu |
| 862 | 33 | 66.8 | 506 | 2 | JC7226 | endo-1,3(4)-beta-g | 935 | 32 | 66.7 | 154 | 2 | B87029 | hypothetical prote |
| 863 | 33 | 66.8 | 512 | 2 | F86196 | hypothetical prote | 936 | 32 | 66.7 | 155 | 2 | JC7732 | trypsin-plasmin in |
| 864 | 33 | 66.8 | 524 | 2 | F96572 | protein F12M16.10 | 937 | 32 | 66.7 | 156 | 2 | B85814 | DNA mismatch endon |
| 865 | 33 | 66.8 | 530 | 2 | T50498 | myc-like protein - | 938 | 32 | 66.7 | 156 | 2 | B90966 | DNA mismatch endon |
| 866 | 33 | 66.8 | 538 | 1 | S12570 | homeotic protein b | 939 | 32 | 66.7 | 156 | 2 | AC0754 | patch repair prote |
| 867 | 33 | 66.8 | 540 | 2 | S21825 | vicilin-like stora | 940 | 32 | 66.7 | 156 | 2 | US0264 | DNA mismatch endon |
| 868 | 33 | 66.8 | 543 | 2 | S35047 | globulin-1S, GLB1S | 941 | 32 | 66.7 | 157 | 2 | F95313 | hypothetical prote |
| 869 | 33 | 66.8 | 573 | 2 | AS3234 | mucin JUK7 - huma | 942 | 32 | 66.7 | 161 | 2 | H85120 | probable prolina-r |
| 870 | 33 | 66.8 | 574 | 2 | T04249 | hypothetical prote | 943 | 32 | 66.7 | 162 | 2 | A55969 | Fp21 protein - sai |
| 871 | 33 | 66.8 | 583 | 2 | B53249 | vicilin-like stora | 944 | 32 | 66.7 | 163 | 2 | D87293 | Fur family protein |
| 872 | 33 | 66.8 | 583 | 2 | T12576 | probable phosphate | 945 | 32 | 66.7 | 164 | 2 | T07759 | disease resistance |
| 873 | 33 | 66.8 | 609 | 2 | F84824 | hypothetical prote | 946 | 32 | 66.7 | 168 | 2 | T22447 | hypothetical prote |
| 874 | 33 | 66.8 | 610 | 2 | S35049 | mucin JERS7 - huma | 947 | 32 | 66.7 | 171 | 2 | T10904 | sporamin - sweet p |
| 875 | 33 | 66.8 | 615 | 2 | T20839 | hypothetical prote | 948 | 32 | 66.7 | 171 | 2 | A83458 | urase accessory p |
| 876 | 33 | 66.8 | 638 | 2 | T47569 | hypothetical prote | 949 | 32 | 66.7 | 172 | 2 | T00924 | hypothetical prote |
| 877 | 33 | 66.8 | 647 | 2 | C66834 | unknown protein P5 | 950 | 32 | 66.7 | 172 | 2 | D82642 | conserved hypotet |
| 878 | 33 | 66.8 | 647 | 2 | T26240 | hypothetical prote | 951 | 32 | 66.7 | 173 | 2 | B41841 | hypothetical prote |
| 879 | 33 | 66.8 | 695 | 2 | C86731 | copper-potassium t | 952 | 32 | 66.7 | 173 | 2 | AF1872 | bilin biosynthesis |
| 880 | 33 | 66.8 | 697 | 2 | B86239 | protein T10O24.19 | 953 | 32 | 66.7 | 174 | 2 | B69979 | urase accessory p |
| 881 | 33 | 66.8 | 702 | 2 | T27730 | hypothetical prote | 954 | 32 | 66.7 | 185 | 2 | G64075 | urase accessory p |
| 882 | 33 | 66.8 | 720 | 2 | J01676 | AB13 protein - Ara | 955 | 32 | 66.7 | 185 | 2 | T51844 | RING-H2 finger pro |
| 883 | 33 | 66.8 | 754 | 2 | S50601 | hypothetical prote | 956 | 32 | 66.7 | 190 | 1 | WMBE28 | structural phospho |
| 884 | 33 | 66.8 | 764 | 2 | T48446 | hypothetical prote | 957 | 32 | 66.7 | 195 | 2 | AC0778 | probable membrane |
| 885 | 33 | 66.8 | 800 | 2 | S54623 | probable mitochond | 958 | 32 | 66.7 | 195 | 2 | T21300 | hypothetical prote |
| 886 | 33 | 66.8 | 833 | 2 | T01547 | probable phospholi | 959 | 32 | 66.7 | 195 | 2 | AD0024 | peptidylprolyl iso |
| 887 | 33 | 66.8 | 839 | 2 | B96576 | hypothetical prote | 960 | 32 | 66.7 | 203 | 2 | G85850 | hypothetical prote |
| 888 | 33 | 66.8 | 853 | 2 | S74279 | hypothetical prote | 961 | 32 | 66.7 | 203 | 2 | F64981 | hypothetical 22.4 |
| 889 | 33 | 66.8 | 1042 | 2 | T25644 | hypothetical prote | 962 | 32 | 66.7 | 203 | 2 | F91006 | hypothetical prote |
| 890 | 33 | 66.8 | 1440 | 2 | T33813 | hypothetical prote | 963 | 32 | 66.7 | 204 | 2 | G83482 | probable transcrip |
| 891 | 33 | 66.8 | 1476 | 2 | A45773 | keich protein, lon | 964 | 32 | 66.7 | 205 | 2 | F85363 | hypothetical prote |
| 892 | 33 | 66.8 | 2145 | 2 | JC4747 | adenylate cyclase | 965 | 32 | 66.7 | 211 | 2 | C84751 | hypothetical prote |
| 893 | 33 | 66.8 | 2145 | 2 | B96750 | hypothetical prote | 966 | 32 | 66.7 | 213 | 2 | C84200 | hypothetical prote |
| 894 | 33.5 | 67.7 | 512 | 2 | T23166 | hypothetical prote | 967 | 32 | 66.7 | 219 | 2 | T10563 | proline-rich phosp |
| 895 | 32 | 66.7 | 13 | 2 | AB0764 | his operon leader | 968 | 32 | 66.7 | 225 | 2 | C88633 | protein P5683.3 (i |
| 896 | 32 | 66.7 | 69 | 2 | S17518 | opa protein - friu | 969 | 32 | 66.7 | 230 | 2 | T19161 | dysetonin isoform 2 |
| 897 | 32 | 66.7 | 69 | 2 | AE2474 | hypothetical prote | 970 | 32 | 66.7 | 232 | 2 | T16873 | hypothetical prote |
| 898 | 32 | 66.7 | 73 | 2 | T18013 | hypothetical prote | 971 | 32 | 66.7 | 234 | 2 | T14301 | hypothetical prote |
| 899 | 32 | 66.7 | 83 | 2 | A44465 | sodium ion pump ox | 972 | 32 | 66.7 | 236 | 2 | C82566 | hypothetical prote |
| 900 | 32 | 66.7 | 87 | 2 | T16439 | hypothetical prote | 973 | 32 | 66.7 | 241 | 2 | H84864 | hypothetical prote |
| 901 | 32 | 66.7 | 88 | 2 | AP1283 | conserved hypotet | 974 | 32 | 66.7 | 243 | 2 | T51652 | mbp-related transc |
| 902 | 32 | 66.7 | 88 | 2 | A11654 | conserved hypotet | 975 | 32 | 66.7 | 244 | 2 | T00449 | hypothetical prote |
| 903 | 32 | 66.7 | 94 | 2 | S32939 | Au1 protein - yea | 976 | 32 | 66.7 | 244 | 2 | H84853 | hypothetical prote |
| 904 | 32 | 66.7 | 97 | 2 | T23850 | hypothetical prote | 977 | 32 | 66.7 | 244 | 2 | JC2379 | cell-specific heli |
| 905 | 32 | 66.7 | 102 | 2 | AD1420 | PTS cellobiose-spe | 978 | 32 | 66.7 | 245 | 2 | S10658 | hypothetical prote |

979 32 66.7 245 2 G72064 ABC transporter AT
 980 32 66.7 245 2 B86558 ABC transporter AT
 981 32 66.7 248 2 S20886 MADS box protein s
 982 32 66.7 250 2 T36868 hypothetical prote
 983 32 66.7 251 2 AG0132 probable hydroxyc
 984 32 66.7 257 2 AC1879 hypothetical prote
 985 32 66.7 257 2 S01165 achaeae-scute locu
 986 32 66.7 260 2 T18909 hypothetical prote
 987 32 66.7 264 2 PNO681 nitrogennase (EC 1.
 988 32 66.7 271 2 T49956 hypothetical prote
 989 32 66.7 273 1 S69189 myb-related protei
 990 32 66.7 276 2 AH0244 probable esterase
 991 32 66.7 276 2 T51685 myb-related transc
 992 32 66.7 278 1 S57643 stearyl-CoA 9-des
 993 32 66.7 278 2 H64029 hypothetical prote
 994 32 66.7 278 2 T49276 hypothetical prote
 995 32 66.7 279 2 B86402 protein T22C5.19 f
 996 32 66.7 281 2 E64216 hypothetical prote
 997 32 66.7 285 2 T05777 hypothetical prote
 998 32 66.7 288 2 G02629 Rev interacting pr
 999 32 66.7 289 2 T01257 probable GT-1-like
 1000 32 66.7 290 2 T36205 hypothetical prote

ALIGNMENTS

RESULT 1

LPECH

his operon leader peptide - Escherichia coli (strain K-12)

C:Species: Escherichia coli
 C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004

C:Accession: A03594; I41073; A64967

R:Verde, P.; Funzio, R.; di Nocera, P.P.; Blasi, F.; Bruni, C.B.

Nucleic Acids Res. 9, 2075-2086, 1981

A:Title: Identification, nucleotide sequence and expression of the regulatory region of

A:Reference number: A03594; MUID:82059525; PMID:6170941

A:Accession: A03594

A:Molecule type: DNA

A:Residues: 1-16 <RES>

A:Cross-references: UNIPROT:P60995; UNIPARC:UPI000012E854; GB:V00284; GB:J01627; GB:J016

A:Note: this protein is involved in the attenuation mechanism for the control of the exp

R:Di Nocera, P.P.; Blasi, F.; Di Lauro, R.; Funzio, R.; Bruni, C.B.

Proc. Natl. Acad. Sci. U.S.A. 75, 4276-4280, 1978

A:Title: Nucleotide sequence of the attenuator region of the histidine operon of Escheri

A:Reference number: I41073; MUID:79033821; PMID:360215

A:Accession: I41073

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-16 <RES>

A:Cross-references: UNIPARC:UPI000012E854; EMBL:V00285; NID:G41701; PIDN:CAA23550.1; PID

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A64967

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-16 <BLAT>

A:Cross-references: UNIPARC:UPI000012E854; GB:AE000293; GB:U00096; NID:G2367127; PIDN:AA

A:Experimental source: strain K-12, substrain MG1655

C:Genetics:

A:Gene: hisl

C:Superfamily: his leader peptide

C:Keywords: histidine biosynthesis

Query Match 100.0%; Score 48; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HHHHHH 6
 |||||

Db 8 HHHHHH 13

RESULT 2

his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain RMD

C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: C90981

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G

gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc

A:Reference number: A96429; MUID:21156231; PMID:11258796

A:Accession: C90981

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-16 <RAY>

A:Cross-references: UNIPROT:Q8X8T5; UNIPARC:UPI00000D08D2; GB:BA000007; PIDN:BA036242.1,

A:Experimental source: strain O157:H7, substrain RMD 0509952

C:Genetics:

A:Gene: EC82819

Query Match 100.0%; Score 48; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
 |||||
 Db 9 HHHHHH 14

RESULT 3

his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: A85827

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A85827

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-16 <STO>

A:Cross-references: UNIPROT:Q8X8T5; UNIPARC:UPI00000D08D2; GB:AE005174; NID:G12516199; P

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: hisl

Query Match 100.0%; Score 48; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
 |||||
 Db 9 HHHHHH 14

RESULT 4

histidine and glutamine-rich protein - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: H64698

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodex, A.; McKenne

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: H64698
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-57 <TOM>
 A:Cross-references: UNIPROT:O25973; UNIPARC:UPI000017A919; GB:AE000511; TIGR:HP1432

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 16 HHHHHH 21

RESULT 5
 C64698
 probable histidine-rich metal-binding protein - Helicobacter pylori
 C:Species: Helicobacter pylori
 A:Variety: strains J99, 26695
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: C64698; C71821
 R:Alm, R.A.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalik, H.G.; Glodex, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujik, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frazer, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: C64698
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-60 <TOM>
 A:Cross-references: UNIPROT:Q48251; UNIPARC:UPI000014897A; GB:AE000643; GB:AE000511; NID:16436
 A:Experimental source: strain 26695
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: C71821
 A:Molecule type: DNA
 A:Residues: 1-60 <ARN>
 A:Cross-references: UNIPARC:UPI000014897A; GB:AE001555; GB:AE001439; NID:94155929; PIDN: A:Experimental source: strain J99
 C:Genetics:
 A:Gene: HP1427; jhp1320

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 11 HHHHHH 16

RESULT 6
 S57787
 hypothetical protein 2 (clone ES1A) - barley
 C:Species: Hordeum vulgare (barley)
 C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S57787
 R:Spelman, E.; Salamini, F.
 Plant Mol. Biol. 28, 915-926, 1995
 A:Title: GA(3)-regulated cDNAs from Hordeum vulgare leaves.
 A:Reference number: S57787; MUID:95367651; PMID:7640362
 A:Accession: S57787
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-64 <SP>
 A:Cross-references: UNIPROT:Q40049; UNIPARC:UPI000009D67D; EMBL:X78884; NID:9929666; PID

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 64;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 25 HHHHHH 30

RESULT 7
 D71821
 probable histidine and glutamine-rich metal-binding protein - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: D71821
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: D71821
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 <ARN>
 A:Cross-references: UNIPROT:Q92J18; UNIPARC:UPI00000D3729; GB:AE001555; GB:AE001439; NID: A:Experimental source: strain J99
 C:Genetics:
 A:Gene: jhp1321

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 77;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 21 HHHHHH 26

RESULT 8
 T16436
 hypothetical protein F53A9.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T16436
 R:Miller, N.
 submitted to the EMBL Data Library, March 1995
 A:Description: The sequence of C. elegans cosmid F53A9.
 A:Reference number: Z18513
 A:Accession: T16436
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-77 <ML>
 A:Cross-references: UNIPROT:Q20690; UNIPARC:UPI000007C69D; EMBL:U23523; NID:9746551; P1 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:F53A9.1

Query Match
 Best Local Similarity 100.0%; Score 48; DB 2; Length 77;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 46 HHHHHH 51

RESULT 9
 T16435
 hypothetical protein F53A9.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T16435
 R/Miller, N.
 submitted to the EMBL Data Library, March 1995
 A/Description: The sequence of *C. elegans* cosmid F53A9.
 A/Reference number: Z18513
 A/Accession: T16435
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-83 <ML>
 A/Cross-references: UNIPROT:Q20689; UNIPARC:UPI000007808B; EMBL:U23523; NID:g746551; PID
 A/Experimental source: strain Bristol N2
 C/Genetics:
 A/Gene: CESP:F53A9.2

Query Match 100.0%; Score 48; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 45 HHHHHH 50

RESULT 10
 T34146
 hypothetical protein C33H5.13 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T34146
 R/Bradshaw, H.; Steillyes, L.
 submitted to the EMBL Data Library, November 1995
 A/Description: The sequence of *C. elegans* cosmid C33H5.
 A/Reference number: Z21482
 A/Accession: T34146
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-92 <BRA>
 A/Cross-references: UNIPROT:Q18410; UNIPARC:UPI0000079A72; EMBL:U41007; PIDN:AAA82273.1;
 A/Experimental source: strain Bristol N2
 C/Genetics:
 A/Gene: CESP:C33H5.13
 A/Introns: 13/3; 53/2

Query Match 100.0%; Score 48; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 58 HHHHHH 63

RESULT 11
 B4971
 hypothetical protein 2 - *Plasmodium brasiliannu*
 C/Species: *Plasmodium brasiliannu*
 C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
 C/Accession: B4971
 R/Killejian, A.; Yang, Y.F.; Cochran, A.H.; Rashid, M.A.
 Mol. Biochem. Parasitol. 38, 291-293, 1990
 A/Title: Homologous sequences in *Plasmodium cynomolgi* and the gene of the histidine-rich
 A/Reference number: A44971; MUID:90220761; PMID:2183051
 A/Accession: B44971
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-101 <KIT>
 A/Cross-references: UNIPROT:Q25652; UNIPARC:UPI000017B5DD; GB:M28064

Query Match 100.0%; Score 48; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 0.87;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

Db 5 HHHHHH 10
 |||||

RESULT 12
 T30119
 hypothetical protein F22H10.2 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T30119
 R/Langston, Y.; Hawkins, J.
 submitted to the EMBL Data Library, September 1996
 A/Description: The sequence of *C. elegans* cosmid F22H10.
 A/Reference number: Z20740
 A/Accession: T30119
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-102 <LAN>
 A/Cross-references: UNIPROT:Q94189; UNIPARC:UPI000007E413; EMBL:U70845; PIDN:AAB09100.1;
 A/Experimental source: strain Bristol N2; clone F22H10
 C/Genetics:
 A/Gene: CESP:F22H10.2
 A/Map position: X
 A/Introns: 16/1

Query Match 100.0%; Score 48; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 61 HHHHHH 66

RESULT 13
 S37150
 aar2 protein - tomato
 C/Species: *Lycopersicon esculentum* (tomato)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S37150
 R/Amitai, H.; Scolnik, P.A.; Bar-Zvi, D.
 submitted to the EMBL Data Library, September 1993
 A/Reference number: S37150
 A/Accession: S37150
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-114 <AMT>
 A/Cross-references: UNIPROT:P37219; UNIPARC:UPI0000126164; EMBL:X74907; NID:g400468; PID
 C/Genetics:
 A/Introns: 53/3

Query Match 100.0%; Score 48; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.98;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 108 HHHHHH 113

RESULT 14
 H72583
 hypothetical protein APE1948 - *Aeropyrum pernix* (strain K1)
 C/Species: *Aeropyrum pernix*
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C/Accession: H72583
 R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakeyama, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyr*
 A/Reference number: A72450; MUID:99310339; PMID:10382966
 A/Accession: H72583
 A/Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-115 <KAM>
 A:Cross-references: UNIPROT:Q9YAJ2; UNIPARC:UPI000005E159; DDBJ:AP000062; NID:G5105244;
 A:Experimental source: strain KI
 C:Genetics:
 A:Gene: APE1948

Query Match 100.0%; Score 48; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 0.99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 32 HHHHHH 37

RESULT 15

T01558
 auxin-induced protein homolog A.TM018A10.6 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 31-Dec-2004
 C:Accession: T01558
 R:Dempsey, S.; Harper, M.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of A. thaliana TM018A10.
 A:Reference number: Z14348
 A:Accession: T01558
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-122 <DEM>
 A:Cross-references: UNIPROT:Q23089; UNIPARC:UPI000004A87A; EMBL:AF013294; NID:G2252848;
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Map position: 4
 A:Note: A.TM018A10.6
 C:Superfamily: auxin-induced protein 10A

Query Match 100.0%; Score 48; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 108 HHHHHH 113

RESULT 16

S14983
 extensin class I (clone w10-1 L) - tomato (fragment)
 C:Species: Lycopersicon esculentum (tomato)
 C>Date: 07-May-1998 #sequence_revision 15-May-1998 #text_change 17-Jul-1998
 C:Accession: S14983
 R>Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
 Plant Mol. Biol. 16, 547-565, 1991
 A>Title: Tomato extensin and extensin-like cDNAs: structure and expression in response to
 A:Reference number: S14970; MUID:91329690; PMID:1714316
 A:Accession: S14983
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-130 <SHO>
 A:Cross-references: UNIPARC:UPI000017B08A; EMBL:X55694
 A:Experimental source: cv. UC82B
 C:Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 100.0%; Score 48; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 54 HHHHHH 59

RESULT 17

139193
 gene HOXA1 protein - human
 C:Species: Homo sapiens (man)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
 C:Accession: 139193
 R:Charlot, A.; Moreau, L.; Senterre, G.; Sobel, M.; Castronovo, V.
 Biochem. Biophys. Res. Commun. 215, 713-720, 1995
 A>Title: Retinoic acid induces three newly cloned HOXA1 transcripts in MCF7 breast cancer
 A:Reference number: 139192; MUID:96011836; PMID:7488013
 A:Accession: 139193
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-132 <RES>
 A:Cross-references: UNIPARC:UPI000015FF40; EMBL:U37431; NID:G1051226; PIDN:AAC50250.1; P
 C:Genetics:
 A:Gene: GDB:HOXA1
 A:Cross-references: GDB:120652; OMIM:142955
 A:Map position: 7p15.3-7p15.3
 A:Introns: 113/3
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 100.0%; Score 48; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 60 HHHHHH 65

RESULT 18

B30242
 stem cell protein ERA-1-199, retinoic acid-induced - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Dec-2004
 C:Accession: B30242
 R:LaRosa, G.J.; Gudas, L.J.
 Mol. Cell. Biol. 8, 3906-3917, 1988
 A>Title: Early retinoic acid-induced F9 teratocarcinoma stem cell gene ERA-1: alternate
 A:Reference number: A30242; MUID:89127233; PMID:2906112
 A:Accession: B30242
 A:Molecule type: mRNA
 A:Residues: 1-133 <LAR>
 A:Cross-references: UNIPROT:P09022; UNIPARC:UPI000002AB6D; GB:M22115; NID:G193047; PIDN:
 C:Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulation

Query Match 100.0%; Score 48; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 Db 60 HHHHHH 65

RESULT 19

T22959
 hypothetical protein F58H10.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22959
 R:McMurray, A.
 submitted to the EMBL Data Library, September 1996
 A:Reference number: Z19643
 A:Accession: T22959
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-136 <MII>
 A:Cross-references: UNIPROT:Q93827; UNIPARC:UPI000007ERCA; EMBL:Z79697; PIDN:CAB01975.1;
 A:Experimental source: clone F58H10
 C:Genetics:
 A:Gene: CESP:F58H10.1

A:Map position: 1
A:introns: 103/2

Query Match 100.0%; Score 48; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
DB 77 HHHHHH 82

RESULT 20
T33968
hypothetical protein F46E10.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33968
R:Johnson, D.; Bradshaw, H.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid F46E10.
A:Reference number: Z21446
A:Accession: T33968
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Structure: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-139 <J0H>
A:Molecule type: DNA
A:Cross-references: UNIPROT:Q9UAV7; UNIPARC:UPI000007704D; EMBL:AF125955; P1DN:AD14713.
C:Genetic8:
A:Gene: CESP:F46E10.2
A:Map position: 5
A:introns: 22/1; 82/2

Query Match 100.0%; Score 48; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
DB 121 HHHHHH 126

RESULT 21
T06554
probable profilin PRO3 - wheat
C:Species: *Triticum aestivum* (common wheat)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06554
R:Rihns, H.P.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z15756
A:Accession: T06554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-140 <RIH>
A:Cross-references: UNIPROT:P49234; UNIPARC:UPI0000132294; EMBL:X89827; NID:G1008444; PI
A:Experimental source: cv. Tam 107; 13 day seedlings
C:Genetics:
A:Gene: PRO3
C:Superfamily: profilin
C:Keywords: actin binding; cytoskeleton

Query Match 100.0%; Score 48; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
DB 135 HHHHHH 140

RESULT 22
A54523

histidine-rich protein - *Plasmodium lophurae* (fragment)
C:Species: *Plasmodium lophurae*
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 31-Dec-2004
C:Accession: A54523
R:Irving, D.O.; Cross, G.A.M.; Feder, R.; Wallach, M.
Mol. Biochem. Parasitol. 18, 223-234, 1986
A:Title: Structure and organization of the histidine-rich protein gene of *Plasmodium lopi*
A:Reference number: A54523; MUID:86174893; PMID:3007981
A:Accession: A54523
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <IRV>
A:Cross-references: UNIPROT:Q26056; UNIPARC:UPI000007C1E6; GB:M15317; NID:G160331; P1DN::

C:Superfamily: surface antigen spar
C:Keywords: tandem repeat

Query Match 100.0%; Score 48; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
DB 1 HHHHHH 6

RESULT 23
T19083
hypothetical protein C08B6.10 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19083
R:Wilkinson, J.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19070
A:Accession: T19083
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-140 <WIL>
A:Cross-references: UNIPROT:Q17821; UNIPARC:UPI00000793A5; EMBL:Z72502; P1DN:CAA96592.1;
A:Experimental source: clone C08B6
C:Genetics:
A:Gene: CESP:C08B6.10
A:Map position: 5
A:introns: 22/2

Query Match 100.0%; Score 48; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
DB 102 HHHHHH 107

RESULT 24
T06553
probable profilin PRO2 - wheat
C:Species: *Triticum aestivum* (common wheat)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06553
R:Rihns, H.P.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z15756
A:Accession: T06553
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-141 <RIH>
A:Cross-references: UNIPROT:P49233; UNIPARC:UPI000013228A; EMBL:X89826; NID:G1008442; PI
A:Experimental source: cv. Tam 107; 13 day seedlings
C:Genetics:
A:Gene: PRO2
C:Superfamily: profilin
C:Keywords: actin binding; cytoskeleton

Query Match 100.0%; Score 48; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||
Db 136 HHHHHH 141

RESULT 25

B64421 conserved hypotheoretical protein MJ0970 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Jul-2004

C:Accession: B64421
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodok, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087

A:Accession: B64421

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-143 <BU>

A:Cross-references: UNIPROT:O58380; UNIPARC:UPI000013959A; GB:U67540; GB:L77117; NID:915

C:Genetics:

A:Map position: REV904629-904198

C:Superfamily: cobaltochelatase/ferrochelatase CblX/SixB

Query Match 100.0%; Score 48; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||
Db 99 HHHHHH 104

RESULT 26

T51065 hypotheoretical protein B12F1.170 [imported] - Neurospora crassa

C:Species: Neurospora crassa
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000

C:Accession: T51065
R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25286

A:Accession: T51065

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-172 <SCH>

A:Cross-references: UNIPARC:UPI0000179F4B; EMBL:AL390091; GSPDB:GN00116; NCSP:B12F1.170

A:Experimental source: BAC clone B12F1; strain OR74A

C:Genetics:

A:Gene: NCSP:B12F1.170

A:Map position: 6

A:introns: 51/3; 125/2

C:Superfamily: Neurospora crassa hypotheoretical protein B12F1.170

Query Match 100.0%; Score 48; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||
Db 83 HHHHHH 88

RESULT 27

T48265

hypotheoretical protein T22P11.30 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C:Accession: T48265

R:Beyan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24490

A:Accession: T48265

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-176 <BY>

A:Cross-references: UNIPROT:O9LZ58; UNIPARC:UPI000090DABC; EMBL:AL162971

A:Experimental source: cultivar Columbia; BAC clone T22P11

C:Genetics:

A:Map position: 5

A:introns: 4/3; 61/3

A:Note: T22P11.30

Query Match 100.0%; Score 48; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||
Db 27 HHHHHH 32

RESULT 28

B84774 probable RING zinc finger protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: B84774

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Wolfat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: B84774

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-180 <STO>

A:Cross-references: UNIPROT:O9SJS9; UNIPARC:UPI000009EB11; GB:AE002093; NID:94510378; P

C:Genetics:

A:Gene: At2g35910

A:Map position: 2

Query Match 100.0%; Score 48; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||
Db 71 HHHHHH 76

RESULT 29

T39367 hypotheoretical protein SPBC1289.16c - fission yeast (Schizosaccharomyces pombe) (fragment)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T39367

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D.

submitted to the EMBL Data Library, March 1999

A:Reference number: Z21848

A:Accession: T39367

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-192 <WOO>

A:Cross-references: UNIPROT:O42890; UNIPARC:UPI0000162111; EMBL:AL035675; PIDN:CAB3869

A:Experimental source: strain 972h-; cosmid c1289

C:Genetics:

A:Gene: SPDB:SPBC1289.16c
A:Map position: 2

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 192;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
140 HHHHHH 145

RESULT 30

T25384
hypothetical protein T27F6.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25384

R:DoBson, R.
submitted to the EMBL Data Library, November 1996
A:Accession: T25384

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-206 <WIL>
A:Cross-references: UNIPROT:O45868; UNIPARC:UPI000007F4P2; EMBL:Z82060; PIDN:CAB04883.1;
A:Experimental source: clone T27F6

C:Genetics:
A:Gene: CESP:T27F6.4
A:Map position: 1
A:Introns: 61/3; 154/3

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 206;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
116 HHHHHH 121

RESULT 31

T24446
hypothetical protein T04C10.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24446

R:Burton, J.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19891

A:Accession: T24446
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-208 <WIL>
A:Cross-references: UNIPROT:Q22156; UNIPARC:UPI000007C102; EMBL:Z69885; PIDN:CAA93757.1;
A:Experimental source: clone T04C10

C:Genetics:
A:Gene: CESP:T04C10.4
A:Map position: X
A:Introns: 91/3; 183/3

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 208;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
30 HHHHHH 35

RESULT 32

I53100
ehand - mouse

C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I53100

R:Caerjeff, P.; Brown, D.; Lyons, G.E.; Olson, E.N.
Dev. Biol. 170, 664-678, 1995
A:Title: Expression of the novel basic helix-loop-helix gene ehAND in neural crest deriv

A:Reference number: I53100; MUID:95377552; PMID:7649392
A:Accession: I53100

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-216 <RES>
A:Cross-references: UNIPARC:UPI0000024164; GB:S79216; NID:g1086931; PIDN:AAB35104.1; PII

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 216;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
9 HHHHHH 14

RESULT 33

T32443
hypothetical protein T28B4.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T32443

R:Wilson, R.; Greco, T.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid T28B4.

A:Reference number: Z21168
A:Accession: T32443
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-219 <WIL>
A:Cross-references: UNIPARC:UPI000017BBFB; EMBL:AF026206; PIDN:AAB71260.1; GSPDB:GN00028

A:Experimental source: strain Bristol N2; clone T28B4
C:Genetics:
A:Gene: CESP:T28B4.4
A:Map position: X
A:Introns: 34/2; 138/2; 184/3

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 219;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
38 HHHHHH 43

RESULT 34

I59192
gene HOXA1 protein - human

C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
C:Accession: I59192

R:Chariot, A.; Moreau, L.; Senferrer, G.; Sobel, M.; Castronovo, V.
Biochem. Biophys. Res. Commun. 215, 713-720, 1995
A:Title: Retinoic acid induces three newly cloned HOXA1 transcripts in MCF7 breast cancer

A:Reference number: I59192; MUID:96011836; PMID:7488013
A:Accession: I59192
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-222 <RES>
A:Cross-references: UNIPARC:UPI000016A264; EMBL:U37431; NID:g1051226; PIDN:AAC50248.1; P

C:Genetics:
A:Gene: GDB:HOXA1
A:Cross-references: GDB:120652; OMIM:142955
A:Map position: 7p15.3-7p15.3

C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

```

Query Match          100.0%; Score 48; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
    |||||
Db 60 HHHHHH 65

RESULT 35
T47866
regulatory protein-like - Arabidopsis thaliana
N:Alternate names: protein T8B10.210
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 12-Jul-2004
C:Accession: T47866
R:Reiger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224478
A:Accession: T47866
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <RIB>
A:CROSS-references: UNIPROT:Q9M205; UNIPARC:UPI000009F73B; EMBL:AL138646
C:Genetics:
A:Map position: 3
A:introns: 137/2
A>Note: T8B10.210
C:Superfamily: negative regulatory factor PREG

Query Match          100.0%; Score 48; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
    |||||
Db 218 HHHHHH 223

RESULT 36
D89101
protein F25E5.8 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89101
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: See websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elg
A>Note: published extra appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D89101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-235 <STO>
A:CROSS-references: UNIPROT:Q76647; UNIPARC:UPI000007715A; GB:chr_V; PIRN:AAC27331.1; PI
C:Genetics:
A>Note: weak similarity to POU transcription factors
A:Gene: F25E5.8
A:Map position: 5

Query Match          100.0%; Score 48; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
    |||||
Db 114 HHHHHH 119

RESULT 37
S41512

```

```

Brn-3b protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
C:Accession: S41512
R:Theil, T.; McLean-Hunter, S.; Zoernig, M.; Moeroy, T.
Nucleic Acids Res. 21, 5921-5929, 1993
A>Title: Mouse Brn-3 family of POU transcription factors: a new aminoterminal domain is
A:Reference number: S41511; MUID:94119691; PMID:8290353
A:Accession: S41512
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-236 <THE>
A:CROSS-references: UNIPARC:UPI00000E5952
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:91-161/Domain: POU domain homology <POU>
F:180-236/Domain: homeobox homology <HOX>

Query Match          100.0%; Score 48; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
    |||||
Db 78 HHHHHH 83

RESULT 38
E86346
F16F4.1 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86346
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewart, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86346
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <STO>
A:CROSS-references: UNIPROT:Q9LMP5; UNIPARC:UPI00000A94EA; GB:AE005172; NID:G8920630; P
C:Genetics:
A:Map position: 1

Query Match          100.0%; Score 48; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
    |||||
Db 154 HHHHHH 159

RESULT 39
S41511
Brn-3a protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
C:Accession: S41511
R:Theil, T.; McLean-Hunter, S.; Zoernig, M.; Moeroy, T.
Nucleic Acids Res. 21, 5921-5929, 1993
A>Title: Mouse Brn-3 family of POU transcription factors: a new aminoterminal domain is
A:Reference number: S41511; MUID:94119691; PMID:8290353
A:Accession: S41511
A:Status: preliminary
A:Molecule type: mRNA

```

A;Residues: 1-255 <THE>
 A;Cross-references: UNIPARC:UPI000017A2E0
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;110-180/Domain: POU domain homology <POU>
 F;199-255/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 48; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 100 HHHHHH 105

RESULT 40
 T51679
 myb-related transcription factor MYB74 [imported] - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Dec-2004
 C;Accession: T51679

R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
 Paz-Ares, J.; Weisshart, B.
 Plant J. 16, 263-276, 1998

A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
 A;Reference number: 214349; MUID:9839469; PMID:9839469

A;Accession: T51679

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-259 <KRA>

A;Cross-references: UNIPROT:Q9ZTC8; UNIPARC:UPI00009052B; EMBL:AF062907; PIDN:MAC83629.

A;Experimental source: cultivar Columbia

C;Genetics:

A;Gene: MYB74

A;Map position: IV

C;Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

C;Keywords: transcription factor

Query Match 100.0%; Score 48; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 84 HHHHHH 89

RESULT 41
 A70359
 hydrogenase expression/formation protein B - Aquifex aeolicus

C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 31-Dec-2004
 C;Accession: A70359

R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
 V.

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: A70359

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-259 <AOQ>

A;Cross-references: UNIPROT:O66901; UNIPARC:UPI0000563FF; GB:AE000701; NID:g2983260; PI

A;Experimental source: strain VFS

C;Genetics:

A;Gene: hysB

C;Superfamily: N1(2+)-binding GTPase ([Nife]-hydrogenase/urease maturation factor)

Query Match 100.0%; Score 48; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

DB 18 HHHHHH 23

RESULT 42

E86300
 protein F309.30 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E86300

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasey, T.H.; Dewar, K.,
 ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltl, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E86300

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-259 <STO>

A;Cross-references: UNIPROT:Q9SA48; UNIPARC:UPI00005EB54; GB:AE005172; NID:g4966370; PI

C;Genetics:

A;Map position: 1

C;Superfamily: Arabidopsis thaliana hypothetical protein YUPH12R.23

Query Match 100.0%; Score 48; DB 2; Length 259;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 96 HHHHHH 101

RESULT 43

A56446
 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C;Species: Mus musculus (house mouse)

C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C;Accession: A56446

R;Tang, P.M.; Folz, L.A.; Mahoney, W.C.; Schueler, P.A.
 J. Biol. Chem. 270, 7829-7835, 1995

A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identic

A;Reference number: A56446; MUID:95229583; PMID:7713873

A;Accession: A56446

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-268 <TAN>

A;Cross-references: UNIPARC:UPI000017C6D0; GB:U20617

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 48; DB 2; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 DB 246 HHHHHH 251

RESULT 44

F96506
 hypothetical protein T12C22.4 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: F96506

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasey, T.H.; Dewar, K.,

ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Malt, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.M.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: P96506
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-269 <STO>
 A:Cross-references: UNIPROT:Q9LPR4; UNIPARC:UPI00000A76A7; GB:AE005173; NID:g8655987; PI
 A:Gene: T12C22.4
 A:Map position: 1

Query Match 100.0%; Score 48; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 28 HHHHHH 33

RESULT 45
 knob protein - malaria parasite (*Plasmodium falciparum*) (fragments)
 C:Species: *Plasmodium falciparum*
 C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
 C:Accession: A26480
 R:Kilejian, A.; Sharma, Y.D.; Karoui, H.; Naslund, L.
 Proc. Natl. Acad. Sci. U.S.A. 83, 7938-7941, 1986
 A:Title: Histidine-rich domain of the knob protein of the human malaria parasite *Plasmod*
 A:Reference number: A26480; MUID:87017062; PMID:3532126
 A:Accession: A26480
 A:Molecule type: mRNA
 A:Residues: 1-270 <KIL>
 A:Cross-references: UNIPROT:P09346; UNIPARC:UPI000016B96; GB:M14210; NID:g160361; PIDN:
 C:Superfamily: knob-associated histidine-rich protein

Query Match 100.0%; Score 48; DB 2; Length 270;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 63 HHHHHH 68

RESULT 46
 T02334
 probable urease accessory protein [imported] - *Arabidopsis thaliana*
 N:Alternate names: urease accessory protein G homolog F13P17.30
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 31-Dec-2004
 C:Accession: T02334; A84757
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, July 1998
 A:Description: *Arabidopsis thaliana* chromosome II BAC F13P17 genomic sequence.
 A:Reference number: Z14657
 A:Accession: T02334
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-275 <ROU>
 A:Cross-references: UNIPROT:O64700; UNIPARC:UPI000000C5C0; EMBL:AC004481; NID:g3337347;
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Motilal, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J
 Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84757
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <STO>
 A:Cross-references: UNIPARC:UPI000000C5C0; GB:AE002093; NID:g3128220; PIDN:AAC26700.1; G
 C:Gene: At2g34470; F13P17.30
 A:Map position: 2
 A:introns: 18/2; 85/2; 105/3; 173/1; 213/3; 248/3
 C:Superfamily: N1(2+)-binding GTPase ([N1fe]-hydrogenase/urease maturation factor)

Query Match 100.0%; Score 48; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 6 HHHHHH 11

RESULT 47
 E84766
 probable AT-hook DNA-binding protein [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 05-Oct-2004
 C:Accession: E84766
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Motilal, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84766
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-285 <STO>
 A:Cross-references: UNIPROT:O82166; UNIPARC:UPI00000A14DC; GB:AE002093; NID:g3668079; PI
 C:Gene: At2g35270
 A:Map position: 2
 C:Superfamily: AT-hook DNA-binding protein

Query Match 100.0%; Score 48; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 40 HHHHHH 45

RESULT 48
 T21868
 hypothetical protein F36G9.11 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T21868
 R:Wall, M.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19481
 A:Accession: T21868
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-290 <WIL>
 A:Cross-references: UNIPROT:O45469; UNIPARC:UPI0000061011; EMBL:Z81533; PIDN:CAB04330.1
 A:Experimental source: clone F36G9
 C:Gene: CESP:F36G9.11
 A:Map position: 5
 A:introns: 130/3; 234/2

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:00:40 ; Search time 235 Seconds
(without alignments)
18.013 Million cell updates/sec

Title: US-10-719-523-5
Perfect score: 48
Sequence: 1 HHHHHH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------|----------------------|
| 1 | 48 | 100.0 | 15 | 1 LPHI_YERPE | Q8d079 yerxina pe |
| 2 | 48 | 100.0 | 16 | 1 LPHI_ECO57 | Q8xct5 escherichia |
| 3 | 48 | 100.0 | 16 | 1 LPHI_ECOL6 | P60996 escherichia |
| 4 | 48 | 100.0 | 16 | 1 LPHI_ECOL1 | P60995 escherichia |
| 5 | 48 | 100.0 | 16 | 1 LPHI_KUEPN | Q48439 klebsiella |
| 6 | 48 | 100.0 | 30 | 1 LPHI_SALTY | P60997 salmoneila |
| 7 | 48 | 100.0 | 30 | 2 Q5C5K5_SCHJA | Q5C5K5 schistosoma |
| 8 | 48 | 100.0 | 31 | 2 Q6UGP2_PEA | Q6UGP2 pium sativ |
| 9 | 48 | 100.0 | 31 | 2 Q6UGP3_PEA | Q6UGP3 pium sativ |
| 10 | 48 | 100.0 | 31 | 2 Q6UGP5_PEA | Q6UGP5 pium sativ |
| 11 | 48 | 100.0 | 31 | 2 Q6UGP7_PEA | Q6UGP7 pium sativ |
| 12 | 48 | 100.0 | 31 | 2 Q5S0G0_MOUSE | Q5S0G0 mus musculu |
| 13 | 48 | 100.0 | 34 | 2 Q4YAH2_PLABE | Q4YAH2 plasmodium |
| 14 | 48 | 100.0 | 44 | 2 Q65825_9BACU | Q65825 plasmodium |
| 15 | 48 | 100.0 | 46 | 2 Q5ISMI_MACFA | Q5ISMI macaca fasc |
| 16 | 48 | 100.0 | 48 | 2 Q8SAS0_PINSY | Q8SAS0 pinus sylve |
| 17 | 48 | 100.0 | 48 | 2 Q8SAS1_PINSY | Q8SAS1 pinus sylve |
| 18 | 48 | 100.0 | 53 | 2 Q5C2J2_SCHJA | Q5C2J2 schistosoma |
| 19 | 48 | 100.0 | 53 | 2 Q55244_92ZZZ | Q55244 plasmod pet |
| 20 | 48 | 100.0 | 54 | 2 Q4WHB8_ASPFU | Q4WHB8 aspergillus |
| 21 | 48 | 100.0 | 58 | 2 Q6TH19_DROME | Q6TH19 drosophila |
| 22 | 48 | 100.0 | 59 | 1 HPN_HELPU | HPNHELPU helicobacte |
| 23 | 48 | 100.0 | 59 | 1 HPN_HELPU | HPNHELPU helicobacte |
| 24 | 48 | 100.0 | 64 | 2 Q40049_HORVU | Q40049 hordeum vul |
| 25 | 48 | 100.0 | 66 | 2 Q6IYH9_DROME | Q6IYH9 drosophila |
| 26 | 48 | 100.0 | 69 | 2 Q6R2V8_TRIPE | Q6R2V8 trichoderma |
| 27 | 48 | 100.0 | 69 | 2 Q4TOL0_GIBZE | Q4TOL0 gibberella |
| 28 | 48 | 100.0 | 69 | 2 Q9PT65_XETLA | Q9PT65 xenopus lae |
| 29 | 48 | 100.0 | 72 | 2 Q54KT2_DICDI | Q54KT2 dictyostei |
| 30 | 48 | 100.0 | 72 | 2 Q8T1A1_DICDI | Q8T1A1 dictyostei |
| 31 | 48 | 100.0 | 72 | 2 Q25973_HELPU | Q25973 helicobacte |

| | | | | | |
|-----|----|-------|-----|-----------------|---------------------|
| 32 | 48 | 100.0 | 75 | 2 Q8T3D9_CAEEL | Q8T3D9 caenorhabdi |
| 33 | 48 | 100.0 | 76 | 2 Q9VTH4_DROME | Q9VTH4 drosophila |
| 34 | 48 | 100.0 | 77 | 2 Q20690_CAEEL | Q20690 caenorhabdi |
| 35 | 48 | 100.0 | 77 | 2 Q9ZJ18_HELPU | Q9ZJ18 helicobacte |
| 36 | 48 | 100.0 | 80 | 2 Q61310_CAEER | Q61310 caenorhabdi |
| 37 | 48 | 100.0 | 80 | 2 Q7JPU3_CAEEL | Q7JPU3 caenorhabdi |
| 38 | 48 | 100.0 | 82 | 2 Q61DQ0_CAEER | Q61DQ0 caenorhabdi |
| 39 | 48 | 100.0 | 83 | 2 Q20689_CAEEL | Q20689 caenorhabdi |
| 40 | 48 | 100.0 | 84 | 2 Q615X5_CAEER | Q615X5 caenorhabdi |
| 41 | 48 | 100.0 | 85 | 2 Q58WZ3_ORENT | Q58WZ3 orochromis |
| 42 | 48 | 100.0 | 86 | 2 Q5TRG3_ANOGA | Q5TRG3 anopheles g |
| 43 | 48 | 100.0 | 87 | 2 Q61311_CAEER | Q61311 caenorhabdi |
| 44 | 48 | 100.0 | 87 | 2 Q61HCE_DROME | Q61HCE drosophila |
| 45 | 48 | 100.0 | 89 | 2 Q861J4_DICDI | Q861J4 dictyostei |
| 46 | 48 | 100.0 | 89 | 2 Q6EPJ7_ORYSA | Q6EPJ7 oryza sativ |
| 47 | 48 | 100.0 | 89 | 2 Q598K8_AGRXA | Q598K8 agrostodon |
| 48 | 48 | 100.0 | 91 | 2 Q5Z4U9_ORYSA | Q5Z4U9 oryza sativ |
| 49 | 48 | 100.0 | 92 | 2 Q18410_CAEEL | Q18410 caenorhabdi |
| 50 | 48 | 100.0 | 93 | 2 Q861J4_DICDI | Q861J4 dictyostei |
| 51 | 48 | 100.0 | 94 | 2 Q5MTV4_AEDAL | Q5MTV4 aedes albop |
| 52 | 48 | 100.0 | 94 | 2 Q6ND72_RHOPA | Q6ND72 rhodopseudo |
| 53 | 48 | 100.0 | 97 | 2 Q5MIX7_AEDAL | Q5MIX7 aedes albop |
| 54 | 48 | 100.0 | 101 | 2 Q5AHK9_CANAL | Q5AHK9 candida alb |
| 55 | 48 | 100.0 | 102 | 2 Q59QY5_CANAL | Q59QY5 candida alb |
| 56 | 48 | 100.0 | 102 | 2 Q9VUEL_DROME | Q9VUEL drosophila |
| 57 | 48 | 100.0 | 102 | 2 Q94189_CAEEL | Q94189 caenorhabdi |
| 58 | 48 | 100.0 | 103 | 2 Q970X8_SULTO | Q970X8 sulfolobus |
| 59 | 48 | 100.0 | 104 | 2 Q7PKYA_ANOGA | Q7PKYA anopheles g |
| 60 | 48 | 100.0 | 104 | 2 Q6ETKI_DICDI | Q6ETKI dictyostei |
| 61 | 48 | 100.0 | 104 | 2 Q46246_SUIPT | Q46246 drosophila |
| 62 | 48 | 100.0 | 107 | 2 Q9VQW5_DROME | Q9VQW5 drosophila |
| 63 | 48 | 100.0 | 108 | 2 Q5ADL5_CANAL | Q5ADL5 candida alb |
| 64 | 48 | 100.0 | 109 | 2 Q8WXA9_9ECAN | Q8WXA9 holopneuste |
| 65 | 48 | 100.0 | 109 | 2 Q9D6B9_MOUSE | Q9D6B9 mus musculu |
| 66 | 48 | 100.0 | 112 | 2 Q8WXB0_9ECAN | Q8WXB0 holopneuste |
| 67 | 48 | 100.0 | 113 | 2 Q5A9C8_CANAL | Q5A9C8 candida alb |
| 68 | 48 | 100.0 | 113 | 2 Q5TWL5_ANOGA | Q5TWL5 anopheles g |
| 69 | 48 | 100.0 | 113 | 2 Q7PL00_ANOGA | Q7PL00 anopheles g |
| 70 | 48 | 100.0 | 113 | 2 Q5OL74_ORYSA | Q5OL74 oryza sativ |
| 71 | 48 | 100.0 | 113 | 2 Q6Z1U5_ORYSA | Q6Z1U5 oryza sativ |
| 72 | 48 | 100.0 | 114 | 1 A8R2_LYCES | P37219 lycopersico |
| 73 | 48 | 100.0 | 114 | 2 Q61GR9_DROME | Q61GR9 drosophila |
| 74 | 48 | 100.0 | 114 | 2 Q40165_LYCES | Q40165 lycopersico |
| 75 | 48 | 100.0 | 114 | 2 Q7XYV3_LYCES | Q7XYV3 lycopersico |
| 76 | 48 | 100.0 | 114 | 2 Q7XYV4_LYCES | Q7XYV4 lycopersico |
| 77 | 48 | 100.0 | 114 | 2 Q7XYV6_LYCHI | Q7XYV6 lycopersico |
| 78 | 48 | 100.0 | 114 | 2 Q84ZL8_ORYSA | Q84ZL8 oryza sativ |
| 79 | 48 | 100.0 | 115 | 2 Q9YAU2_AERPE | Q9YAU2 aetopyrum p |
| 80 | 48 | 100.0 | 115 | 2 Q5MIX6_AEDAL | Q5MIX6 aedes albop |
| 81 | 48 | 100.0 | 115 | 2 Q559F6_DICDI | Q559F6 dictyostei |
| 82 | 48 | 100.0 | 116 | 2 Q59L13_CANAL | Q59L13 candida alb |
| 83 | 48 | 100.0 | 117 | 2 Q59U45_CANAL | Q59U45 candida alb |
| 84 | 48 | 100.0 | 117 | 2 Q67WD5_ORYSA | Q67WD5 oryza sativ |
| 85 | 48 | 100.0 | 118 | 2 Q60WMS_CAEER | Q60WMS caenorhabdi |
| 86 | 48 | 100.0 | 118 | 2 Q7JJP1_CAEEL | Q7JJP1 caenorhabdi |
| 87 | 48 | 100.0 | 119 | 2 Q59JW6_CANAL | Q59JW6 candida alb |
| 88 | 48 | 100.0 | 119 | 2 Q938Z7_CAEEL | Q938Z7 caenorhabdi |
| 89 | 48 | 100.0 | 120 | 2 Q592P7_LYMST | Q592P7 lymanea tra |
| 90 | 48 | 100.0 | 122 | 2 Q96Z09_SULTO | Q96Z09 sulfolobus |
| 91 | 48 | 100.0 | 122 | 2 Q23089_ARATH | Q23089 arabidopsis |
| 92 | 48 | 100.0 | 122 | 2 Q9FJCS_ARATH | Q9FJCS arabidopsis |
| 93 | 48 | 100.0 | 122 | 2 Q4SXT2_TETNG | Q4SXT2 terradon n |
| 94 | 48 | 100.0 | 123 | 2 Q54CDS_DICDI | Q54CDS dictyostei |
| 95 | 48 | 100.0 | 124 | 2 Q5D9C9_SCHJA | Q5D9C9 schistosoma |
| 96 | 48 | 100.0 | 124 | 2 Q61IK5_DROME | Q61IK5 drosophila |
| 97 | 48 | 100.0 | 127 | 2 Q7QUP8_ANOGA | Q7QUP8 anopheles g |
| 98 | 48 | 100.0 | 127 | 2 Q84LH6_ORYSA | Q84LH6 oryza sativ |
| 99 | 48 | 100.0 | 127 | 2 Q82ZN4_ENTFA | Q82ZN4 enterococcu |
| 100 | 48 | 100.0 | 128 | 2 Q4JBM7_SULAC | Q4JBM7 sulfolobus |
| 101 | 48 | 100.0 | 132 | 2 Q59S89_CANAL | Q59S89 candida alb |
| 102 | 48 | 100.0 | 132 | 2 Q61L47_DROME | Q61L47 drosophila |
| 103 | 48 | 100.0 | 132 | 2 Q7X1Z6_ORYSA | Q7X1Z6 oryza sativ |
| 104 | 48 | 100.0 | 132 | 2 Q9XY97_LAMPFL | Q9XY97 lampectra fl |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|--------------|---------------------|-----|----|-------|-----|---|--------------|---------------------|
| 105 | 48 | 100.0 | 135 | 2 | Q4TES1_TETNG | Q4tes1 tetraodon n | 178 | 48 | 100.0 | 164 | 2 | Q8N033_9D1PT | Q8n033 drosophila |
| 106 | 48 | 100.0 | 136 | 2 | Q08657_RAT | Q08657 rattus norv | 179 | 48 | 100.0 | 164 | 2 | Q69J28_ORYSA | Q69j28 oryza sativ |
| 107 | 48 | 100.0 | 137 | 2 | Q54KZ0_DICDI | Q54kz0 dictyosteli | 180 | 48 | 100.0 | 165 | 2 | Q8N016_9D1PT | Q8n016 drosophila |
| 108 | 48 | 100.0 | 137 | 2 | Q61I16_DROME | Q61i16 drosophila | 181 | 48 | 100.0 | 165 | 2 | Q8N019_9D1PT | Q8n019 drosophila |
| 109 | 48 | 100.0 | 137 | 2 | Q8ENS9_OCBRI | Q8ens9 oceanobacti | 182 | 48 | 100.0 | 165 | 2 | Q8N022_9D1PT | Q8n022 drosophila |
| 110 | 48 | 100.0 | 138 | 2 | Q4TVN3_SHEEP | Q4tvn3 ovis aries | 183 | 48 | 100.0 | 165 | 2 | Q8N024_9D1PT | Q8n024 drosophila |
| 111 | 48 | 100.0 | 138 | 2 | Q4TV04_MALZE | Q4tv04 zea mays (m | 184 | 48 | 100.0 | 165 | 2 | Q8N026_9D1PT | Q8n026 drosophila |
| 112 | 48 | 100.0 | 139 | 2 | Q9UAV7_CABEL | Q9uav7 caenorhabdi | 185 | 48 | 100.0 | 165 | 2 | Q8N031_DROAV | Q8n031 drosophila |
| 113 | 48 | 100.0 | 140 | 1 | PROF3_WHEAT | PROF3 tritlicum ae | 186 | 48 | 100.0 | 165 | 2 | Q8N034_9D1PT | Q8n034 drosophila |
| 114 | 48 | 100.0 | 140 | 1 | Q26056_PLALO | Q26056 plasmodium | 187 | 48 | 100.0 | 165 | 2 | Q6BD24_XENLA | Q6bd24 xenopus lae |
| 115 | 48 | 100.0 | 140 | 2 | Q17821_CABEL | Q17821 caenorhabdi | 188 | 48 | 100.0 | 166 | 2 | Q8N021_9D1PT | Q8n021 drosophila |
| 116 | 48 | 100.0 | 140 | 2 | Q8RZM6_ORYSA | Q8rzm6 oryza sativ | 189 | 48 | 100.0 | 166 | 2 | Q8N037_9D1PT | Q8n037 drosophila |
| 117 | 48 | 100.0 | 140 | 2 | Q61G65_BRARE | Q61g65 brachydantio | 190 | 48 | 100.0 | 166 | 2 | Q61T41_DROME | Q61t41 drosophila |
| 118 | 48 | 100.0 | 140 | 2 | Q4TH05_TETNG | Q4th05 tetraodon n | 191 | 48 | 100.0 | 166 | 2 | Q5XG6_XENTR | Q5xg6 xenopus tro |
| 119 | 48 | 100.0 | 141 | 1 | PROF2_WHEAT | P49J33 tritlicum ae | 192 | 48 | 100.0 | 166 | 2 | Q61P57_XENLA | Q61p57 xenopus lae |
| 120 | 48 | 100.0 | 141 | 2 | Q6HL00_BACHK | Q6hl00 bacillus th | 193 | 48 | 100.0 | 167 | 2 | Q8N025_DROSR | Q8n025 drosophila |
| 121 | 48 | 100.0 | 141 | 2 | Q63DH7_BACCZ | Q63dh7 bacillus ce | 194 | 48 | 100.0 | 167 | 2 | Q8N038_9D1PT | Q8n038 drosophila |
| 122 | 48 | 100.0 | 142 | 2 | Q6NPG2_ARATH | Q6npg2 arabidopsis | 195 | 48 | 100.0 | 167 | 2 | Q8N044_9D1PT | Q8n044 drosophila |
| 123 | 48 | 100.0 | 142 | 2 | Q81FM0_BACCR | Q81fm0 bacillus ce | 196 | 48 | 100.0 | 167 | 2 | Q8N057_DROAI | Q8n057 drosophila |
| 124 | 48 | 100.0 | 142 | 2 | Q8U216_9PAPI | Q8u216 phocoena sp | 197 | 48 | 100.0 | 167 | 2 | O17346_CABEL | O17346 caenorhabdi |
| 125 | 48 | 100.0 | 143 | 1 | CBIX_METUA | Q58380 methanococc | 198 | 48 | 100.0 | 168 | 2 | Q7PX82_ANGGA | Q7px82 anopheles g |
| 126 | 48 | 100.0 | 143 | 1 | CBIX_METUA | Q8Y777 methanopyru | 199 | 48 | 100.0 | 168 | 2 | Q8N018_9D1PT | Q8n018 drosophila |
| 127 | 48 | 100.0 | 143 | 2 | Q615Y1_CABER | Q615y1 caenorhabdi | 200 | 48 | 100.0 | 169 | 2 | Q61H82_CABER | Q61h82 caenorhabdi |
| 128 | 48 | 100.0 | 143 | 2 | Q86N07_DROME | Q86nq7 drosophila | 201 | 48 | 100.0 | 169 | 2 | Q8N055_DROTO | Q8n055 drosophila |
| 129 | 48 | 100.0 | 144 | 1 | CBIX_METNP | P61819 methanococc | 202 | 48 | 100.0 | 169 | 2 | Q8N058_DROPS | Q8n058 drosophila |
| 130 | 48 | 100.0 | 145 | 2 | Q59LJ7_CANAL | Q59lj7 candida alb | 203 | 48 | 100.0 | 169 | 2 | Q8N059_DROPE | Q8n059 drosophila |
| 131 | 48 | 100.0 | 145 | 2 | O31510_BACSU | O31510 bacillus su | 204 | 48 | 100.0 | 169 | 2 | Q8N060_DROAM | Q8n060 drosophila |
| 132 | 48 | 100.0 | 145 | 2 | Q90Z07_ORYLA | Q90z07 oryzae lat | 205 | 48 | 100.0 | 170 | 2 | Q7SG33_NEUCR | Q7sg33 neurospora |
| 133 | 48 | 100.0 | 146 | 2 | Q91891_CHICK | Q91891 gallus gall | 206 | 48 | 100.0 | 171 | 2 | Q59Y98_CANAL | Q59y98 candida alb |
| 134 | 48 | 100.0 | 146 | 2 | Q4RCM5_TETNG | Q4rcm5 tetraodon n | 207 | 48 | 100.0 | 171 | 2 | Q8N056_DROBF | Q8n056 drosophila |
| 135 | 48 | 100.0 | 147 | 2 | Q5TX37_ANGGA | Q5tx37 anopheles g | 208 | 48 | 100.0 | 172 | 2 | Q502A3_BRARE | Q502a3 brachydantio |
| 136 | 48 | 100.0 | 148 | 2 | Q6BW81_DEBHA | Q6bw81 debaryomyce | 209 | 48 | 100.0 | 173 | 2 | Q59Y43_CANAL | Q59y43 candida alb |
| 137 | 48 | 100.0 | 148 | 1 | Q6LD46_9MURI | Q6ld46 rattus sp. | 210 | 48 | 100.0 | 174 | 2 | Q5E280_VIBF0 | Q5e280 vibrio fisc |
| 138 | 48 | 100.0 | 149 | 1 | Q8399B_DROME | Q8399b drosophila | 211 | 48 | 100.0 | 174 | 2 | Q951E0_CANFA | Q951e0 canis famli |
| 139 | 48 | 100.0 | 152 | 2 | Q8N014_DROEL | Q8n014 drosophila | 212 | 48 | 100.0 | 176 | 2 | Q81A55_CABEL | Q81a55 caenorhabdi |
| 140 | 48 | 100.0 | 152 | 2 | Q8N052_DROTK | Q8n052 drosophila | 213 | 48 | 100.0 | 176 | 2 | Q91Z58_ARATH | Q91z58 arabidopsis |
| 141 | 48 | 100.0 | 153 | 2 | Q8N050_9D1PT | Q8n050 drosophila | 214 | 48 | 100.0 | 178 | 2 | Q91TP3_ARATH | Q91tp3 arabidopsis |
| 142 | 48 | 100.0 | 154 | 2 | Q8N041_DROEU | Q8n041 drosophila | 215 | 48 | 100.0 | 181 | 2 | Q61K24_DROME | Q61k24 drosophila |
| 143 | 48 | 100.0 | 154 | 2 | Q8N048_9D1PT | Q8n048 drosophila | 216 | 48 | 100.0 | 183 | 2 | Q5D6J0_SCHJA | Q5d6j0 schistosoma |
| 144 | 48 | 100.0 | 155 | 2 | Q8N051_DROLT | Q8n051 drosophila | 217 | 48 | 100.0 | 183 | 2 | Q5Z8B9_ORYSA | Q5z8b9 oryza sativ |
| 145 | 48 | 100.0 | 155 | 2 | Q8N013_DROFC | Q8n013 drosophila | 218 | 48 | 100.0 | 185 | 2 | Q00837_LEIBR | Q00837 leishmania |
| 146 | 48 | 100.0 | 155 | 2 | Q8N039_DROYA | Q8n039 drosophila | 219 | 48 | 100.0 | 185 | 2 | Q4RFA3_TETNG | Q4rfa3 tetraodon n |
| 147 | 48 | 100.0 | 155 | 2 | Q8N040_DROYE | Q8n040 drosophila | 220 | 48 | 100.0 | 187 | 2 | Q6NLES_ARATH | Q6nles arabidopsis |
| 148 | 48 | 100.0 | 155 | 2 | Q8N042_9D1PT | Q8n042 drosophila | 221 | 48 | 100.0 | 188 | 2 | Q5AF41_CANAL | Q5af41 candida alb |
| 149 | 48 | 100.0 | 155 | 2 | Q8N047_DROAN | Q8n047 drosophila | 222 | 48 | 100.0 | 188 | 2 | Q61HR6_DROME | Q61hr6 drosophila |
| 150 | 48 | 100.0 | 156 | 2 | Q8N053_9D1PT | Q8n053 drosophila | 223 | 48 | 100.0 | 191 | 2 | Q59NL6_CANAL | Q59nl6 candida alb |
| 151 | 48 | 100.0 | 157 | 2 | Q8N043_9D1PT | Q8n043 drosophila | 224 | 48 | 100.0 | 191 | 2 | Q61KE7_DROME | Q61ke7 drosophila |
| 152 | 48 | 100.0 | 157 | 2 | Q8N045_9D1PT | Q8n045 drosophila | 225 | 48 | 100.0 | 192 | 2 | Q56WX8_ORENI | Q56wx8 oreochromis |
| 153 | 48 | 100.0 | 157 | 2 | Q8N049_9D1PT | Q8n049 drosophila | 226 | 48 | 100.0 | 192 | 1 | HUNB_DROAD | Q46232 drosophila |
| 154 | 48 | 100.0 | 157 | 2 | Q8N054_9D1PT | Q8n054 drosophila | 227 | 48 | 100.0 | 193 | 1 | HUNB_DROTA | Q46260 drosophila |
| 155 | 48 | 100.0 | 157 | 2 | Q8N054_9D1PT | Q8n054 drosophila | 228 | 48 | 100.0 | 193 | 1 | HUNB_DROIK | Q46242 drosophila |
| 156 | 48 | 100.0 | 158 | 1 | HUNB_DROMM | Q94F72 charina tri | 229 | 48 | 100.0 | 193 | 1 | Q7QIH3_ANGGA | Q7qih3 anopheles g |
| 157 | 48 | 100.0 | 158 | 1 | Q94577_HELER | Q94577 helicoidari | 230 | 48 | 100.0 | 195 | 1 | HUNB_DROPA | Q46262 drosophila |
| 158 | 48 | 100.0 | 159 | 1 | HUNB_DROSO | Q46258 drosophila | 231 | 48 | 100.0 | 196 | 1 | HUNB_DROXA | Q46234 drosophila |
| 159 | 48 | 100.0 | 159 | 2 | Q9YMT6_NPYLD | Q9ymt6 lymantria d | 232 | 48 | 100.0 | 196 | 1 | HUNB_DROSL | Q46236 drosophila |
| 160 | 48 | 100.0 | 159 | 2 | Q8JIL5_9CICH | Q8jil5 astrotocliap | 233 | 48 | 100.0 | 196 | 2 | Q7PPI4_ANGGA | Q7ppi4 anopheles g |
| 161 | 48 | 100.0 | 159 | 2 | Q8JIL6_ASPAL | Q8jil6 astatoreoch | 234 | 48 | 100.0 | 196 | 2 | Q61LFI_DROME | Q61lfi drosophila |
| 162 | 48 | 100.0 | 159 | 2 | Q8JIL7_9CICH | Q8jil7 trophus du | 235 | 48 | 100.0 | 197 | 2 | Q94F76_MALZE | Q94f76 zea mays (m |
| 163 | 48 | 100.0 | 159 | 2 | Q8JIL8_9CICH | Q8jil8 labidochrom | 236 | 48 | 100.0 | 198 | 1 | HUNB_DROCY | Q46238 drosophila |
| 164 | 48 | 100.0 | 160 | 2 | Q8N046_DROYA | Q8n046 drosophila | 237 | 48 | 100.0 | 198 | 1 | HUNB_DRODS | Q46240 drosophila |
| 165 | 48 | 100.0 | 161 | 2 | Q8N015_DROEC | Q8n015 drosophila | 238 | 48 | 100.0 | 198 | 1 | HUNB_DROLI | Q46244 drosophila |
| 166 | 48 | 100.0 | 161 | 2 | Q8N030_9D1PT | Q8n030 drosophila | 239 | 48 | 100.0 | 198 | 2 | Q61KWI_DROME | Q61kwi drosophila |
| 167 | 48 | 100.0 | 161 | 2 | Q54YM7_DICDI | Q54ym7 dictyosteli | 240 | 48 | 100.0 | 198 | 2 | Q7XQSO_ORYSA | Q7xqso oryza sativ |
| 168 | 48 | 100.0 | 162 | 2 | Q8N020_9D1PT | Q8n020 drosophila | 241 | 48 | 100.0 | 198 | 2 | Q61AM2_ORYSA | Q61am2 oryza sativ |
| 169 | 48 | 100.0 | 162 | 2 | Q8N035_DROBN | Q8n035 drosophila | 242 | 48 | 100.0 | 199 | 2 | Q61GJ3_DROME | Q61gj3 drosophila |
| 170 | 48 | 100.0 | 163 | 2 | Q8N017_9D1PT | Q8n017 drosophila | 243 | 48 | 100.0 | 199 | 2 | Q6YUUS_ORYSA | Q6yuus oryza sativ |
| 171 | 48 | 100.0 | 163 | 2 | Q8N036_9D1PT | Q8n036 drosophila | 244 | 48 | 100.0 | 199 | 2 | Q751R7_ORYSA | Q751r7 oryza sativ |
| 172 | 48 | 100.0 | 163 | 2 | Q7YTA3_9MYRI | Q7yta3 glomeris ma | 245 | 48 | 100.0 | 200 | 2 | Q61WN4_BRARE | Q61wn4 brachioosto |
| 173 | 48 | 100.0 | 164 | 2 | Q8N023_DROTS | Q8n023 drosophila | 246 | 48 | 100.0 | 200 | 2 | Q7Q0Z7_ANGGA | Q7q0z7 anopheles g |
| 174 | 48 | 100.0 | 164 | 2 | Q8N027_DROLN | Q8n027 drosophila | 247 | 48 | 100.0 | 200 | 2 | Q4STZ9_TETNG | Q4stz9 tetraodon n |
| 175 | 48 | 100.0 | 164 | 2 | Q8N028_DROKI | Q8n028 drosophila | 248 | 48 | 100.0 | 201 | 2 | Q4R176_CABEL | Q4r176 caenorhabdi |
| 176 | 48 | 100.0 | 164 | 2 | Q8N029_9D1PT | Q8n029 drosophila | 249 | 48 | 100.0 | 202 | 1 | HAND1_CHICK | Q90691 gallus gall |
| 177 | 48 | 100.0 | 164 | 2 | Q8N032_9D1PT | Q8n032 drosophila | 250 | 48 | 100.0 | 202 | 2 | Q6AV25_ORYSA | Q6av25 oryza sativ |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|--------------|---------------------|-----|----|-------|-----|---|--------------|---------------------|
| 251 | 48 | 100.0 | 203 | 2 | Q7S411_NEUCR | Q7S411_neurospora | 324 | 48 | 100.0 | 235 | 2 | Q76647_CABEL | Q76647_caenorhabdi |
| 252 | 48 | 100.0 | 203 | 2 | Q6S2S4_HUMAN | Q6S2S4_homo sapien | 325 | 48 | 100.0 | 235 | 2 | Q7X8E2_ORYSA | Q7X8E2_oryza sativ |
| 253 | 48 | 100.0 | 204 | 1 | HAND1_SHEEP | O28E55 ovis aries | 326 | 48 | 100.0 | 235 | 2 | Q6QPY7_MIMRI | Q6QPY7_mimulus rin |
| 254 | 48 | 100.0 | 206 | 2 | Q4S868_CABEL | O4S868 caenorhabdi | 327 | 48 | 100.0 | 236 | 2 | Q4MMU8_ASPFU | Q4MMU8_aspergillus |
| 255 | 48 | 100.0 | 207 | 2 | Q5TYJ3_BRARE | O5TYJ3 brachydanio | 328 | 48 | 100.0 | 236 | 2 | Q5T0S5_ANOGA | O5T0S5_anopheles g |
| 256 | 48 | 100.0 | 208 | 2 | Q9NFP3_LEIMA | O9NFP3 leishmania | 329 | 48 | 100.0 | 236 | 2 | Q6L1T5_CAEBR | Q6L1T5_caenorhabdi |
| 257 | 48 | 100.0 | 208 | 2 | Q6IGL9_DROME | O6IGL9 drosophila | 330 | 48 | 100.0 | 236 | 2 | Q7XPC7_ORYSA | Q7XPC7_oryza sativ |
| 258 | 48 | 100.0 | 208 | 2 | Q221S6_CABEL | O221S6 caenorhabdi | 331 | 48 | 100.0 | 236 | 2 | Q9QWE1_SMURI | Q9QWE1_mus sp. cla |
| 259 | 48 | 100.0 | 209 | 2 | Q5CPB5_CRYPV | O5CPB5 cryptospori | 332 | 48 | 100.0 | 237 | 2 | Q6QVK6_MIMCU | Q6QVK6_mimulus gut |
| 260 | 48 | 100.0 | 209 | 2 | Q5S8Z0_DICDI | O5S8Z0 dictyosteli | 333 | 48 | 100.0 | 238 | 2 | Q8C173_MOUSE | Q8C173_mus muscicu |
| 261 | 48 | 100.0 | 212 | 2 | Q564Y0_CABEL | O564Y0 caenorhabdi | 334 | 48 | 100.0 | 239 | 1 | CU058_HUMAN | P58S05 homo sapien |
| 262 | 48 | 100.0 | 212 | 2 | Q6RYE4_TRIMO | O6RYE4 triticum tu | 335 | 48 | 100.0 | 239 | 2 | Q9STB3_DROME | Q9STB3_drosophila |
| 263 | 48 | 100.0 | 212 | 2 | Q6RYE6_TRIMO | O6RYE6 triticum tu | 336 | 48 | 100.0 | 239 | 2 | Q721G6_TRYCR | Q721G6_trypanosoma |
| 264 | 48 | 100.0 | 212 | 2 | Q6RY79_TRIMO | O6RY79 triticum mo | 337 | 48 | 100.0 | 239 | 2 | Q9LMP5_ARATH | Q9LMP5_arabidopsis |
| 265 | 48 | 100.0 | 213 | 2 | Q6RY74_TRIMO | O6RY74 triticum mo | 338 | 48 | 100.0 | 240 | 2 | P84136_BACST | P84136_bacillus st |
| 266 | 48 | 100.0 | 213 | 2 | Q6RY76_TRIMO | O6RY76 triticum mo | 339 | 48 | 100.0 | 241 | 2 | Q54E84_DICDI | O54E84_dictyosteli |
| 267 | 48 | 100.0 | 213 | 2 | Q6RY77_TRIMO | O6RY77 triticum mo | 340 | 48 | 100.0 | 241 | 2 | Q9VYW4_DROME | Q9VYW4_drosophila |
| 268 | 48 | 100.0 | 213 | 2 | Q6RYE4_TRIMO | O6RYE4 triticum mo | 341 | 48 | 100.0 | 242 | 2 | Q4WT78_ASPFU | Q4WT78_aspergillus |
| 269 | 48 | 100.0 | 213 | 2 | Q6S6M0_9MAGN | O6S6M0 hymphaea sp | 342 | 48 | 100.0 | 242 | 2 | Q9N3Z0_CABEL | Q9N3Z0_caenorhabdi |
| 270 | 48 | 100.0 | 213 | 2 | Q6N613_RHOPA | O6N613 rhodospseudo | 343 | 48 | 100.0 | 242 | 2 | Q8LRJ3_ORYSA | Q8LRJ3_oryza sativ |
| 271 | 48 | 100.0 | 214 | 2 | Q5TVW8_ANOGA | O5TVW8 anopheles g | 344 | 48 | 100.0 | 242 | 2 | Q6QVY0_SALCC | Q6QVY0_salvia cocco |
| 272 | 48 | 100.0 | 214 | 2 | Q6RY65_HORYU | O6RY65 hordeum vul | 345 | 48 | 100.0 | 242 | 2 | Q58WY3_ORENT | Q58WY3_oreochromis |
| 273 | 48 | 100.0 | 214 | 2 | Q6QVY5_PAUTO | O6QVY5 paulownia t | 346 | 48 | 100.0 | 243 | 2 | Q9P2R2_HUMAN | Q9P2R2_homo sapien |
| 274 | 48 | 100.0 | 215 | 1 | HAND1_HUMAN | O96004 homo sapien | 347 | 48 | 100.0 | 243 | 2 | Q9N2G1_PONPY | Q9N2G1_pongo pygma |
| 275 | 48 | 100.0 | 215 | 1 | HAND1_RABIT | P57100 coryctolagus | 348 | 48 | 100.0 | 243 | 2 | Q9N2G2_9PRIM | Q9N2G2_gorilla gor |
| 276 | 48 | 100.0 | 216 | 1 | HAND1_MOUSE | O64279 m heart - an | 349 | 48 | 100.0 | 243 | 2 | Q9N2G3_PANTR | Q9N2G3_pan troglod |
| 277 | 48 | 100.0 | 216 | 1 | HAND1_MOUSE | P97832 rattus norv | 350 | 48 | 100.0 | 243 | 2 | Q7TQW2_MOUSE | Q7TQW2_mus muscicu |
| 278 | 48 | 100.0 | 216 | 2 | Q8N7N5_HUMAN | O8N7N5 homo sapien | 351 | 48 | 100.0 | 244 | 2 | Q693M4_9PIPT | Q693M4_haematopota |
| 279 | 48 | 100.0 | 216 | 2 | Q5SQG1_MOUSE | O5SQG1 mus muscicu | 352 | 48 | 100.0 | 244 | 2 | Q8UHA3_CHICK | Q8UHA3_gallus gall |
| 280 | 48 | 100.0 | 216 | 2 | Q80UL7_MOUSE | O80UL7 rattus norv | 353 | 48 | 100.0 | 245 | 2 | Q4WSR3_ASPFU | Q4WSR3_aspergillus |
| 281 | 48 | 100.0 | 216 | 2 | Q4V8L8_RAT | O4V8L8 rattus norv | 354 | 48 | 100.0 | 245 | 2 | Q54125_DICDI | Q54125_dictyosteli |
| 282 | 48 | 100.0 | 216 | 2 | Q9W7C7_ORYIA | O9W7C7 oryzaia lat | 355 | 48 | 100.0 | 246 | 2 | Q5L1H3_ORYSA | Q5L1H3_oryza sativ |
| 283 | 48 | 100.0 | 217 | 1 | ATL2I1_ARATH | O8RXZ2 arabidopsis | 356 | 48 | 100.0 | 247 | 2 | Q5ABO8_CANAL | Q5ABO8_candida alb |
| 284 | 48 | 100.0 | 217 | 2 | Q7Q1J3_ANOGA | O7Q1J3 anopheles g | 357 | 48 | 100.0 | 247 | 2 | Q7PEFX_ANOGA | Q7PEFX_anopheles g |
| 285 | 48 | 100.0 | 217 | 2 | Q51SL6_MACPA | O51SL6 macaca fasc | 358 | 48 | 100.0 | 247 | 2 | Q5BPF0_ARATH | Q5BPF0_arabidopsis |
| 286 | 48 | 100.0 | 217 | 2 | Q58L58_PIG | O58L58 sus scrofa | 359 | 48 | 100.0 | 248 | 2 | Q6K5X1_ORYSA | Q6K5X1_oryza sativ |
| 287 | 48 | 100.0 | 218 | 2 | Q754W7_ASHGO | Q754W7 ashyga goss | 360 | 48 | 100.0 | 249 | 2 | Q75K45_ORYSA | Q75K45_oryza sativ |
| 288 | 48 | 100.0 | 219 | 1 | Q6OVX7_MIMLE | Q6OVX7 mimulus lew | 361 | 48 | 100.0 | 250 | 2 | Q8BKX7_MOUSE | Q8BKX7_mus muscicu |
| 289 | 48 | 100.0 | 219 | 1 | MTBM_DROVA | P83733 drosophila | 362 | 48 | 100.0 | 250 | 2 | Q7PW25_ANOGA | Q7PW25_anopheles g |
| 290 | 48 | 100.0 | 219 | 2 | Q5TRN0_ANOGA | O5TRN0 anopheles g | 363 | 48 | 100.0 | 252 | 2 | Q6QPY8_MAZRE | Q6QPY8_marus rept |
| 291 | 48 | 100.0 | 219 | 2 | Q9VDM8_DROME | Q9VDM8 drosophila | 364 | 48 | 100.0 | 254 | 2 | Q9V582_DROME | Q9V582_drosophila |
| 292 | 48 | 100.0 | 219 | 2 | P83699_BACST | P83699 bacillus st | 365 | 48 | 100.0 | 254 | 2 | Q4RNP8_TETNG | Q4RNP8_tetradodon n |
| 293 | 48 | 100.0 | 219 | 2 | Q55579_NPYLS | O55579 leucania se | 366 | 48 | 100.0 | 255 | 2 | Q6KBO5_MOUSE | Q6KBO5_mus muscicu |
| 294 | 48 | 100.0 | 220 | 2 | Q7S6T5_NEUCR | Q7S6T5 neurospora | 367 | 48 | 100.0 | 256 | 2 | Q7RWY3_NEUCR | Q7RWY3_neurospora |
| 295 | 48 | 100.0 | 220 | 2 | Q557E5_DICDI | O557E5 dictyosteli | 368 | 48 | 100.0 | 256 | 2 | Q13722_HUMAN | Q13722_homo sapien |
| 296 | 48 | 100.0 | 220 | 2 | Q86HZ5_DICDI | O86HZ5 dictyosteli | 369 | 48 | 100.0 | 256 | 2 | Q653X1_ORYSA | Q653X1_oryza sativ |
| 297 | 48 | 100.0 | 221 | 2 | Q5XJN5_BRARE | O5XJN5 brachydanio | 370 | 48 | 100.0 | 256 | 2 | Q7XD98_ORYSA | Q7XD98_oryza sativ |
| 298 | 48 | 100.0 | 224 | 2 | Q6WGU1_TRIRE | O6WGU1 trichoderma | 371 | 48 | 100.0 | 256 | 2 | Q8W365_ORYSA | Q8W365_oryza sativ |
| 299 | 48 | 100.0 | 224 | 2 | Q4WPH8_ASPFU | O4WPH8 aspergillus | 372 | 48 | 100.0 | 259 | 2 | Q7SSM0_NEUCR | Q7SSM0_neurospora |
| 300 | 48 | 100.0 | 224 | 2 | Q9N9W1_HAIRO | O9N9W1 halocynthia | 373 | 48 | 100.0 | 259 | 2 | O5CPB3_CRYPV | O5CPB3_cryptospori |
| 301 | 48 | 100.0 | 224 | 2 | Q9N9W2_HAIRO | O9N9W2 halocynthia | 374 | 48 | 100.0 | 259 | 2 | Q9V7K6_DROME | Q9V7K6_drosophila |
| 302 | 48 | 100.0 | 225 | 2 | Q7XZF0_ORYSA | Q7XZF0 oryza sativ | 375 | 48 | 100.0 | 259 | 2 | Q9SA48_ARATH | Q9SA48_arabidopsis |
| 303 | 48 | 100.0 | 225 | 2 | Q6QPY1_MIMKE | Q6QPY1 mimulus kel | 376 | 48 | 100.0 | 259 | 2 | Q9ZTC8_ARATH | Q9ZTC8_arabidopsis |
| 304 | 48 | 100.0 | 225 | 2 | Q90XZ3_ERPCA | Q90XZ3 erpetolichn | 377 | 48 | 100.0 | 259 | 2 | Q66901_AQUAE | Q66901_aquilex aeo |
| 305 | 48 | 100.0 | 225 | 2 | Q4RVT9_TETNG | Q4RVT9 tetradodon n | 378 | 48 | 100.0 | 259 | 2 | Q7T1L0_9SMEG | Q7T1L0_odontesthes |
| 306 | 48 | 100.0 | 226 | 2 | Q9QZD2_RAT | Q9QZD2 rattus norv | 379 | 48 | 100.0 | 260 | 2 | Q9ST44_DROME | Q9ST44_drosophila |
| 307 | 48 | 100.0 | 227 | 2 | Q6QPY2_GLAMI | Q6QPY2 leucocarpus | 380 | 48 | 100.0 | 261 | 2 | Q4SGT5_TETNG | Q4SGT5_tetradodon n |
| 308 | 48 | 100.0 | 229 | 2 | Q7PIS3_ANOGA | Q7PIS3 anopheles g | 381 | 48 | 100.0 | 263 | 2 | Q9ARB0_FLATR | Q9ARB0_flaveria tr |
| 309 | 48 | 100.0 | 229 | 2 | Q65124_9MAGN | O65124 dicentra ex | 382 | 48 | 100.0 | 267 | 2 | Q7SE09_NEUCR | Q7SE09_neurospora |
| 310 | 48 | 100.0 | 230 | 2 | Q7S263_HUMAN | Q7S263 homo sapien | 383 | 48 | 100.0 | 268 | 2 | Q59VW7_CANAL | Q59VW7_candida alb |
| 311 | 48 | 100.0 | 230 | 2 | O5CPB6_CRYPV | O5CPB6 cryptospori | 384 | 48 | 100.0 | 268 | 2 | Q7S806_HUMAN | Q7S806_homo sapien |
| 312 | 48 | 100.0 | 230 | 2 | Q7RDB4_PLAYO | Q7RDB4 plasmodium | 385 | 48 | 100.0 | 268 | 2 | O5CV53_CRYPV | O5CV53_cryptospori |
| 313 | 48 | 100.0 | 230 | 2 | Q6ZCWA_ORYSA | Q6ZCWA oryza sativ | 386 | 48 | 100.0 | 268 | 2 | Q5RQW6_ANOGA | O5RQW6_anopheles g |
| 314 | 48 | 100.0 | 230 | 2 | Q9W205_ARATH | Q9W205 arabidopsis | 387 | 48 | 100.0 | 268 | 2 | Q9HAX7_DICDI | Q9HAX7_dictyosteli |
| 315 | 48 | 100.0 | 231 | 2 | Q81QK7_DROME | Q81QK7 drosophila | 388 | 48 | 100.0 | 269 | 2 | Q9LPE4_ARATH | Q9LPE4_arabidopsis |
| 316 | 48 | 100.0 | 232 | 2 | Q7S3F2_NEUCR | Q7S3F2 neurospora | 389 | 48 | 100.0 | 270 | 2 | Q9FFC8_ARATH | Q9FFC8_arabidopsis |
| 317 | 48 | 100.0 | 232 | 2 | Q7PYS3_ANOGA | Q7PYS3 anopheles g | 390 | 48 | 100.0 | 271 | 1 | HM8_XENLA | P14837 xenopus lae |
| 318 | 48 | 100.0 | 233 | 2 | O8TCS3_HUMAN | O8TCS3 homo sapien | 391 | 48 | 100.0 | 271 | 2 | O5C1T2_SCHJA | O5C1T2_schistosoma |
| 319 | 48 | 100.0 | 233 | 2 | O6PIU3_HUMAN | O6PIU3 homo sapien | 392 | 48 | 100.0 | 271 | 2 | O4H2U1_CLOIN | O4H2U1_ciona intes |
| 320 | 48 | 100.0 | 233 | 2 | O8MP30_DICDI | O8MP30 dictyosteli | 393 | 48 | 100.0 | 271 | 2 | O84WK2_ARATH | O84WK2_arabidopsis |
| 321 | 48 | 100.0 | 233 | 2 | Q7XTV6_ORYSA | Q7XTV6 oryza sativ | 394 | 48 | 100.0 | 271 | 2 | O5VR71_ORYSA | O5VR71_oryza sativ |
| 322 | 48 | 100.0 | 234 | 2 | O8STF5_DICDI | O8STF5 dictyosteli | 395 | 48 | 100.0 | 272 | 1 | HX49_HUMAN | P31269 homo sapien |
| 323 | 48 | 100.0 | 234 | 2 | O551Q1_DICDI | O551Q1 dictyosteli | 396 | 48 | 100.0 | 272 | 2 | O5CMT6_CRYHO | O5CMT6_cryptospori |

| | | | | | | | | | | | | | | | | | |
|-----|----|-------|-----|---|---------|--------|---------|--------------|-----|----|-------|-----|---|--------|--------|--------|---------------|
| 397 | 48 | 100.0 | 273 | 2 | 0540Y5 | DICDI | 0544Y5 | dictyosteli | 470 | 48 | 100.0 | 305 | 2 | 091346 | XENLA | 091346 | xenopus lae |
| 398 | 48 | 100.0 | 273 | 2 | 04T2H7 | TEING | 04T2H7 | tetradon n | 471 | 48 | 100.0 | 306 | 1 | PRRT1 | HUMAN | 099946 | homo sapien |
| 399 | 48 | 100.0 | 274 | 2 | 09XGS2 | SOYBN | 09XGS2 | glycine max | 472 | 48 | 100.0 | 306 | 1 | PRRT1 | MOUSE | 035446 | mus musculus |
| 400 | 48 | 100.0 | 274 | 2 | 05KYZ27 | GEOKA | 05KYZ27 | geobacillus | 473 | 48 | 100.0 | 306 | 2 | 054CU2 | DICDI | 054CU2 | dictyosteli |
| 401 | 48 | 100.0 | 275 | 2 | 05KFFV8 | CRYNE | 05KFFV8 | cryptococcus | 474 | 48 | 100.0 | 306 | 2 | 08LH59 | ORYSA | 08LH59 | oryza sativ |
| 402 | 48 | 100.0 | 275 | 2 | 05SQAB | CRYNE | 05SQAB | cryptococcus | 475 | 48 | 100.0 | 307 | 1 | YK55 | YEAST | YK55 | saccharomyc |
| 403 | 48 | 100.0 | 275 | 2 | 064700 | ARATH | 064700 | arabidopsis | 476 | 48 | 100.0 | 307 | 2 | 075H63 | ORYSA | 075H63 | oryza sativ |
| 404 | 48 | 100.0 | 276 | 2 | 04R946 | MAGFA | 04R946 | macaca fasc | 477 | 48 | 100.0 | 308 | 2 | 054G56 | DICDI | 054G56 | dictyosteli |
| 405 | 48 | 100.0 | 276 | 2 | 09DGB3 | LAMJA | 09DGB3 | lametpra ja | 478 | 48 | 100.0 | 308 | 2 | 067168 | AQUAE | 067168 | aquilex aeo |
| 406 | 48 | 100.0 | 276 | 2 | P79788 | CHICK | P79788 | gallus gall | 479 | 48 | 100.0 | 308 | 2 | 06GBB3 | STRAS | 06GBB3 | staphylococ |
| 407 | 48 | 100.0 | 277 | 2 | 05A4K1 | CANAL | 05A4K1 | candida alb | 480 | 48 | 100.0 | 308 | 2 | 06GIV5 | STRAR | 06GIV5 | staphylococ |
| 408 | 48 | 100.0 | 277 | 2 | 04PHR7 | USMA | 04PHR7 | ureliago ma | 481 | 48 | 100.0 | 308 | 2 | 05MHY1 | STRAC | 05MHY1 | staphylococ |
| 409 | 48 | 100.0 | 277 | 2 | 06S2W5 | ORYSA | 06S2W5 | oryza sativ | 482 | 48 | 100.0 | 308 | 2 | 07A6X1 | STRAN | 07A6X1 | staphylococ |
| 410 | 48 | 100.0 | 277 | 2 | 04S3L7 | TEING | 04S3L7 | tetradon n | 483 | 48 | 100.0 | 308 | 2 | 08BXQ1 | STRAM | 08BXQ1 | staphylococ |
| 411 | 48 | 100.0 | 277 | 2 | 04VOD4 | GASAC | 04VOD4 | gaasteroste | 484 | 48 | 100.0 | 308 | 2 | 099VT4 | STRAM | 099VT4 | staphylococ |
| 412 | 48 | 100.0 | 278 | 2 | 08LEB5 | ARATH | 08LEB5 | arabidopsis | 485 | 48 | 100.0 | 309 | 2 | 05DHK3 | SCJJA | 05DHK3 | schistosoma |
| 413 | 48 | 100.0 | 278 | 2 | 094EJ7 | MAIZE | 094EJ7 | zea mays (m | 486 | 48 | 100.0 | 309 | 2 | 018751 | CABEL | 018751 | caenorhabdi |
| 414 | 48 | 100.0 | 279 | 2 | 06SXEB | ORYSA | 06SXEB | oryza sativ | 487 | 48 | 100.0 | 309 | 2 | 084M6 | ORYSA | 084M6 | oryza sativ |
| 415 | 48 | 100.0 | 279 | 2 | 04RA01 | TEING | 04RA01 | tetradon n | 488 | 48 | 100.0 | 311 | 2 | 06B415 | DBSHA | 06B415 | debrayomyce |
| 416 | 48 | 100.0 | 280 | 2 | 057Z17 | PTTYP | 057Z17 | trypanosoma | 489 | 48 | 100.0 | 311 | 2 | 08H077 | ORYSA | 08H077 | oryza sativ |
| 417 | 48 | 100.0 | 280 | 2 | 09AR63 | SOLTU | 09AR63 | solanium tub | 490 | 48 | 100.0 | 311 | 2 | 090370 | COTJA | 090370 | coturnix co |
| 418 | 48 | 100.0 | 283 | 2 | 05JK41 | ORYSA | 05JK41 | oryza sativ | 491 | 48 | 100.0 | 311 | 2 | 090888 | CHICK | 090888 | gallus gall |
| 419 | 48 | 100.0 | 285 | 2 | 082166 | ARATH | 082166 | arabidopsis | 492 | 48 | 100.0 | 312 | 2 | 081RR4 | DBOME | 081RR4 | drosophi |
| 420 | 48 | 100.0 | 285 | 2 | 09LGP3 | ORYSA | 09LGP3 | oryza sativ | 493 | 48 | 100.0 | 312 | 2 | 09LHP0 | ARATH | 09LHP0 | arabidopsis |
| 421 | 48 | 100.0 | 285 | 2 | 09L5S4 | ARATH | 09L5S4 | arabidopsis | 494 | 48 | 100.0 | 312 | 2 | 06T150 | BRARE | 06T150 | brachydantio |
| 422 | 48 | 100.0 | 286 | 2 | 042290 | CHICK | 042290 | gallus gall | 495 | 48 | 100.0 | 313 | 2 | 06DBE4 | XENLA | 06DBE4 | xenopus lae |
| 423 | 48 | 100.0 | 286 | 2 | 057342 | COTJA | 057342 | coturnix co | 496 | 48 | 100.0 | 313 | 2 | 09PUA6 | XENLA | 09PUA6 | xenopus lae |
| 424 | 48 | 100.0 | 286 | 2 | 08AMH8 | CHICK | 08AMH8 | gallus gall | 497 | 48 | 100.0 | 314 | 2 | 04RNI4 | TEING | 04RNI4 | tetradon n |
| 425 | 48 | 100.0 | 286 | 2 | 04RM07 | TEING | 04RM07 | tetradon n | 498 | 48 | 100.0 | 314 | 2 | 09SPJ7 | GOSHI | 09SPJ7 | goshelydium h |
| 426 | 48 | 100.0 | 288 | 2 | 0524M2 | MAGCR | 0524M2 | magnaporthe | 499 | 48 | 100.0 | 314 | 2 | 09M9A3 | ARATH | 09M9A3 | arabidopsis |
| 427 | 48 | 100.0 | 288 | 2 | 07PPD2 | ANOGA | 07PPD2 | anopheles g | 500 | 48 | 100.0 | 314 | 2 | 04S508 | TEING | 04S508 | tetradon n |
| 428 | 48 | 100.0 | 288 | 2 | 08RTA39 | HERGL | 08RTA39 | heterodera | 501 | 48 | 100.0 | 315 | 2 | 08LT06 | ORYSA | 08LT06 | oryza sativ |
| 429 | 48 | 100.0 | 289 | 2 | 07XV64 | ORYSA | 07XV64 | oryza sativ | 502 | 48 | 100.0 | 315 | 2 | 05L2G4 | GEOKA | 05L2G4 | geobacillus |
| 430 | 48 | 100.0 | 289 | 2 | 04UIU2 | XENTR | 04UIU2 | xenopus tro | 503 | 48 | 100.0 | 315 | 2 | 098UK3 | BRARE | 098UK3 | brachydantio |
| 431 | 48 | 100.0 | 290 | 2 | 086P14 | DBOME | 086P14 | drosophi | 504 | 48 | 100.0 | 316 | 2 | 06K6C4 | ORYSA | 06K6C4 | oryza sativ |
| 432 | 48 | 100.0 | 290 | 2 | 04S466 | CABEL | 04S466 | caenorhabdi | 505 | 48 | 100.0 | 316 | 2 | 0504L8 | XENTR | 0504L8 | xenopus tro |
| 433 | 48 | 100.0 | 290 | 2 | 06ZGY7 | ORYSA | 06ZGY7 | oryza sativ | 506 | 48 | 100.0 | 317 | 2 | 05UIP7 | ORYSA | 05UIP7 | oryza sativ |
| 434 | 48 | 100.0 | 292 | 2 | 06YUVO | ORYSA | 06YUVO | oryza sativ | 507 | 48 | 100.0 | 317 | 2 | 06P4L0 | XENTR | 06P4L0 | xenopus tro |
| 435 | 48 | 100.0 | 292 | 2 | 0857E3 | ORYSA | 0857E3 | oryza sativ | 508 | 48 | 100.0 | 317 | 2 | 07T0X1 | XENLA | 07T0X1 | xenopus lae |
| 436 | 48 | 100.0 | 292 | 2 | 07XC01 | ORYSA | 07XC01 | oryza sativ | 509 | 48 | 100.0 | 318 | 2 | 07SA92 | NEUCR | 07SA92 | neurospora |
| 437 | 48 | 100.0 | 292 | 2 | 05O2E8 | IDILLO | 05O2E8 | idiomatina | 510 | 48 | 100.0 | 318 | 2 | 04GYV8 | PTTYP | 04GYV8 | trypanosoma |
| 438 | 48 | 100.0 | 292 | 2 | 091294 | RANCA | 091294 | rana catesb | 511 | 48 | 100.0 | 318 | 2 | 08H301 | ORYSA | 08H301 | oryza sativ |
| 439 | 48 | 100.0 | 294 | 2 | 05TKH1 | ORYSA | 05TKH1 | oryza sativ | 512 | 48 | 100.0 | 318 | 2 | 08S026 | ORYSA | 08S026 | oryza sativ |
| 440 | 48 | 100.0 | 294 | 2 | P94395 | BACSV | P94395 | bacillus su | 513 | 48 | 100.0 | 318 | 2 | 06NB56 | RHOPA | 06NB56 | rhodospheo |
| 441 | 48 | 100.0 | 295 | 2 | 054CT9 | DICDI | 054CT9 | dictyosteli | 514 | 48 | 100.0 | 319 | 2 | 06XZHO | BRARE | 06XZHO | brachydantio |
| 442 | 48 | 100.0 | 295 | 2 | 08SMU6 | DBOME | 08SMU6 | drosophi | 515 | 48 | 100.0 | 320 | 2 | 0504T7 | HUMAN | 0504T7 | homo sapien |
| 443 | 48 | 100.0 | 296 | 2 | 09SSA2 | ARATH | 09SSA2 | arabidopsis | 516 | 48 | 100.0 | 320 | 2 | 07PDB9 | ANOGA | 07PDB9 | anopheles g |
| 444 | 48 | 100.0 | 297 | 2 | 05A295 | CANAL | 05A295 | candida alb | 517 | 48 | 100.0 | 320 | 2 | 05LTM6 | SILIPO | 05LTM6 | silicibacte |
| 445 | 48 | 100.0 | 297 | 2 | 041122 | PHAVU | 041122 | phaseolus v | 518 | 48 | 100.0 | 320 | 2 | 09KCO0 | BACHD | 09KCO0 | baclillus ha |
| 446 | 48 | 100.0 | 297 | 2 | 0627B6 | ORYSA | 0627B6 | oryza sativ | 519 | 48 | 100.0 | 321 | 2 | 05TNR2 | ANOGA | 05TNR2 | anopheles g |
| 447 | 48 | 100.0 | 297 | 2 | 08B2C7 | MOUSE | 08B2C7 | mus musculu | 520 | 48 | 100.0 | 321 | 2 | 06K5Y1 | ORYSA | 06K5Y1 | oryza sativ |
| 448 | 48 | 100.0 | 298 | 1 | MEOX2 | XENLA | MEOX2 | xenopus lae | 521 | 48 | 100.0 | 321 | 2 | 06YX13 | ORYSA | 06YX13 | oryza sativ |
| 449 | 48 | 100.0 | 298 | 2 | 06IKF0 | DBOME | 06IKF0 | drosophi | 522 | 48 | 100.0 | 321 | 2 | 023891 | ORYSA | 023891 | oryza sativ |
| 450 | 48 | 100.0 | 298 | 2 | 07ZX12 | XENLA | 07ZX12 | xenopus lae | 523 | 48 | 100.0 | 321 | 2 | 07WU57 | PORGI | 07WU57 | porphyromon |
| 451 | 48 | 100.0 | 299 | 2 | 05TFG4 | ANOGA | 05TFG4 | anopheles g | 524 | 48 | 100.0 | 322 | 2 | 07S197 | PIABE | 07S197 | plasmodium |
| 452 | 48 | 100.0 | 299 | 2 | 05LV18 | SILIPO | 05LV18 | silicibacte | 525 | 48 | 100.0 | 322 | 2 | 06ZKS4 | ORYSA | 06ZKS4 | oryza sativ |
| 453 | 48 | 100.0 | 300 | 2 | 06K722 | ORYSA | 06K722 | oryza sativ | 526 | 48 | 100.0 | 323 | 1 | MAFB | HUMAN | 0955q3 | homo sapien |
| 454 | 48 | 100.0 | 300 | 2 | 06WM82 | RAT | 06WM82 | rattus norv | 527 | 48 | 100.0 | 323 | 1 | MAFB | MOUSE | P54881 | mus musculu |
| 455 | 48 | 100.0 | 301 | 2 | 0656T1 | ORYSA | 0656T1 | oryza sativ | 528 | 48 | 100.0 | 323 | 1 | MAFB | RAT | P54882 | rattus norv |
| 456 | 48 | 100.0 | 302 | 1 | HYPB | BRANA | 054X57 | birdytriazib | 529 | 48 | 100.0 | 323 | 1 | ORYX1 | BRARE | 091994 | brachydantio |
| 457 | 48 | 100.0 | 302 | 2 | 054VX0 | DICDI | 054VX0 | dictyosteli | 530 | 48 | 100.0 | 323 | 2 | 066835 | DBOME | 096835 | drosophi |
| 458 | 48 | 100.0 | 302 | 2 | 090YH7 | CHICK | 090YH7 | gallus gall | 531 | 48 | 100.0 | 323 | 2 | 09SDW0 | ARATH | 09SDW0 | arabidopsis |
| 459 | 48 | 100.0 | 303 | 1 | MEOX2 | HUMAN | P50222 | homo sapien | 532 | 48 | 100.0 | 323 | 2 | 04ST17 | TEING | 04ST17 | tetradon n |
| 460 | 48 | 100.0 | 303 | 1 | MEOX2 | MOUSE | P32443 | mus musculu | 533 | 48 | 100.0 | 323 | 2 | 07ZU54 | BRARE | 07ZU54 | brachydantio |
| 461 | 48 | 100.0 | 303 | 1 | MEOX2 | RAT | P39020 | rattus norv | 534 | 48 | 100.0 | 324 | 2 | 0756L9 | ASHGA | 0756L9 | ashhya goss |
| 462 | 48 | 100.0 | 303 | 2 | 06FHYE | HUMAN | 06FHYE | homo sapien | 535 | 48 | 100.0 | 324 | 2 | 07X6C5 | ORYSA | 07X6C5 | oryza sativ |
| 463 | 48 | 100.0 | 303 | 2 | 095UAB | PIG | 095UAB | sus scrofa | 536 | 48 | 100.0 | 324 | 2 | 06R077 | ARATH | 06R077 | arabidopsis |
| 464 | 48 | 100.0 | 303 | 2 | 0544T6 | MOUSE | 0544T6 | mus musculu | 537 | 48 | 100.0 | 324 | 2 | 09M0Y5 | ARATH | 09M0Y5 | arabidopsis |
| 465 | 48 | 100.0 | 303 | 2 | 099M23 | MOUSE | 099M23 | mus musculu | 538 | 48 | 100.0 | 324 | 2 | 09W6B1 | BRARE | 09W6B1 | brachydantio |
| 466 | 48 | 100.0 | 304 | 2 | 04SAL9 | TEING | 04SAL9 | tetradon n | 539 | 48 | 100.0 | 325 | 2 | 09BSNO | HUMAN | 09BSNO | homo sapien |
| 467 | 48 | 100.0 | 304 | 1 | GSH2 | HUMAN | 09b5m3 | homo sapien | 540 | 48 | 100.0 | 325 | 1 | 06KZW6 | BRARE | 06KZW6 | brachydantio |
| 468 | 48 | 100.0 | 304 | 1 | GSH2 | MAGCR | 0511C5 | magnaporthe | 541 | 48 | 100.0 | 326 | 1 | PIRX2 | XENLA | 09pwr3 | xenopus lae |
| 469 | 48 | 100.0 | 305 | 1 | GSH2 | MOUSE | P31316 | mus musculu | 542 | 48 | 100.0 | 326 | 2 | QTXUT3 | ORYSA | QTXUT3 | oryza sativ |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|---------------|---------------------|-----|----|-------|-----|---|---------------|---------------------|
| 543 | 48 | 100.0 | 326 | 2 | 091447_PSEAE | 091447_pseudomonas | 616 | 48 | 100.0 | 352 | 2 | 06NHW3_HUMAN | 06nhw3_homo sapien |
| 544 | 48 | 100.0 | 326 | 2 | 090W66_9GCOBI | 090w66_leucoparario | 617 | 48 | 100.0 | 352 | 2 | 05QLF4_ORYSA | 05qlf4_oryza sativ |
| 545 | 48 | 100.0 | 327 | 2 | 098U64_BRARE | 098u64_brachydantio | 618 | 48 | 100.0 | 352 | 2 | 08DGP0_SYNEL | 08dgp0_synelococc |
| 546 | 48 | 100.0 | 328 | 1 | 098U64_BRARE | 098u64_homo sapien | 619 | 48 | 100.0 | 353 | 2 | 04T358_TETNG | 04t358_tetradon n |
| 547 | 48 | 100.0 | 328 | 1 | 09Y1_YEAST | P38271_baccharomyc | 620 | 48 | 100.0 | 354 | 1 | 09X1_HUMAN | P33242_homo sapien |
| 548 | 48 | 100.0 | 328 | 2 | 053Q0V_HUMAN | 053quv_homo sapien | 621 | 48 | 100.0 | 354 | 2 | 033T06_HUMAN | 033t06_homo sapien |
| 549 | 48 | 100.0 | 328 | 2 | 05VQ11_ORYSA | 05vq11_oryza sativ | 622 | 48 | 100.0 | 354 | 2 | 054D06_DICDI | 054d06_dicystostei |
| 550 | 48 | 100.0 | 328 | 2 | 062U00_BACLD | 062u00_bacillus 11 | 623 | 48 | 100.0 | 354 | 2 | 051M4_DICDI | 051m4_dicystostei |
| 551 | 48 | 100.0 | 329 | 2 | 08N1Y1_NEURCR | 08n1y1_neurospora | 624 | 48 | 100.0 | 355 | 1 | 09X1_MOUSE | P80205_mus musculu |
| 552 | 48 | 100.0 | 329 | 2 | 0945N2_ARATH | 0945n2_arabidopsis | 625 | 48 | 100.0 | 355 | 1 | 09X1_MOUSE | 064140_rattus norv |
| 553 | 48 | 100.0 | 329 | 2 | 080ZK5_MOUSE | 080zk5_mus musculu | 626 | 48 | 100.0 | 355 | 2 | 09W4B1_DROME | 09w4b1_drosophila |
| 554 | 48 | 100.0 | 330 | 2 | 05CEA1_CRYHO | 05ceal_cryptospori | 627 | 48 | 100.0 | 355 | 2 | 09S7W5_ARATH | 09s7w5_arabidopsis |
| 555 | 48 | 100.0 | 330 | 2 | 07XEZ4_ORYSA | 07xez4_oryza sativ | 628 | 48 | 100.0 | 355 | 2 | 091ZU3_MOUSE | 091zj3_mus musculu |
| 556 | 48 | 100.0 | 330 | 2 | 065JDT_BACLD | 065jdt_bacillus 11 | 629 | 48 | 100.0 | 355 | 2 | 05SS54_MOUSE | 05ss54_mus musculu |
| 557 | 48 | 100.0 | 331 | 1 | 09X1_MOUSE | P09022_mus musculu | 630 | 48 | 100.0 | 356 | 2 | 09ATR4_ORYSA | 09atr4_oryza sativ |
| 558 | 48 | 100.0 | 331 | 2 | 06K5X2_ORYSA | 06k5x2_oryza sativ | 631 | 48 | 100.0 | 356 | 2 | 09LZFT_ARATH | 09lzf7_arabidopsis |
| 559 | 48 | 100.0 | 331 | 2 | 04KSV9_9NUCL | 04ksv9_chrysodeixi | 632 | 48 | 100.0 | 356 | 2 | 073679_BRARE | 073679_brachydantio |
| 560 | 48 | 100.0 | 332 | 1 | DLX2_MOUSE | P40764_mus musculu | 633 | 48 | 100.0 | 356 | 2 | 098UK5_BRARE | 098uks_brachydantio |
| 561 | 48 | 100.0 | 332 | 2 | 05B4K6_EBENI | 05b4k6_aspergillus | 634 | 48 | 100.0 | 357 | 2 | 08B0C1_MOUSE | 08bgc1_mus musculu |
| 562 | 48 | 100.0 | 332 | 2 | 052KJ2_MOUSE | 052kj2_mus musculu | 635 | 48 | 100.0 | 357 | 2 | 07T2W1_BRARE | 07t2w1_brachydantio |
| 563 | 48 | 100.0 | 333 | 1 | HXA1_RAT | 008656_rattus norv | 636 | 48 | 100.0 | 358 | 2 | 080411_IPONI | 080411_ipomoea n11 |
| 564 | 48 | 100.0 | 333 | 1 | SP18_ARATH | 08gx13_arabidopsis | 637 | 48 | 100.0 | 358 | 2 | 076K80_ARATH | 076k80_arabidopsis |
| 565 | 48 | 100.0 | 333 | 2 | 08LCT0_ARATH | 08lctv0_arabidopsis | 638 | 48 | 100.0 | 358 | 2 | 070418_HCMV | 070418_human cytom |
| 566 | 48 | 100.0 | 333 | 2 | 04LIQ2_LACRE | 04liq2_lactobacill | 639 | 48 | 100.0 | 358 | 2 | 069215_HCMV | 069215_human cytom |
| 567 | 48 | 100.0 | 333 | 2 | 04SGC1_TETNG | 04sgc1_tetradon n | 640 | 48 | 100.0 | 358 | 2 | 0789F2_CHICK | 0789f2_gallus gall |
| 568 | 48 | 100.0 | 334 | 2 | 05SG11_DICDI | 05sg11_dicystostei | 641 | 48 | 100.0 | 358 | 2 | 09DG32_XENLA | 09dg32_xenopus lae |
| 569 | 48 | 100.0 | 334 | 2 | 06T4R4_9BILA | 06t4r4_ptychodera | 642 | 48 | 100.0 | 358 | 2 | 04S148_TETNG | 04s148_tetradon n |
| 570 | 48 | 100.0 | 334 | 2 | 09F1W9_ARATH | 09f1w9_arabidopsis | 643 | 48 | 100.0 | 359 | 1 | KX1_MALIZE | P24345_zea mays (m |
| 571 | 48 | 100.0 | 335 | 1 | HXA1_HUMAN | P49639_homo sapien | 644 | 48 | 100.0 | 359 | 1 | YOM3_CABEL | 009556_caenorhabdi |
| 572 | 48 | 100.0 | 335 | 2 | 09SG82_ARATH | 09sg82_arabidopsis | 645 | 48 | 100.0 | 359 | 2 | 053ZFL_MALIZE | 053zfl_zea mays (m |
| 573 | 48 | 100.0 | 335 | 2 | 09J889_9NUCL | 09j889_spodoptera | 646 | 48 | 100.0 | 359 | 2 | 08CF90_MOUSE | 08cf90_mus musculu |
| 574 | 48 | 100.0 | 336 | 2 | 04LIU7_HELTB | 04liu7_hellicodacti | 647 | 48 | 100.0 | 359 | 2 | 0789F3_CHICK | 0789f3_gallus gall |
| 575 | 48 | 100.0 | 336 | 2 | 04LIU8_HELTB | 04liu8_hellicodacti | 648 | 48 | 100.0 | 359 | 2 | 04R1R1_TETNG | 04r1r1_tetradon n |
| 576 | 48 | 100.0 | 336 | 2 | 09AY44_ORYSA | 09ay44_oryza sativ | 649 | 48 | 100.0 | 361 | 2 | 054MY4_DICDI | 054my4_dicystostei |
| 577 | 48 | 100.0 | 336 | 2 | 07XC32_ORYSA | 07xc32_oryza sativ | 650 | 48 | 100.0 | 361 | 2 | 060EU0_ORYSA | 06e0u0_oryza sativ |
| 578 | 48 | 100.0 | 336 | 2 | 08BN18_MOUSE | 08bn18_mus musculu | 651 | 48 | 100.0 | 362 | 2 | 09AT58_9POAL | 09at58_cymbopogon |
| 579 | 48 | 100.0 | 336 | 2 | 06P4Y7_XENTR | 06p4y7_xenopus tro | 652 | 48 | 100.0 | 363 | 2 | 05A5V5_CANAL | 05a5v5_candida alb |
| 580 | 48 | 100.0 | 337 | 2 | 080ZAZ_MOUSE | 080zaz_mus musculu | 653 | 48 | 100.0 | 364 | 2 | 06VM30_LUPDE | 06vm30_lupinus den |
| 581 | 48 | 100.0 | 337 | 2 | 0566M1_XENTR | 0566m1_xenopus tro | 654 | 48 | 100.0 | 364 | 2 | 06VM32_LUPDE | 06vm32_lupinus den |
| 582 | 48 | 100.0 | 337 | 2 | 06DEB7_XENLA | 06deb7_xenopus lae | 655 | 48 | 100.0 | 364 | 2 | 06YU11_ORYSA | 06yu11_oryza sativ |
| 583 | 48 | 100.0 | 338 | 1 | IAR1_ARATH | 09me47_arabidopsis | 656 | 48 | 100.0 | 364 | 2 | 06Y196_BRARE | 06y196_brachydantio |
| 584 | 48 | 100.0 | 338 | 2 | 080YR1_MOUSE | 080yrt1_mus musculu | 657 | 48 | 100.0 | 365 | 2 | 09AB80_CAUCR | 09ab80_calobacter |
| 585 | 48 | 100.0 | 338 | 2 | 05FR31_CHICK | 05fr31_gallus gall | 658 | 48 | 100.0 | 366 | 2 | 09AT50_9POAL | 09at50_borhriochlo |
| 586 | 48 | 100.0 | 338 | 2 | 04RNC8_TETNG | 04rnc8_tetradon n | 659 | 48 | 100.0 | 366 | 2 | 09AT54_9POAL | 09at54_capillipedi |
| 587 | 48 | 100.0 | 339 | 2 | 05HYJ3_HUMAN | 05hyj3_homo sapien | 660 | 48 | 100.0 | 366 | 2 | 08S7W9_ORYSA | 08s7w9_oryza sativ |
| 588 | 48 | 100.0 | 339 | 2 | 05TTT5_ARATH | 05ttt5_anopheles g | 661 | 48 | 100.0 | 366 | 2 | 05K549_BRARE | 05k549_brachydantio |
| 589 | 48 | 100.0 | 339 | 2 | 081NR1_DROME | 081nr1_drosophila | 662 | 48 | 100.0 | 366 | 2 | 07SZN6_BRARE | 07szn6_brachydantio |
| 590 | 48 | 100.0 | 339 | 2 | 05ZE66_ORYSA | 05ze66_oryza sativ | 663 | 48 | 100.0 | 367 | 1 | SELP4_BRARE | 0986v1_brechydantio |
| 591 | 48 | 100.0 | 339 | 2 | 080XP8_MOUSE | 080xp8_mus musculu | 664 | 48 | 100.0 | 367 | 2 | 07PXF8_ANOGA | 07pxf8_anopheles g |
| 592 | 48 | 100.0 | 340 | 2 | 098S17_XENLA | 098s17_xenopus lae | 665 | 48 | 100.0 | 367 | 2 | 06P3K0_BRARE | 06p3k0_brechydantio |
| 593 | 48 | 100.0 | 340 | 2 | 0941Y5_ORYSA | 0941y5_oryza sativ | 666 | 48 | 100.0 | 368 | 2 | 05TOY4_ANOGA | 05tcy4_anopheles g |
| 594 | 48 | 100.0 | 340 | 2 | 07W1L1_BORPA | 07w1l1_bordetella | 667 | 48 | 100.0 | 368 | 2 | 09S7Y1_ARATH | 09s7y1_arabidopsis |
| 595 | 48 | 100.0 | 340 | 2 | 07WPK2_BORBR | 07wpk2_bordetella | 668 | 48 | 100.0 | 368 | 2 | 092LZ1_RHIME | 092lzt1_rhizobium m |
| 596 | 48 | 100.0 | 342 | 2 | 05AGV0_CANAL | 05agv0_candida alb | 669 | 48 | 100.0 | 368 | 2 | 04SHV5_TETNG | 04shv5_tetradon n |
| 597 | 48 | 100.0 | 342 | 2 | 06EN34_ORYSA | 06en34_oryza sativ | 670 | 48 | 100.0 | 369 | 1 | MAF_AVIS4 | P23091_avian muscu |
| 598 | 48 | 100.0 | 342 | 2 | 076BT1_ORYSA | 076bt1_oryza sativ | 671 | 48 | 100.0 | 369 | 1 | MAF_AVIS4 | P54844_rattus norv |
| 599 | 48 | 100.0 | 343 | 2 | 09DG50_XENLA | 09dg50_xenopus lae | 672 | 48 | 100.0 | 369 | 2 | 059K07_CANAL | 059k07_candida alb |
| 600 | 48 | 100.0 | 344 | 2 | 091BA2_NPST | 091ba2_spodoptera | 673 | 48 | 100.0 | 369 | 2 | 06DN06_SHEEP | 06dn06_ovis aries |
| 601 | 48 | 100.0 | 345 | 2 | 059Y92_CANAL | 059y92_candida alb | 674 | 48 | 100.0 | 369 | 2 | 07W213_BORPA | 07w213_bordetella |
| 602 | 48 | 100.0 | 345 | 2 | 04ZL62_PSEBSM | 04zl62_pseudomonas | 675 | 48 | 100.0 | 369 | 2 | 07WQZ1_BORBR | 07wqzt1_bordetella |
| 603 | 48 | 100.0 | 345 | 2 | 087TY3_PSEBSM | 087ty3_pseudomonas | 676 | 48 | 100.0 | 369 | 2 | 092171_CHICK | 092171_gallus gall |
| 604 | 48 | 100.0 | 346 | 2 | 04K3D2_PSEBS | 04k3d2_pseudomonas | 677 | 48 | 100.0 | 370 | 1 | MAF_MOUSE | P54843_mus musculu |
| 605 | 48 | 100.0 | 346 | 2 | 04UIU0_XENTR | 04uiu0_xenopus tro | 678 | 48 | 100.0 | 370 | 2 | 071A33_HUMAN | 071a33_homo sapien |
| 606 | 48 | 100.0 | 347 | 2 | 04T9B1_TETNG | 04t9b1_tetradon n | 679 | 48 | 100.0 | 370 | 2 | 086AD2_DICDI | 086ad2_dicystostei |
| 607 | 48 | 100.0 | 348 | 2 | 07PT15_ANOGA | 07pt15_anopheles g | 680 | 48 | 100.0 | 370 | 2 | 09W368_DROME | 09w368_drosophila |
| 608 | 48 | 100.0 | 348 | 2 | 049457_ARATH | 049457_arabidopsis | 681 | 48 | 100.0 | 370 | 2 | 06H666_ORYSA | 06h666_oryza sativ |
| 609 | 48 | 100.0 | 348 | 2 | 06VBA4_ORYSA | 06vba4_oryza sativ | 682 | 48 | 100.0 | 371 | 2 | 05PPD0_9ALPH | 05ppd0_suid herpes |
| 610 | 48 | 100.0 | 349 | 2 | 092X29_RHIME | 092x29_rhizobium m | 683 | 48 | 100.0 | 371 | 2 | 09MAL7_ARATH | 09mal7_arabidopsis |
| 611 | 48 | 100.0 | 349 | 2 | 08YNF0_ANASP | 08ynf0_anabaena sp | 684 | 48 | 100.0 | 371 | 2 | 07VUK2_BORPE | 07vuk2_bordetella |
| 612 | 48 | 100.0 | 350 | 1 | ROUGH_DROME | P10181_drosophila | 685 | 48 | 100.0 | 372 | 2 | 05AMK8_CANAL | 05amk8_candida alb |
| 613 | 48 | 100.0 | 350 | 1 | 04V714_DROME | 04v714_drosophila | 686 | 48 | 100.0 | 372 | 2 | 08N7W6_HUMAN | 08n7w6_homo sapien |
| 614 | 48 | 100.0 | 351 | 1 | CAV2_CABEL | 018879_caenorhabdi | 687 | 48 | 100.0 | 373 | 2 | 066147_HUMAN | 066147_homo sapien |
| 615 | 48 | 100.0 | 351 | 1 | HRPX_PLALO | P04929_plasmodium | 688 | 48 | 100.0 | 373 | 2 | 05CDR3_CRYHO | 05cdr3_cryptospori |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|---------------|---------------------|-----|----|-------|-----|---|---------------|---------------------|
| 669 | 48 | 100.0 | 373 | 2 | 081369_ARATH | 081369_arabidopsis | 762 | 48 | 100.0 | 394 | 2 | 06QB01_STRPU | 06qb01_strongyloce |
| 690 | 48 | 100.0 | 374 | 1 | YMP4_CAEEL | Q10948 caenorhabdi | 763 | 48 | 100.0 | 394 | 2 | Q9XYQ3_ANOGA | Q9xyq3_anopheles |
| 691 | 48 | 100.0 | 375 | 1 | CAR2_DICDI | P34907 dictyosteli | 764 | 48 | 100.0 | 394 | 2 | Q7PMQ4_ANOGA | Q7pmq4_anopheles |
| 692 | 48 | 100.0 | 375 | 1 | MPBP_ARATH | Q6dbm arabidopsis | 765 | 48 | 100.0 | 395 | 2 | Q4RJS5_TETNG | Q4rjs5_tetradon n |
| 693 | 48 | 100.0 | 375 | 2 | Q54J91_DICDI | Q54j91 dictyosteli | 766 | 48 | 100.0 | 395 | 2 | Q7SKS7_AVTIS3 | Q7skst7_avian sarco |
| 694 | 48 | 100.0 | 375 | 2 | Q54U61_DICDI | Q54u6 dictyosteli | 767 | 48 | 100.0 | 396 | 2 | Q7PY34_ANOGA | Q7py34_anopheles |
| 695 | 48 | 100.0 | 376 | 1 | TF2AA_HUMAN | P52655 h transcript | 768 | 48 | 100.0 | 396 | 2 | Q76KV0_PEA | Q76kv0_plum savi |
| 696 | 48 | 100.0 | 376 | 1 | TF2AA_PONPY | Q5c00 p transcript | 769 | 48 | 100.0 | 397 | 2 | Q6MYU4_ASFPU | Q6myu4_apepigi |
| 697 | 48 | 100.0 | 376 | 2 | Q7OLH2_ANOGA | Q7olh2 anopheles | 770 | 48 | 100.0 | 397 | 2 | Q6S9V4_MUSDO | Q6s9v4_musca domes |
| 698 | 48 | 100.0 | 376 | 2 | Q7XA55_GNENGA | Q7x55 gnemum gnem | 771 | 48 | 100.0 | 397 | 2 | Q7YIE4_ORYSA | Q7yie4_oryza savi |
| 699 | 48 | 100.0 | 377 | 1 | TF2AA_RAT | Q08949 r transcript | 772 | 48 | 100.0 | 398 | 1 | GAT24_ARATH | Q512q arabidopsis |
| 700 | 48 | 100.0 | 377 | 2 | Q7X9Z1_PAGES | Q7x9z1 fagopyrum e | 773 | 48 | 100.0 | 398 | 2 | Q54LO8_DICDI | Q54lq8 dictyosteli |
| 701 | 48 | 100.0 | 377 | 2 | Q7XA00_9CARY | Q7xa00 fagopyrum h | 774 | 48 | 100.0 | 398 | 2 | Q70119_ANTMA | Q70119_antirrhium |
| 702 | 48 | 100.0 | 377 | 2 | Q7XA02_9CARY | Q7xa02 fagopyrum u | 775 | 48 | 100.0 | 398 | 2 | Q6QS35_PEBTA | Q6qs35_pongine her |
| 703 | 48 | 100.0 | 377 | 2 | Q6D75_BRARE | Q6d75 brachydanto | 776 | 48 | 100.0 | 399 | 2 | Q52A85_MAGGR | Q52a85_magnaporthe |
| 704 | 48 | 100.0 | 377 | 2 | Q80482_BRARE | Q80482 brachydanto | 777 | 48 | 100.0 | 399 | 2 | Q4WU7_ASFPU | Q4wuv7_aspergillus |
| 705 | 48 | 100.0 | 378 | 1 | TF2AA_MOUSE | Q09pm3 m transcript | 778 | 48 | 100.0 | 401 | 1 | NMA1_YEAST | Q06178 saccharomyc |
| 706 | 48 | 100.0 | 378 | 1 | Q7SGL1_ORYSA | Q7sgl1 oryza savi | 779 | 48 | 100.0 | 401 | 2 | Q615J2_CABBR | Q615j2_caenorhabdi |
| 707 | 48 | 100.0 | 378 | 2 | Q7X9Z2_9CARY | Q7x9z2 fagopyrum c | 780 | 48 | 100.0 | 402 | 1 | POXM_DROME | P23757 drosophila |
| 708 | 48 | 100.0 | 378 | 2 | Q7XA05_9CARY | Q7xa05 fagopyrum u | 781 | 48 | 100.0 | 402 | 1 | Q7PDB0_ANOGA | Q7pdb0_anopheles |
| 709 | 48 | 100.0 | 379 | 1 | HSBH1_SOYBN | P46608 glycine max | 782 | 48 | 100.0 | 402 | 2 | Q7OKT8_ANOGA | Q7okt8_anopheles |
| 710 | 48 | 100.0 | 379 | 2 | Q5CTA5_CRYPV | Q5cta5 cryptospori | 783 | 48 | 100.0 | 402 | 2 | Q9GDP9_DROME | Q9gdp9_drosophila |
| 711 | 48 | 100.0 | 379 | 2 | Q7X9Y8_9CARY | Q7x9y8 fagopyrum s | 784 | 48 | 100.0 | 402 | 2 | Q8MLD0_DROME | Q8mld0_drosophila |
| 712 | 48 | 100.0 | 379 | 2 | Q7X9Z3_9CARY | Q7x9z3 fagopyrum s | 785 | 48 | 100.0 | 403 | 1 | MAF_HUMAN | Q75444_homo sapien |
| 713 | 48 | 100.0 | 379 | 2 | Q7X9Z5_9CARY | Q7x9z5 fagopyrum p | 786 | 48 | 100.0 | 403 | 2 | Q93WJ9_ARATH | Q93wj9_arabidopsis |
| 714 | 48 | 100.0 | 379 | 2 | Q7X9Z8_9CARY | Q7x9z8 fagopyrum c | 787 | 48 | 100.0 | 403 | 2 | Q90Y49_AMBME | Q90y49_ambystoma m |
| 715 | 48 | 100.0 | 379 | 2 | Q7XA04_9CARY | Q7xa04 fagopyrum g | 788 | 48 | 100.0 | 404 | 2 | Q90J96_ARATH | Q90j96_arabidopsis |
| 716 | 48 | 100.0 | 379 | 2 | Q5BJV8_RAT | Q5bjv8 rattus norv | 789 | 48 | 100.0 | 404 | 2 | Q64875_ARATH | Q64875_arabidopsis |
| 717 | 48 | 100.0 | 380 | 1 | CAR2_CHARE | P23258 chlamdomon | 790 | 48 | 100.0 | 404 | 2 | Q8UVJ4_PETMA | Q8uvj4_petromyzon |
| 718 | 48 | 100.0 | 380 | 1 | Q7X9T_9CARY | Q7x9t fagopyrum s | 791 | 48 | 100.0 | 406 | 2 | Q5QLP5_ORYSA | Q5qlf5_oryza savi |
| 719 | 48 | 100.0 | 380 | 2 | Q7X9Z7_9CARY | Q7x9z7 fagopyrum s | 792 | 48 | 100.0 | 407 | 2 | Q4FL4_DICDI | Q54f14 dictyosteli |
| 720 | 48 | 100.0 | 380 | 2 | Q7X9Z9_9CARY | Q7x9z9 fagopyrum c | 793 | 48 | 100.0 | 407 | 2 | Q84WQ3_ARATH | Q84wq3_arabidopsis |
| 721 | 48 | 100.0 | 380 | 2 | Q4QY62_MOUSE | Q4qy62 fagopyrum c | 794 | 48 | 100.0 | 407 | 2 | Q9ZQA3_ARATH | Q9zqa3_arabidopsis |
| 722 | 48 | 100.0 | 380 | 2 | Q7X9Y9_9CARY | Q7x9y9 fagopyrum g | 795 | 48 | 100.0 | 407 | 2 | Q7V242_PROMP | Q7v242_prochloroco |
| 723 | 48 | 100.0 | 381 | 2 | Q7X9V6_9CARY | Q7x9v6 fagopyrum g | 796 | 48 | 100.0 | 409 | 1 | BAG7_YEAST | Q12128 saccharomyc |
| 724 | 48 | 100.0 | 381 | 2 | Q7XKU0_ORYSA | Q7xku0 oryza savi | 797 | 48 | 100.0 | 410 | 1 | PO4F2_HUMAN | Q12837_homo sapien |
| 725 | 48 | 100.0 | 381 | 2 | Q5UK17_ORYSA | Q5uk17 oryza savi | 798 | 48 | 100.0 | 411 | 1 | PO4F2_MOUSE | Q63934_mus musculu |
| 726 | 48 | 100.0 | 381 | 2 | Q92MD8_RHIME | Q92md8 rhizobium m | 799 | 48 | 100.0 | 411 | 2 | P78701_METAN | P78701_methanazium |
| 727 | 48 | 100.0 | 382 | 2 | Q4WAA9_ASFPU | Q4waa9 aspergillus | 800 | 48 | 100.0 | 411 | 2 | Q504X5_HUMAN | Q504x5_homo sapien |
| 728 | 48 | 100.0 | 382 | 2 | Q7X9Z4_9CARY | Q7x9z4 fagopyrum r | 801 | 48 | 100.0 | 411 | 2 | Q9SSV1_DROME | Q9ssv1_drosophila |
| 729 | 48 | 100.0 | 384 | 2 | Q61XU1_CABBR | Q61xu1 caenorhabdi | 802 | 48 | 100.0 | 411 | 2 | Q9VVM5_DROME | Q9vwm5_drosophila |
| 730 | 48 | 100.0 | 384 | 2 | Q5QLF6_ORYSA | Q5qlf6 oryza savi | 803 | 48 | 100.0 | 411 | 2 | Q8CHJ4_RAT | Q8chj4_rattus norv |
| 731 | 48 | 100.0 | 384 | 2 | Q82136_PEA | Q82136 plium savi | 804 | 48 | 100.0 | 412 | 2 | Q51XZ7_MAGGR | Q51xz7_magnaporthe |
| 732 | 48 | 100.0 | 384 | 2 | Q6XZH1_BRARE | Q6xzh1 brachydanto | 805 | 48 | 100.0 | 412 | 2 | Q98U15_LAMJA | Q98u15_lampectra ja |
| 733 | 48 | 100.0 | 385 | 1 | SEPP1_RAT | P25336 rattus norv | 806 | 48 | 100.0 | 412 | 2 | Q4UIT8_BRARE | Q4uit8_brechydanto |
| 734 | 48 | 100.0 | 385 | 2 | Q5AS77_CANAL | Q5as77 candida alb | 807 | 48 | 100.0 | 413 | 2 | Q8J0Y8_CRYNV | Q8j0y8_cryptococcu |
| 735 | 48 | 100.0 | 385 | 2 | Q17909_CAEEL | Q17909 caenorhabdi | 808 | 48 | 100.0 | 413 | 2 | Q8J108_CRYNV | Q8j108_cryptococcu |
| 736 | 48 | 100.0 | 387 | 1 | Q1N_AVTIS3 | P56260 avian sarco | 809 | 48 | 100.0 | 413 | 2 | Q4GYR6_PRRYP | Q4gyr6_rypanosoma |
| 737 | 48 | 100.0 | 387 | 2 | Q7PXZ4_ANOGA | Q7pxz4 anopheles g | 810 | 48 | 100.0 | 413 | 2 | Q6NLK3_ARATH | Q6nlk3_arabidopsis |
| 738 | 48 | 100.0 | 387 | 2 | Q941Q6_ORYSA | Q941q6 oryza savi | 811 | 48 | 100.0 | 413 | 2 | Q5ICW3_LAMFL | Q5icw3_lampectra fl |
| 739 | 48 | 100.0 | 388 | 2 | Q9SR32_DROME | Q9sr32 drosophila | 812 | 48 | 100.0 | 414 | 1 | TYV1_HUMAN | P25490_homo sapien |
| 740 | 48 | 100.0 | 388 | 2 | Q9VP48_DROME | Q9vp48 drosophila | 813 | 48 | 100.0 | 414 | 2 | TYV1_MOUSE | Q00899_mus musculu |
| 741 | 48 | 100.0 | 388 | 2 | Q7Y1X7_ORYSA | Q7y1x7 oryza savi | 814 | 48 | 100.0 | 414 | 2 | Q6ZOB3_MOUSE | Q6zob3_mus musculu |
| 742 | 48 | 100.0 | 388 | 2 | Q8LNE8_ORYSA | Q8lne8 oryza savi | 815 | 48 | 100.0 | 415 | 2 | Q7XIX9_ORYSA | Q7xix9_oryza savi |
| 743 | 48 | 100.0 | 388 | 2 | Q941M8_ORYSA | Q941m8 oryza savi | 816 | 48 | 100.0 | 419 | 2 | Q5T2Z7_HUMAN | Q5t2z7_homo sapien |
| 744 | 48 | 100.0 | 388 | 2 | Q4S7V3_TETNG | Q4s7v3 tetradon n | 817 | 48 | 100.0 | 419 | 2 | Q9SY80_CLARKA | Q9sy80_clarkia bre |
| 745 | 48 | 100.0 | 389 | 2 | Q7X910_ARATH | P23192 caa-nb-1 mu | 818 | 48 | 100.0 | 419 | 2 | Q5WMS9_ORYSA | Q5wms9_oryza savi |
| 746 | 48 | 100.0 | 390 | 1 | CB1_MLYCN | P26017 drosophila | 819 | 48 | 100.0 | 419 | 2 | Q7T2N8_BRARE | Q7t2n8_brechydanto |
| 747 | 48 | 100.0 | 390 | 1 | PC_DROME | Q526k4 magnaporthe | 820 | 48 | 100.0 | 420 | 1 | YBE1_SCHPO | Q42980_schizosacch |
| 748 | 48 | 100.0 | 390 | 2 | Q5ZER4_MAGGR | Q5zer4 magnaporthe | 821 | 48 | 100.0 | 420 | 2 | Q5CFT4_CRYHO | Q5cft4_cryptospori |
| 749 | 48 | 100.0 | 390 | 2 | Q541F9_DROME | Q541f9 drosophila | 822 | 48 | 100.0 | 420 | 2 | Q90VZ9_WMORI | Q90vz9_mus sp. . b |
| 750 | 48 | 100.0 | 390 | 2 | Q4QB70_LEIWA | Q4qb70 leiishmania | 823 | 48 | 100.0 | 420 | 2 | Q73862_BRARE | Q73862_brechydanto |
| 751 | 48 | 100.0 | 390 | 2 | Q661T4_XENLA | Q661t4 xenopus lae | 824 | 48 | 100.0 | 420 | 2 | Q568V0_BRARE | Q568v0_brechydanto |
| 752 | 48 | 100.0 | 390 | 2 | Q4V872_XENLA | Q4v872 xenopus lae | 825 | 48 | 100.0 | 420 | 2 | Q4SON1_TETNG | Q4son1_tetradon n |
| 753 | 48 | 100.0 | 391 | 2 | Q7SB14_NEYCR | Q7sb14 neurospora | 826 | 48 | 100.0 | 421 | 1 | PO4FL1_MOUSE | P17208_mus musculu |
| 754 | 48 | 100.0 | 391 | 2 | Q9WAH8_ARATH | Q9wah8 arabidopsis | 827 | 48 | 100.0 | 421 | 2 | Q64FW2_MOUSE | Q64fm2_mus musculu |
| 755 | 48 | 100.0 | 392 | 1 | ODD_DROME | P23038 arabidopsis | 828 | 48 | 100.0 | 421 | 2 | Q7BNAS_MOUSE | Q7bnas_mus musculu |
| 756 | 48 | 100.0 | 392 | 1 | ODD_DROME | P23038 arabidopsis | 829 | 48 | 100.0 | 422 | 2 | Q7BNAS_MOUSE | Q7bnas_mus musculu |
| 757 | 48 | 100.0 | 392 | 2 | Q5DE72_SCHJA | Q5de72 schistosoma | 830 | 48 | 100.0 | 422 | 2 | Q9W4B5_DROME | Q9w4b5_herdmania c |
| 758 | 48 | 100.0 | 392 | 2 | Q5CV98_CRYPV | Q5cv98 cryptospori | 831 | 48 | 100.0 | 422 | 2 | Q4SZ36_TETNG | Q4sz36_tetradon n |
| 759 | 48 | 100.0 | 392 | 2 | Q614Y5_CABBR | Q614y5 caenorhabdi | 832 | 48 | 100.0 | 423 | 1 | PO4FL1_HUMAN | Q01851_homo sapien |
| 760 | 48 | 100.0 | 392 | 2 | Q810A6_CAEEL | Q810a6 caenorhabdi | 833 | 48 | 100.0 | 423 | 2 | OS1JF1_MAGGR | OS1jf1_magnaporthe |
| 761 | 48 | 100.0 | 394 | 2 | Q5D114_SCHJA | Q5d114 schistosoma | 834 | 48 | 100.0 | 423 | 2 | O10417_HCMV | O10417_human cytom |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|---------------|-----------------------|-----|----|-------|-----|---|---------------|---------------------|
| 835 | 48 | 100.0 | 424 | 2 | Q5CU23_CRYHO | Q5CJ23_cryptospori | 908 | 48 | 100.0 | 456 | 2 | Q95WD6_9ANNE | Q95WD6_pristina lae |
| 836 | 48 | 100.0 | 424 | 2 | Q4RG16_TERING | Q4RG16_tetradon n | 909 | 48 | 100.0 | 456 | 2 | Q7X637_ORYSA | Q7X637 oryza sativ |
| 837 | 48 | 100.0 | 425 | 1 | LE756_CAERL | Q1184 caenorhabdi | 910 | 48 | 100.0 | 456 | 2 | Q8BS83_MOUSE | Q8BS83 mus musculu |
| 838 | 48 | 100.0 | 425 | 1 | POU1_BRARE | P31366 brachydantio | 911 | 48 | 100.0 | 456 | 2 | Q6MYT7_BRARE | Q6MYT7 brachydantio |
| 839 | 48 | 100.0 | 425 | 2 | Q6OV83_CAEBR | Q6OV83 caenorhabdi | 912 | 48 | 100.0 | 456 | 2 | Q5MD20_BRARE | Q5MD20 brachydantio |
| 840 | 48 | 100.0 | 425 | 2 | Q5CUTI_CRYPV | Q5CUTI_cryptospori | 913 | 48 | 100.0 | 457 | 2 | Q7SGR7_NEUCR | Q7SGR7 neurospora |
| 841 | 48 | 100.0 | 425 | 2 | Q5VWM2_ORYSA | Q5VWM2 oryza sativ | 914 | 48 | 100.0 | 457 | 2 | Q6P440_HUMAN | Q6P440 homo sapien |
| 842 | 48 | 100.0 | 426 | 2 | Q9JZP9_ARATH | Q9JZP9 arabidopsi | 915 | 48 | 100.0 | 457 | 2 | Q5JY75_HUMAN | Q5JY75 homo sapien |
| 843 | 48 | 100.0 | 426 | 2 | Q9LXK1_ARATH | Q9LXK1 arabidopsi | 916 | 48 | 100.0 | 459 | 2 | Q4ST96_TERING | Q4ST96 tetradon n |
| 844 | 48 | 100.0 | 427 | 1 | CP1A_DROME | P16241 drosophila | 917 | 48 | 100.0 | 460 | 2 | Q9YLO3_DROME | Q9YLO3 drosophila |
| 845 | 48 | 100.0 | 427 | 1 | Q86P26_DROME | Q86P26 drosophila | 918 | 48 | 100.0 | 461 | 2 | Q7QZ08_ANOGA | Q7QZ08 anopheles g |
| 846 | 48 | 100.0 | 427 | 2 | Q6VM73_LUPAL | Q6VM73 lupinus alb | 919 | 48 | 100.0 | 461 | 2 | Q9D709_MOUSE | Q9D709 mus musculu |
| 847 | 48 | 100.0 | 427 | 2 | Q6S3Q9_ORYSA | Q6S3Q9 oryza sativ | 920 | 48 | 100.0 | 461 | 2 | Q9JY45_MOUSE | Q9JY45 mus musculu |
| 848 | 48 | 100.0 | 427 | 2 | Q6ZJG0_ORYSA | Q6ZJG0 oryza sativ | 921 | 48 | 100.0 | 461 | 2 | Q8VE28_MOUSE | Q8VE28 mus musculu |
| 849 | 48 | 100.0 | 427 | 2 | Q5YNG3_NOCFA | Q5YNG3 nocardia fa | 922 | 48 | 100.0 | 461 | 2 | Q6PHC9_BRARE | Q6PHC9 brachydantio |
| 850 | 48 | 100.0 | 428 | 1 | FOX82_MOUSE | Q64733 mus musculu | 923 | 48 | 100.0 | 461 | 2 | Q5MD19_BRARE | Q5MD19 brachydantio |
| 851 | 48 | 100.0 | 428 | 2 | Q811L7_PLAF7 | Q811L7 plasmodium | 924 | 48 | 100.0 | 462 | 2 | Q7SYH2_XENLA | Q7SYH2 xenopus lae |
| 852 | 48 | 100.0 | 428 | 2 | Q5NKS7_SORBI | Q5NKS7 sorghum bic | 925 | 48 | 100.0 | 462 | 2 | Q7ZY91_XENLA | Q7ZY91 xenopus lae |
| 853 | 48 | 100.0 | 429 | 2 | Q51088_XENTR | Q51088 xenopus tro | 926 | 48 | 100.0 | 463 | 2 | Q54ZC9_DICDI | Q54ZC9 dictyosteli |
| 854 | 48 | 100.0 | 430 | 2 | Q624C6_CAEBR | Q624C6 caenorhabdi | 927 | 48 | 100.0 | 463 | 2 | Q54Y39_DICDI | Q54Y39 dictyosteli |
| 855 | 48 | 100.0 | 431 | 2 | Q81QG2_DROME | Q81QG2 drosophila | 928 | 48 | 100.0 | 463 | 2 | Q4ST87_TERING | Q4ST87 tetradon n |
| 856 | 48 | 100.0 | 431 | 2 | Q9YFP2_DROME | Q9YFP2 drosophila | 929 | 48 | 100.0 | 465 | 1 | HNF6_HUMAN | HNF6_HUMAN |
| 857 | 48 | 100.0 | 432 | 2 | Q5YVVO_HUMAN | Q5YVVO homo sapien | 930 | 48 | 100.0 | 465 | 1 | HNF6_MOUSE | HNF6_MOUSE |
| 858 | 48 | 100.0 | 434 | 2 | Q91765_XENLA | Q91765 xenopus lae | 931 | 48 | 100.0 | 465 | 1 | HNF6_RAT | HNF6_RAT |
| 859 | 48 | 100.0 | 434 | 2 | Q7T1R4_XENTR | Q7T1R4 xenopus tro | 932 | 48 | 100.0 | 465 | 1 | Q801E5_XENLA | Q801E5 xenopus lae |
| 860 | 48 | 100.0 | 435 | 2 | Q4WULO_ASPFU | Q4WULO aspergillus | 933 | 48 | 100.0 | 466 | 1 | Z1C3_MOUSE | Z1C3_MOUSE |
| 861 | 48 | 100.0 | 435 | 2 | Q53PPE_ORYSA | Q53PPE oryza sativ | 934 | 48 | 100.0 | 466 | 2 | Q5CDD8_CRYHO | Q5CDD8 cryho |
| 862 | 48 | 100.0 | 436 | 2 | Q9YHCS_XENLA | Q9YHCS xenopus lae | 935 | 48 | 100.0 | 466 | 2 | Q6AVV5_ORYSA | Q6AVV5 oryza sativ |
| 863 | 48 | 100.0 | 437 | 1 | POU12_BRARE | P56224 brachydantio | 936 | 48 | 100.0 | 467 | 1 | Z1C3_HUMAN | Z1C3_HUMAN |
| 864 | 48 | 100.0 | 437 | 2 | Q5CXM3_CRYPV | Q5CXM3 cryptospori | 937 | 48 | 100.0 | 467 | 2 | Q9ZVX2_ARATH | Q9ZVX2 arath |
| 865 | 48 | 100.0 | 437 | 2 | Q60S46_CAEBR | Q60S46 caenorhabdi | 938 | 48 | 100.0 | 467 | 2 | Q9ML17_ARATH | Q9ML17 arath |
| 866 | 48 | 100.0 | 437 | 2 | Q7YWN5_CAEBL | Q7YWN5 caenorhabdi | 939 | 48 | 100.0 | 467 | 2 | Q9YGC6_XENLA | Q9YGC6 xenopus lae |
| 867 | 48 | 100.0 | 437 | 2 | Q6VM69_GIBZE | Q6VM69 gibberella ten | 940 | 48 | 100.0 | 469 | 1 | ADA2C2_DIDMA | ADA2C2 didyma |
| 868 | 48 | 100.0 | 439 | 2 | Q4IE45_GIBZE | Q4IE45 gibberella | 941 | 48 | 100.0 | 469 | 1 | FOXGA_HUMAN | FOXGA_HUMAN |
| 869 | 48 | 100.0 | 439 | 2 | Q9NSV0_HUMAN | Q9NSV0 homo sapien | 942 | 48 | 100.0 | 469 | 2 | Q8H9F6_ARATH | Q8H9F6 arath |
| 870 | 48 | 100.0 | 439 | 2 | Q67U27_ORYSA | Q67U27 oryza sativ | 943 | 48 | 100.0 | 470 | 2 | Q5BC50_EMENT | Q5BC50 aspergillus |
| 871 | 48 | 100.0 | 440 | 2 | Q4QBP5_LEIMA | Q4QBP5 leishmania | 944 | 48 | 100.0 | 470 | 2 | Q621S9_CAEBL | Q621S9 caenohabdi |
| 872 | 48 | 100.0 | 441 | 1 | GATF6_RAT | P46153 rattus norv | 945 | 48 | 100.0 | 470 | 2 | Q9JMA3_MOUSE | Q9JMA3 mus musculu |
| 873 | 48 | 100.0 | 441 | 1 | Q8T1W3_DICDI | P79745 brachydantio | 946 | 48 | 100.0 | 471 | 2 | Q9JAY0_CAEBL | Q9JAY0 caenorhabdi |
| 874 | 48 | 100.0 | 443 | 1 | POU23_BRARE | Q4YX48 homo sapien | 947 | 48 | 100.0 | 473 | 1 | KNOB_PLARA | KNOB_PLARA |
| 875 | 48 | 100.0 | 443 | 2 | Q54YX8_HUMAN | Q54YX8 dictyosteli | 948 | 48 | 100.0 | 474 | 1 | ANA_DROME | ANA_DROME |
| 876 | 48 | 100.0 | 443 | 2 | Q504D2_BRARE | Q504D2 brachydantio | 949 | 48 | 100.0 | 474 | 2 | Q5B4J3_EMENT | Q5B4J3 aspergillus |
| 877 | 48 | 100.0 | 443 | 2 | Q91863_FUGRU | Q91863 fugu rubrip | 950 | 48 | 100.0 | 474 | 2 | Q75GL2_ORYSA | Q75GL2 oryza sativ |
| 878 | 48 | 100.0 | 444 | 1 | FOXFP2_HUMAN | Q12947 homo sapien | 951 | 48 | 100.0 | 474 | 2 | Q6DIT5_XENTR | Q6DIT5 xenopus tro |
| 879 | 48 | 100.0 | 444 | 1 | GATF6_MOUSE | Q61169 mus musculu | 952 | 48 | 100.0 | 475 | 2 | Q6BIV5_DEBHA | Q6BIV5 debrayomyce |
| 880 | 48 | 100.0 | 444 | 2 | Q5TGU1_HUMAN | Q5TGU1 homo sapien | 953 | 48 | 100.0 | 475 | 2 | Q7XQK6_ORYSA | Q7XQK6 oryza sativ |
| 881 | 48 | 100.0 | 444 | 2 | Q657M9_ORYSA | Q657M9 oryza sativ | 954 | 48 | 100.0 | 476 | 2 | Q55FD4_DICDI | Q55FD4 dictyosteli |
| 882 | 48 | 100.0 | 444 | 2 | Q7ZU22_BRARE | Q7ZU22 brachydantio | 955 | 48 | 100.0 | 477 | 1 | FOXGB_HUMAN | FOXGB_HUMAN |
| 883 | 48 | 100.0 | 444 | 2 | Q6PHH6_BRARE | Q6PHH6 brachydantio | 956 | 48 | 100.0 | 477 | 2 | Q815Y7_ARATH | Q815Y7 arath |
| 884 | 48 | 100.0 | 444 | 2 | Q90ZS9_BRARE | Q90ZS9 brachydantio | 957 | 48 | 100.0 | 477 | 2 | Q9MLK5_ARATH | Q9MLK5 arath |
| 885 | 48 | 100.0 | 445 | 2 | Q4RXPT_TERING | Q4RXPT tetradon n | 958 | 48 | 100.0 | 479 | 2 | Q5A726_CANAL | Q5A726 candida alb |
| 886 | 48 | 100.0 | 446 | 2 | Q54QY7_DICDI | Q54QY7 dictyosteli | 959 | 48 | 100.0 | 479 | 2 | Q5A712_CANAL | Q5A712 candida alb |
| 887 | 48 | 100.0 | 446 | 2 | Q95J45_PIG | Q95J45 sus scrofa | 960 | 48 | 100.0 | 479 | 2 | Q5ABT3_CANAL | Q5ABT3 candida alb |
| 888 | 48 | 100.0 | 446 | 2 | Q97727_PIG | Q97727 sus scrofa | 961 | 48 | 100.0 | 479 | 2 | Q5AC55_CANAL | Q5AC55 candida alb |
| 889 | 48 | 100.0 | 446 | 2 | Q8UTU4_BRARE | Q8UTU4 brachydantio | 962 | 48 | 100.0 | 480 | 1 | FOXGB_RAT | FOXGB_RAT |
| 890 | 48 | 100.0 | 447 | 2 | Q55AD2_DICDI | Q55AD2 dictyosteli | 963 | 48 | 100.0 | 481 | 1 | FOXGB_MOUSE | FOXGB_MOUSE |
| 891 | 48 | 100.0 | 447 | 2 | Q9FLD7_ARATH | Q9FLD7 arabidopsi | 964 | 48 | 100.0 | 481 | 2 | Q6ZIC1_ORYSA | Q6ZIC1 oryza sativ |
| 892 | 48 | 100.0 | 448 | 1 | PO3F1_HUMAN | Q03052 homo sapien | 965 | 48 | 100.0 | 481 | 2 | Q8UFP7_BRARE | Q8UFP7 brare |
| 893 | 48 | 100.0 | 448 | 2 | Q7SA40_NEUCR | Q7SA40 neurospora | 966 | 48 | 100.0 | 482 | 2 | Q7SH12_NEUCR | Q7SH12 neurospora |
| 894 | 48 | 100.0 | 449 | 1 | GATF6_HUMAN | Q92908 homo sapien | 967 | 48 | 100.0 | 482 | 2 | Q4POR1_USITMA | Q4POR1 usitlago ma |
| 895 | 48 | 100.0 | 449 | 1 | PO3F1_MOUSE | P21952 mus musculu | 968 | 48 | 100.0 | 483 | 2 | Q7PSP9_ANOGA | Q7PSP9 anopheles g |
| 896 | 48 | 100.0 | 449 | 2 | Q8C4J8_MOUSE | Q8C4J8 mus musculu | 969 | 48 | 100.0 | 483 | 2 | Q5IF1E_AEDAE | Q5IF1E aedes aegypt |
| 897 | 48 | 100.0 | 450 | 2 | Q7QZK7_ANOGA | Q7QZK7 anopheles g | 970 | 48 | 100.0 | 483 | 2 | Q53PPT_ORYSA | Q53PPT oryza sativ |
| 898 | 48 | 100.0 | 451 | 1 | FOXGB_CHICK | Q90964 gallus gall | 971 | 48 | 100.0 | 484 | 1 | MECP2_MOUSE | MECP2_MOUSE |
| 899 | 48 | 100.0 | 451 | 1 | PO3F1_RAT | P20267 rattus norv | 972 | 48 | 100.0 | 484 | 2 | Q6NNC9_DROME | Q6NNC9 drosophila |
| 900 | 48 | 100.0 | 451 | 2 | Q5YFAG2_HUMAN | Q5YFAG2 homo sapien | 973 | 48 | 100.0 | 485 | 1 | ONEC2_HUMAN | ONEC2_HUMAN |
| 901 | 48 | 100.0 | 451 | 2 | Q969P2_HUMAN | Q969P2 homo sapien | 974 | 48 | 100.0 | 485 | 1 | MECP2_MOUSE | MECP2_MOUSE |
| 902 | 48 | 100.0 | 453 | 2 | Q5AN14_CANAL | Q5AN14 candida alb | 975 | 48 | 100.0 | 486 | 1 | MECP22_MACFA | MECP22 macaca faec |
| 903 | 48 | 100.0 | 453 | 2 | Q4XZP4_PLACH | Q4XZP4 plasmodium | 976 | 48 | 100.0 | 486 | 2 | Q6XBJ3_HUMAN | Q6XBJ3 mus musculu |
| 904 | 48 | 100.0 | 453 | 2 | Q50HVE_SORBI | Q50HVE sorghum bic | 977 | 48 | 100.0 | 487 | 2 | Q703G1_BRANA | Q703G1 brassica na |
| 905 | 48 | 100.0 | 454 | 2 | Q66L07_XENLA | Q66L07 xenopus lae | 978 | 48 | 100.0 | 488 | 2 | Q5SK04_CRYNE | Q5SK04 cryptococcu |
| 906 | 48 | 100.0 | 454 | 2 | Q73627_ANOCA | Q73627 anolis caro | 979 | 48 | 100.0 | 488 | 2 | Q5K9J5_CRYNE | Q5K9J5 cryptococcu |
| 907 | 48 | 100.0 | 456 | 2 | Q54YX8_DICDI | Q54YX8 dictyosteli | 980 | 48 | 100.0 | 488 | 2 | Q4Q509_LEIMA | Q4Q509 leishmania |

```

981 48 100.0 489 2 Q66XT7_HUMAN Q66XT7_homo sapien
982 48 100.0 490 1 M073_YEAST P54785_saccharomyc
983 48 100.0 490 2 OSASD9_EMENTI O5aed9_aspergillus
984 48 100.0 490 2 O4IGP4_GIBZE O4igp4_gibberella
985 48 100.0 490 2 OSCUA2_CRYPV O5cuaz_cryptospori
986 48 100.0 491 2 O60122_EPRBU O60122_erythrocyt
987 48 100.0 492 1 MECBP2_RAT Q60566_rattus norv
988 48 100.0 492 2 O6DKH9_HUMAN Q6dkh9_homo sapien
989 48 100.0 492 2 O9FPF2_ARATH Q9fpf2_arabidopsi
990 48 100.0 494 2 O4R113_TENG O4r113_tetradon n
991 48 100.0 495 1 P03F3_MOUSE P13361_mus muscicu
992 48 100.0 495 2 O54QF2_DICDI O54qf2_dicystocell
993 48 100.0 496 1 BAF1_KLUMA P33293_kluyveromye
994 48 100.0 496 2 O642Y3_FUGRU O642y3_fugu rubrip
995 48 100.0 497 1 P03F3_RAT Q63262_rattus norv
996 48 100.0 497 2 O9YIB7_XENLA O9yib7_xenopus lae
997 48 100.0 498 2 O6GHH9_HUMAN O6ghh9_homo sapien
998 48 100.0 498 2 O9VWL3_DROME O9vwl3_drosophila
999 48 100.0 498 2 O9M0F8_ARATH O9m0f8_arabidopsi
1000 48 100.0 498 2 O6YSC5_ORYSA O6ysc5_oryza sativ

```

ALIGNMENTS

```

RESULT 1
LPHI_YERPE
ID LPHI_YERPE STANDARD; PRT; 15 AA.
AC Q8D079;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE His operon leader peptide (Atenuator peptide).
GN Name=hisl; OrderedlocusNames=YPO1550.1, Y2618, YP1439.1;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parthill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holtroyd S., Jagsi K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Staley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Jin L., Qiu H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
avirulent to humans.";

```

```

RL DNA Res. 11:179-197(2004).
CC -!- FUNCTION: This protein is involved in the attenuation mechanism
CC for the control of the expression of the his operon structural
CC genes (By similarity).
CC -!- SIMILARITY: Belongs to the hisL family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AJ414149; -; NOT ANNOTATED CDS; Genomic DNA.
CC EMBL; AE013863; AA06172.1; -; Genomic DNA.
CC EMBL; AE017132; -; NOT ANNOTATED CDS; Genomic DNA.
CC InterPro; IPR012565; His leader.
CC Pfam; PF08047; His leader; 1.
CC Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;
CC Leader peptide.
CC SEQUENCE 15 AA; 1943 MW; EE17FBF6282748D8 CRC64;

```

Query Match 100.0%; Score 48; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 HHHHHH 6
   |||||
DB 8 HHHHHH 13

```

```

RESULT 2
LPHI_ECO57
ID LPHI_ECO57 STANDARD; PRT; 16 AA.
AC O8X8T5;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE His operon leader peptide (Atenuator peptide).
GN Name=hisl; OrderedlocusNames=23180, EC82819;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RX Perna N.T., Plunkett G. III, Burland V., Mau B., Glaesner J.D.,
RX Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RX Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RX Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
MEDLINE=21156231; PubMed=11258796;
RX Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RX Han C.-G., Ohtsubo E., Nakayama K., Murata K., Tanaka M., Tobe T.,
RX Iida T., Takami H., Honda T., Sasekawa C., Ogasawara N., Yasunaga T.,
RX Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
CC -!- FUNCTION: This protein is involved in the attenuation mechanism
CC for the control of the expression of the his operon structural
CC genes (By similarity).
CC -!- SIMILARITY: Belongs to the hisL family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

CC the European Bioinformatics Institute. There are no restrictions on its
 CC as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; AE005174; AAG57077.1; -; Genomic_DNA.
 DR EMBL; BA000007; BAB36242.1; -; Genomic_DNA.
 DR PIR; A85827; A85827.
 DR PIR; C90981; C90981.
 DR InterPro; IPR012565; His leader.
 DR Pfam; PF08047; His leader; 1.
 KW Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;
 KW Leader peptide.
 SQ SEQUENCE 16 AA; 2072 MW; D78A907BF6283BBA CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 9 HHHHHH 14

RESULT 3

LPHI_ECOL6 STANDARD; PRT; 16 AA.

AC P60956; P03058; (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE His operon leader peptide (Attenuator peptide).
 GN Name=hisL; OrderedLocustNames=c5496;
 OS Escherichia coli O6.

CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 CC NCBI_TaxID=217992;
 OX [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=O6.H1 / CPT073 / ATCC 700928 / UPEC;
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;

RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Raeko D., Buckles E.L., Lion S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Domeneberg M.S., Blattner F.R.;

RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

CC -!- FUNCTION: This protein is involved in the attenuation mechanism
 for the control of the expression of the his operon structural
 genes (by similarity).

CC -!- SIMILARITY: Belongs to the hisL family.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; AE016762; AAN8100.1; -; Genomic_DNA.
 DR InterPro; IPR012565; His leader.

DR Pfam; PF08047; His leader; 1.

KW Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;
 KW Leader peptide.

SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 8 HHHHHH 13

RESULT 4

LPHI_ECOL1 STANDARD; PRT; 16 AA.

AC P60955; P03058; (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE His operon leader peptide (Attenuator peptide).
 GN Name=hisL; OrderedLocustNames=b2018;

OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 CC NCBI_TaxID=562;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=K12;

RX MEDLINE=79033821; PubMed=360215;

RA Dinocera P.P., Biasi F., Dilauro R., Frunzio R., Bruni C.B.;

RT "Nucleotide sequence of the attenuator region of the histidine operon
 of Escherichia coli K-12.";

RL Proc. Natl. Acad. Sci. U.S.A. 75:4276-4280(1978).

RM [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=K12;

RX MEDLINE=82059525; PubMed=6170941;

RA Verde P., Frunzio R., di Nocera P.P., Biasi F., Bruni C.B.;

RT "Identification, nucleotide sequence and expression of the regulatory
 region of the histidine operon of Escherichia coli K-12.";

RL Nucleic Acids Res. 9:2075-2086(1981).

RM [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=K12;

RX MEDLINE=83094829; PubMed=3062174;

RA Carlomagno M.S., Chiarotelli L., Alfano P., Nappo A.G., Bruni C.B.;

RT "Structure and function of the Salmonella typhimurium and Escherichia
 coli K-12 histidine operons.";

RL J. Mol. Biol. 203:585-606(1988).

RM [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

CC -!- FUNCTION: This protein is involved in the attenuation mechanism
 for the control of the expression of the his operon structural
 genes (by similarity).

CC -!- SIMILARITY: Belongs to the hisL family.

CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; V00285; CAA23550.1; -; Genomic_DNA.
 DR EMBL; V00284; CAA23548.1; -; Genomic_DNA.

DR EMBL; X13462; CAA31810.1; -; Genomic_DNA.

DR EMBL; U00096; AAC75079.1; -; Genomic_DNA.

DR PIR; A03594; LFECH.

DR ECHOBASE; EB1248; -;

DR EcoGene; EG1269; hisL.

DR InterPro; IPR012565; His leader.

DR Pfam; PF08047; His leader; 1.

KW Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis;
 KW Leader peptide.

SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 8 HHHHHH 13

RESULT 5

LPPI_KLEPN STANDARD; PRT; 16 AA.

AC Q48439;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE His operon leader peptide (Attenuator peptide).
GN Name=hisL;
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;

RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=8413578; PubMed=6321433;
RA Rodriguez R.L., West R.W. Jr.;
RT "Histidine operon control region of Klebsiella pneumoniae: analysis with an Escherichia coli promoter-probe plasmid vector."
RL J. Bacteriol. 157:764-771(1984).
CC -1- FUNCTION: This protein is involved in the attenuation mechanism for the control of the expression of the his operon structural genes (By similarity).
CC -1- SIMILARITY: Belongs to the hisL family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; K01997; AAA5072.1; -; Genomic DNA.
DR InterPro; IPR012565; His_leader.
DR Pfam; PF08047; His_leader; 1.
KW Amino-acid biosynthesis; Histidine biosynthesis; Leader peptide.
SQ SEQUENCE 16 AA; 2002 MW; CF29907BF6296248 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 9 HHHHHH 14

RESULT 6
LPPI_SALTY STANDARD; PRT; 16 AA.

AC P60957; P03058;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE His operon leader peptide (Attenuator peptide).
GN Name=hisL; OrderedLocustNames=STM2070.1;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;

RN NUCLEOTIDE SEQUENCE.
RC STRAIN=LT2;
RX MEDLINE=79033822; PubMed=360216;
RA Barnes W.M.;
RT "DNA sequence from the histidine operon control region: seven

RT histidine codons in a row."
RL Proc. Natl. Acad. Sci. U.S.A. 75:4281-4285(1978).

RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LT2;
RX MEDLINE=85094829; PubMed=3062174;
RA Carlomagno W.S., Chiaroteli L., Alfano P., Nappo A.G., Bruni C.B.;
RT "Structure and function of the Salmonella typhimurium and Escherichia coli K-12 histidine operons."
RL J. Mol. Biol. 203:585-606(1988).

RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LT2;
RA Barnes W.M., Huseon R.N., Whittier R.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.

RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2."
RL Nature 413:852-856(2001).

CC -1- FUNCTION: This protein is involved in the attenuation mechanism for the control of the expression of the his operon structural genes (By similarity).
CC -1- SIMILARITY: Belongs to the hisL family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; V01371; CAA24656.1; -; Genomic DNA.
DR EMBL; X13464; XAA31821.1; -; Genomic DNA.
DR EMBL; J01804; AAB8613.1; -; Genomic DNA.
DR EMBL; AB008791; -; NOT_ANNOTATED_CDS; Genomic DNA.
DR StGene; SG10166; hisL.
DR InterPro; IPR012565; His_leader.
DR Pfam; PF08047; His_leader; 1.
KW Amino-acid biosynthesis; Complete proteome; Histidine biosynthesis; Leader peptide.
SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 100.0%; Score 48; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 8 HHHHHH 13

RESULT 7

Q5C5K5_SCHUA PRELIMINARY; PRT; 30 AA.

AC Q5C5K5;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.

OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY809180; AAX25069.1; -, mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 30 AA; 3637 MW; FF50EE3B02EA533D CRC64;

Query Match 100.0%; Score 48; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 10 HHHHHH 15

RESULT 8
 Q6UGP2_PEA PRELIMINARY; PRT; 31 AA.

AC Q6UGP2;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Sats (Fragment).
 OS Pisum sativum subsp. abyssinicum.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=198035;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Stafsstrom J.P., Ingram P.A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY370645; AAO67403.1; -, Genomic_DNA.
 FT NON TER 31 31
 SQ SEQUENCE 31 AA; 3668 MW; B5CC671448C064E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 19 HHHHHH 24

RESULT 9
 Q6UGP3_PEA PRELIMINARY; PRT; 31 AA.

AC Q6UGP3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Sats (Fragment).
 OS Pisum sativum subsp. elatius.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=47742;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Stafsstrom J.P., Ingram P.A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY370644; AAO67402.1; -, Genomic_DNA.
 FT NON TER 31 31
 SQ SEQUENCE 31 AA; 3668 MW; B5CC671448C064E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 19 HHHHHH 24

RESULT 10
 Q6UGP5_PEA PRELIMINARY; PRT; 31 AA.

AC Q6UGP5;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Sats (Fragment).
 OS Pisum sativum var. pumilio.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=51234;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Stafsstrom J.P., Ingram P.A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY370642; AAO67400.1; -, Genomic_DNA.
 FT NON TER 31 31
 SQ SEQUENCE 31 AA; 3668 MW; B5CC671448C064E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 19 HHHHHH 24

RESULT 11
 Q6UGP7_PEA PRELIMINARY; PRT; 31 AA.

AC Q6UGP7;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Sats (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OC NCBI_TaxID=3888;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Stafsstrom J.P., Ingram P.A.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY370640; AAO67398.1; -, Genomic_DNA.
 FT NON TER 31 31
 SQ SEQUENCE 31 AA; 3668 MW; B5CC671448C064E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 Db 19 HHHHHH 24

RESULT 12
 Q5SG0_MOUSE PRELIMINARY; PRT; 31 AA.

AC Q5SG0;
 DT 01-FEB-2005 (TREMBLrel. 29, Created)
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Heart and neural crest derivatives expressed transcript 1
 DE (Fragment).
 GN Name=Hand1; ORFNames=RP23-268K22.4-002;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
-OK NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Matthews L.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL732587; CAI24810.1; -; Genomic_DNA.
FT NON_TER 31
SQ SEQUENCE 31 AA; 3636 MW; 66C64537B1C5FE85 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 9 HHHHHH 14

RESULT 13
Q4YAH2_PLABE PRELIMINARY; PRT; 34 AA.
AC Q4YAH2_
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB401314.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
-OK NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kocij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Omond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janc C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01007077; CAI05235.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4155 MW; BE4AE59E7ED365C4 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 1 HHHHHH 6

RESULT 14
Q65825_9BACU PRELIMINARY; PRT; 44 AA.
AC Q65825_
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE MCS protein precursor.
GN Name=MCS;
OS unidentified baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
-OK NCBI_TaxID=10469;

```

```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96032347; PubMed=7557433; DOI=10.1016/0378-1119(95)00360-1;
RA Kuehn S., Zipfel P.F.;
RT "The baculovirus expression vector pBSV-8His directs secretion of
RT histidine-tagged proteins."
RL Gene 167:225-229(1995).
DR EMBL; X87245; CAA60687.1; -; Genomic_DNA.
KW Signal.
FT SIGNAL 1
SQ SEQUENCE 44 AA; 4961 MW; E042D55613947925 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 34 HHHHHH 39

RESULT 15
Q5ISM1_MACFA PRELIMINARY; PRT; 46 AA.
ID Q5ISM1_
AC Q5ISM1_
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Distal-less homeobox 2 protein (Fragment).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
-OK NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15620360; DOI=10.1016/j.cell.2004.11.040;
RA Dorns S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L.,
RA Mawald M., Wyckoff E.J., Malcom C.M., Lahn B.T.;
RT "Accelerated evolution of nervous system genes in the origin of Homo
RT sapiens."
RL Cell 119:1027-1040(2004).
DR EMBL; AY650359; AA67391.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5081 MW; AF905E0A2829EBCB CRC64;

Query Match 100.0%; Score 48; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 40 HHHHHH 45

RESULT 16
Q8SASO_PINSY PRELIMINARY; PRT; 48 AA.
ID Q8SASO_
AC Q8SASO_
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative N-terminal acetyltransferase (Fragment).
OS Pinus sylvestris (Scots pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
-OK NCBI_TaxID=3349;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21660210; PubMed=11801746;

```

```

RA Dvornyk V., Sirvio A., Mikkonen M., Savolainen O.;
RT "Low nucleotide diversity at the pall locus in the widely distributed
RT Pinus sylvestris.";
RL Mol. Biol. Evol. 19:179-188(2002).
DR EMBL; AF359124; AAL74392.1; -; Genomic_DNA.
KW GO; GO:0016740; F:transferase activity; IEA.
FT NON TER
SQ SEQUENCE 48 AA; 5247 MW; FD0FD03DED4DFDDE CRC64;

Query Match 100.0%; Score 48; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 16 HHHHHH 21

RESULT 17
OBSAS1_PINSY PRELIMINARY; PRT; 48 AA.
AC OBSAS1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative N-terminal acetyltransferase (Fragment).
OS Pinus sylvestris (Scots pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxId=33349;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2160210; PubMed=11801746;
RA Dvornyk V., Sirvio A., Mikkonen M., Savolainen O.;
RT "Low nucleotide diversity at the pall locus in the widely distributed
RT Pinus sylvestris.";
RL Mol. Biol. Evol. 19:179-188(2002).
DR EMBL; AF359123; AAL74391.1; -; Genomic_DNA.
KW GO; GO:0016740; F:transferase activity; IEA.
FT NON TER
SQ SEQUENCE 48 AA; 5302 MW; 6A91AE3DED4DFDDB CRC64;

Query Match 100.0%; Score 48; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 16 HHHHHH 21

RESULT 18
OSC2J2_SCHJA PRELIMINARY; PRT; 53 AA.
AC OSC2J2;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiidae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxId=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF181024; AAX26133.1; -; mRNA.
DR InterPro; IPR012287; Homeodomain-rel.
KW Hypothetical protein.
SQ SEQUENCE 53 AA; 6363 MW; 3B8D373DBF1DC268 CRC64;

```

```

Query Match 100.0%; Score 48; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 13 HHHHHH 18

RESULT 19
O55244_92ZZZ PRELIMINARY; PRT; 53 AA.
ID O55244_92ZZZ PRELIMINARY;
AC O55244;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Histidine hexamer-multiple cloning site-histidine decamer.
GN Name=h1s6-mcs-h1s10;
OS plasmid pETHIS-1.
OC plasmid pETHIS-1.
OX other sequences; plasmids.
OX NCBI_TaxId=64374;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99392473; PubMed=10463177;
RA Schaller A., Kuhn R., Kuhnert P., Nicolet J., Anderson T.J.,
RA MacInnes J.I., Segers R.P., Frey J.;
RT "Characterization of aprIVA, a new RTX determinant of Actinobacillus
RT pleuropneumoniae.";
RL Microbiology 145:2105-2116(1999).
DR EMBL; AF012911; AAB97883.1; -; Genomic_DNA.
KW plasmid
SQ SEQUENCE 53 AA; 5780 MW; BDAC93CC66B9CFF6 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 5 HHHHHH 10

RESULT 20
Q4WHB8_ASPFU PRELIMINARY; PRT; 54 AA.
ID Q4WHB8_ASPFU PRELIMINARY;
AC Q4WHB8;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFName=Atu2g05660;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxId=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley.,
RA Arroya J., Berrian M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farnham M., Fedorova N., Fedorova N., Feldlyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang Y., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Lange J.-P., Li W., Lord A., Lu C.,
RA Majors W.H., May G.S., Miller B.L., Mohammad Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penava M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitch E., Rawlins N., Rajandream M.-A., Reichard U.,

```

RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Varquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Frazer C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B., Denning D.W.,
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT *Aspergillus fumigatus*."
 RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAF0100008; EAL87657.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 54 AA; 6561 MW; B65FC626A6EC9C47 CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 54;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HHHHHH 6
 Db 30 HHHHHH 35
 RESULT 21
 O6IH19 DROME PRELIMINARY; PRT; 58 AA.
 ID O6IH19
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE HDCC02522.
 GN ORFNames=HDC02522;
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed:14709175; DOI=10.1186/gb-2003-5-1-r3;
 RA Hild M., Beckmann B., Haas S.A., Koch B., Solovjev V., Bueold C.,
 RA Fellenberg K., Boultros M., Vingron M., Sauer F., Hohnsbeil J.D.,
 RA Paro R.;
 RT "An integrated gene annotation and transcriptional profiling approach
 RT towards the full gene content of the *Drosophila* genome."
 RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
 CC -!- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK003427; DAA03626.1; -; Genomic DNA.
 SQ SEQUENCE 58 AA; 6523 MW; B6F483484C102231 CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 58;
 Best Local Similarity 100.0%; Pred. No. 4.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HHHHHH 6
 Db 48 HHHHHH 53
 RESULT 22
 HPN_HELPJ STANDARD; PRT; 59 AA.
 AC P0A0V7; Q48251;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Histidine-rich, metal binding polypeptide.
 GN Name=hpN; OrderedLocNames=HP1320;
 OS *Helicobacter pylori* J99 (Campylobacter J99).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deLonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.W., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen *Helicobacter pylori*."
 RL Nature 397:176-180(1999).
 CC -!- FUNCTION: Strongly binds nickel and zinc. Binds other metals less
 CC strongly: cobalt > copper > cadmium > manganese. May act to
 CC increase, or at least to preserve, urease activity. Exact function
 CC is still unknown (By similarity).
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AE001555; AAD06898.1; -; Genomic_DNA.
 DR PIR; C64698; C64698.
 DR HSSP; P13231; IHCE.
 KW Complete proteome; Metal-binding; Nickel; Repeat; Zinc.
 FT INIT MET 0 0 By similarity.
 FT REPEAT 37 41 1.
 FT REPEAT 50 54 2.
 FT REGION 37 54 2 X 5 AA repeats of E-E-G-C-C.
 FT COMBIAS 10 23 Poly-His.
 FT COMBIAS 27 32 Poly-His.
 SQ SEQUENCE 59 AA; 6946 MW; C3AE83F602EC973C CRC64;
 Query Match 100.0%; Score 48; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 HHHHHH 6
 Db 10 HHHHHH 15
 RESULT 23
 HPN_HELPJ STANDARD; PRT; 59 AA.
 ID P0A0V6; Q48251;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Histidine-rich, metal binding polypeptide.
 GN Name=hpN; OrderedLocNames=HP1427;
 OS *Helicobacter pylori* (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 1-18 AND 47-59.
 RC STRAIN=IEU.
 RX MEDLINE=95310028; PubMed=7790085;
 RA Gilbert J.V., Ramakrishna J., Sunderman F.W. Jr., Wright A.,
 RA Platt A.G.;
 RT "Protein HpN: cloning and characterization of a histidine-rich metal-
 RT binding polypeptide in *Helicobacter pylori* and *Helicobacter*
 RT *muselae*."
 RL Infect. Immun. 63:2682-2688(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

```

RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khaila H.G.,
RA Glodok A., McEnney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Wathes L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RA "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -1- FUNCTION: Strongly binds nickel and zinc. Binds other metals less
CC strongly: cobalt > copper > cadmium > manganese. May act to
CC increase, or at least to preserve, urease activity. Exact function
CC is still unknown.
CC -----
CC This Swiss-Pro entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: U26361; AAA85859.1; -; Genomic_DNA.
CC DR EMBL; AE000643; AAD08471.1; -; Genomic_DNA.
CC DR PIR; C64698; C64698.
CC DR HSSP; P13231; IHCE.
CC DR TIGR; HP1427; -.
CC KM Complete proteome: Direct protein sequencing; Metal-binding; Nickel;
CC Repeat; Zinc.
CC FT INIT MET 0 0
CC FT REPEAT 37 41 1.
CC FT REPEAT 50 54 2.
CC FT REGION 37 54 2 X 5 AA repeats of E-E-G-C-C.
CC FT COMBINS 10 23 Poly-His.
CC FT COMBINS 27 32 Poly-His.
CC SQ SEQUENCE 59 AA; 6946 MW; C3AE3F602EC973C CRC64;

Query Match 100.0%; Score 48; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
DB 10 HHHHHH 15

RESULT 24
Q40049 HORVU PRELIMINARY; PRT; 64 AA.
ID Q40049 HORVU PRELIMINARY; PRT; 64 AA.
AC Q40049;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE ES1A protein.
GN Name=ES1A;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaves;
RX MEDLINE=95367651; PubMed=7640362;
RA Speulman B., Salami F.;
RT "GA3-regulated cDNAs from Hordeum vulgare leaves.";
RL Plant Mol. Biol. 28:915-926(1995).
DR EMBL; X78884; CAA55483.1; -; mRNA.
DR PIR; SS7787; SS7787
SQ SEQUENCE 64 AA; 7155 MW; 6DECBEE843616138 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
DB 25 HHHHHH 30

RESULT 25
Q61U99 DROME PRELIMINARY; PRT; 66 AA.
ID Q61U99 DROME PRELIMINARY; PRT; 66 AA.
AC Q61U99;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE HDCL4879.
GN ORFNames=HDCL4879;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
RA Hild M., Beckmann B., Haas S.A., Solovay V., Busold C.,
RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohlseil J.D.,
RA Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome.";
RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK002737; DAA04242.1; -; Genomic DNA.
SQ SEQUENCE 66 AA; 7988 MW; A68D75FCB2DB4BC CRC64;

Query Match 100.0%; Score 48; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
DB 14 HHHHHH 19

RESULT 26
Q6R2V8 TRIRE PRELIMINARY; PRT; 69 AA.
ID Q6R2V8 TRIRE PRELIMINARY; PRT; 69 AA.
AC Q6R2V8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE HEX1 (Fragment).
GN Name=hex1;
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocromycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VT-D-79125;
RC Curach N.C., Te'o V.S.J., Gibbs M.D., Bergquist P.L.,
RA Nevalainen H.K.M.;
RT "Isolation, characterization and expression of the hex1 gene from
RT Trichoderma reesei.";
RL Gene 0:0-01(2004).
DR EMBL; AY51641; AAS07013.1; -; mRNA.
FT NON TER 69 69
SQ SEQUENCE 69 AA; 8197 MW; 006B697BFC73570D CRC64;

Query Match 100.0%; Score 48; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 HHHHHH 6
 OX |||||
 Db 27 HHHHHH 32

RESULT 27
 ID Q410L0 GIBZE PRELIMINARY; PRT; 69 AA.
 Q410L0 GIBZE
 AC Q410L0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=FG00498.1;
 OS Gibberella zeae PH-1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocrymucetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxID=229533;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PH-1;
 RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Archchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
 RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Cornu B., Deatellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
 RA Gargyan S., Gierre S., Graham L., Grand-Pierre N., Halez I.,
 RA Hagopian D., Hages B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-C., Mabbitt R., Maclean C., MacDonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Meneus L.,
 RA Mihova T., Mlangi V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Notbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunhng K., Pierre N., Purcell S.,
 RA Oliver J., Peterson K., Phunhng K., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Rella N., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talama J., Tefaye S., Theodore J., Topham J., Travers M.,
 RA Vassiliev H., Venkateraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zaitoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Fusarium graminearum genome sequence."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACM0100020; EAA68730.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 69 AA; 8441 MW; 60C3558458EDEF22 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
 OX |||||
 Db 27 HHHHHH 32

RESULT 28
 ID Q9PT65 XENLA PRELIMINARY; PRT; 69 AA.
 Q9PT65 XENLA
 AC Q9PT65;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Homeodomain transcription factor (Fragment).
 GN Name=Xp12x2A;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8335;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20054091; PubMed=10585561; DOI=10.1016/S0925-4773(99)00227-0;
 RA Schweickert A., Campione M., Steinbissner H., Blum M.;
 RT "Plex2 isoforms: involvement of P12x2c but not P12x2a or P12x2b in
 RT vertebrate left-right asymmetry.";
 RL Mech. Dev. 90:41-51(2000).
 DR EMBL; AJ243596; CAB65515.1; -; mRNA.
 KW GO: GO:0005634; C:nucleus; IEA.
 FT Nucleic protein.
 KW NON_TER
 SQ SEQUENCE 69 AA; 7576 MW; 19C21A42C7B30B47 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
 OX |||||
 Db 24 HHHHHH 29

RESULT 29
 ID Q54KT2 DICDI PRELIMINARY; PRT; 72 AA.
 Q54KT2 DICDI
 AC Q54KT2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=DDB0218896;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MX4;
 RA Sicking L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugand R., Barriman M., Song J., Olsen R., Szafarski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quilez M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Louiseged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabbinnowltch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinrock G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.A.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum.";
 RL Nature 0:0-0(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAF10100148; EAL63870.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 72 AA; 8561 MW; E495A55F52AB37A CRC64;

Query Match 100.0%; Score 48; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
 OX |||||
 Db 18 HHHHHH 23

```

RESULT 30
Q8T1A1_DICDI PRELIMINARY; PRT; 72 AA.
AC Q8T1A1;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 10-MAY-2005 (TREMblrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DDB0167568;
OS Dictyostella mycetozoa (slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_Taxid=44689;
RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RA Gloeckner G., Eichinger L., Szafrański K., Pachbat J.A.,
RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
RA Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Baumgart C.;
RN Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RC
[3]
RA NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachbat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Bertrman M., Song J., Olsen R., Szafrański K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Baeson N.,
RA Fathroter P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Mazny D., Moutier T., Pain A., Lu M., Harper D., Lindsey R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Salto T., Buchrieser C.,
RA Wardeger A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louisseg H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M.,
RA Urushihara H., Hernandez J., Rabbinnowitsch E., Steffen D., Sanders M.,
RA Ma U., Kohara Y., Sharp S., Simmonds W., Slegler S., Tivy A.,
RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chailom R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
DR EMBL; AC116956; AA08755.1; -; Genomic_DNA.
DR EMBL; AAF10100027; BAL69989.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ
SEQUENCE 72 AA; 8867 MW; 27CDD6A105612FDDCA CRC64;

Query Match 100.0%; Score 48; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 64 HHHHHH 69

```

```

DE Histidine and glutamine-rich protein.
GN OrderedlocusNames=HP1432;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteriaceae; Helicobacter.
OX NCBI_Taxid=210;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khakhal H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori.";
RL Nature 388:539-547(1997).
DR EMBL; AE000643; AAD08472.1; -; Genomic_DNA.
DR PIR; H64698; H64698.
DR TIGR; HP1432; -.
KW Complete proteome.
SQ
SEQUENCE 72 AA; 8779 MW; 1663F1CFCDB4760D CRC64;

```

```

Query Match 100.0%; Score 48; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 16 HHHHHH 21

```

```

RESULT 32
Q8T3D9_CAEEL PRELIMINARY; PRT; 75 AA.
AC Q8T3D9;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Hypothetical protein F53B6.9.
GN ORFNames=F53B6.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG "The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81086; CAD30440.1; -; Genomic_DNA.
DR EMBL; F53B6.9; Caenorhabditis elegans.
DR Wormbase; WBGene0009964; F53B6.9.
DR WormPep; F53B6.9; CE30539.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 75 AA; 8785 MW; 987285B295505F6C CRC64;

```

```

Query Match 100.0%; Score 48; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
DB 34 HHHHHH 39

```

```

RESULT 31
O25973_HELPY PRELIMINARY; PRT; 72 AA.
AC O25973;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)

```

RESULT 33
 O9VLH4 DROME PRELIMINARY; PRT; 76 AA.
 AC O9VLH4
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE CG15867-PA.
 DN Name=CG15867; ORFNames=CG15867;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abilil J.F., Abmayri A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hoeft D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jajaeli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J.H., Liang Y., Lin X.,
 RA Liu X., Mattei J.B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moadarry C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reihart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spiedling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RT Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams W., Champe M., Dugan S.P., Friese E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodegryn E.J.,
 RA Svitskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svitskas R.,
 RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatic
 RT a genomes perspective.";
 RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tuzy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celinker S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svitskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG Flybase;
 RL Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AE003622; AF52716.1; -; Genomic DNA.
 DR Ensembl; CG15867; Drosophila melanogaster.
 DR Flybase; FBgn0040961; CG15867.
 SQ SEQUENCE 76 AA; 8473 MW; 1197816AD64A15F CRC64;
 Qy Best Local Similarity 100.0%; Score 48; DB 2; Length 76;
 Db Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 HHHHHH 6
 13 HHHHHH 18
 RESULT 34
 Q02690 CAEBL PRELIMINARY; PRT; 77 AA.
 AC Q02690
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein F53A9.1.
 DE ORFNames=F53A9.1;
 GN Caenorhabditis elegans.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Felodierinae; Caenorhabditis.
 OC NCBI_TaxId=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology.";
 RT Science 283:2012-2018(1998).
 CC -I- INTERACTION:
 CC Q8MM07.cim-1, NDeExp-1; InAct-EBI-312591, EBI-312477;
 CC EMBL; U23523; AAC46556.1; -; Genomic DNA.
 DR PIR; T16436; T16436.
 DR InAct; Q02690; -;
 DR Ensembl; F53A9.1; Caenorhabditis elegans.
 DR WormBase; WBGene00018724; F53A9.1.
 DR WormPeP; F53A9.1; CE02760.
 DR InterPro; IPR006025; Pept_M_Zn_BS.

```

DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 77 AA; 8577 MW; 23A5D23442541D64 CRC64;
  Query Match 100.0%; Score 48; DB 2; Length 77;
  Best Local Similarity 100.0%; Pred. No. 5.4;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
   |||||
Db 46 HHHHHH 51

RESULT 35
09ZJ18_HELPJ PRELIMINARY; PRT; 77 AA.
ID 09ZJ18_HELPJ PRELIMINARY; PRT; 77 AA.
AC 09ZJ18;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative histidine and glutamine-rich metal-binding protein.
GN OrderedLocusNames=JH1321;
OS OrderedLocusNames=JH1321;
OC Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxId=85963;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tumlin P.J., Carnso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR EMBL; AE001555; AAD06903.1; -; Genomic_DNA.
DR PIR; D71821; D71821.
KW Complete proteome.
SQ SEQUENCE 77 AA; 9409 MW; F259778DBDB39B5 CRC64;
  Query Match 100.0%; Score 48; DB 2; Length 77;
  Best Local Similarity 100.0%; Pred. No. 5.4;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
   |||||
Db 21 HHHHHH 26

RESULT 36
0613L0_CABBR PRELIMINARY; PRT; 80 AA.
ID 0613L0_CABBR PRELIMINARY; PRT; 80 AA.
AC 0613L0;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG16338.
GN Name=CBG16338;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW Hypothetical protein.

```

```

SQ SEQUENCE 80 AA; 8906 MW; 1FF84C346C128F99 CRC64;
  Query Match 100.0%; Score 48; DB 2; Length 80;
  Best Local Similarity 100.0%; Pred. No. 5.6;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
   |||||
Db 74 HHHHHH 79

RESULT 37
07JPJ3_CABEL PRELIMINARY; PRT; 80 AA.
ID 07JPJ3_CABEL PRELIMINARY; PRT; 80 AA.
AC 07JPJ3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Insulin related protein 20.
GN Name=ins-20; ORFNames=ZK84.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RT "The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; U23181; AAR12989.1; -; Genomic DNA.
DR Ensembl; ZK84.7; Caenorhabditis elegans.
DR Wormbase; WBGene00002103; ZK84.7.
DR WormPep; ZK84.7; CE36082.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007582; P:physiological process; IEA.
DR InterPro; IPR003235; Nmrde_ins_beta.
DR ProDom; PD012623; Nmrde_ins_beta; 1.
KW Complete proteome.
SQ SEQUENCE 80 AA; 9357 MW; AB17117D39923D30 CRC64;
  Query Match 100.0%; Score 48; DB 2; Length 80;
  Best Local Similarity 100.0%; Pred. No. 5.6;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
   |||||
Db 25 HHHHHH 30

RESULT 38
061D00_CABBR PRELIMINARY; PRT; 82 AA.
ID 061D00_CABBR PRELIMINARY; PRT; 82 AA.
AC 061D00;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG12395.
GN Name=CBG12395;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

```

DR EMBL; CAAC01000060; CA66997.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 82 AA; 9659 MW; 4039B513C6552F31 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
|
|
|
|
|
|
DB 35 HHHHHH 40
RESULT 39
Q20689 CAEEL PRELIMINARY; PRT; 83 AA.
ID Q20689 CAEEL PRELIMINARY;
AC Q20689
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein F53A9.2.
GN ORFNames=F53A9.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Br1stol N2; PubMed=9651916;
RX MEDLINE=99069613; PubMed=9651916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018 (1998).
CC -1- INTERACTION:
Q8MM07:ctm-1; NDEXP-1; Intact=EBI-312596; EBI-312477;
DR EMBL; U23523; AAC46557.1; -; Genomic_DNA.
DR PIR; T16435; T16435.
DR IntAct; Q20689; -.
DR Ensemble; F53A9.2; Caenorhabditis elegans.
DR WormBase; WBGene00018725; F53A9.2.
DR WormPeP; F53A9.2; CE02762.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 83 AA; 9300 MW; DFF31DFB5C81F18 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
|
|
|
|
|
|
DB 45 HHHHHH 50
RESULT 40
Q615X5 CAEBR PRELIMINARY; PRT; 84 AA.
ID Q615X5 CAEBR PRELIMINARY;
AC Q615X5
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG15407.
GN Name=CBG15407;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The C.briggsae Sequencing Consortium;
RL Submitted (Sep-2003) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAAC01000072; CA69311.1; -; Genomic_DNA.
DR EMBL; CAAC01000072; CA69311.1; -; Genomic_DNA.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 84 AA; 9397 MW; 12C5B95F7AA516F CRC64;
Query Match 100.0%; Score 48; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
|
|
|
|
|
|
DB 46 HHHHHH 51
RESULT 41
Q58WZ3 ORENI PRELIMINARY; PRT; 85 AA.
ID Q58WZ3 ORENI PRELIMINARY;
AC Q58WZ3
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Hox protein (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphae; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapiaini;
OC Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B3b;
RX PubMed=15716008; DOI=10.1016/j.gene.2004.10.027;
RA Santini S.; Bernardi G.;
RT "Organization and base composition of tilapia Hox genes: implications
for the evolution of Hox clusters in fish."
RL Gene 346:51-61 (2005).
DR EMBL; AY57333; AAY97676.2; -; Genomic_DNA.
DR InterPro; IPR001827; Antennapedia.
DR PROSITE; PS00032; ANTENNAPEDIA; UNKNOWN_1.
FT NON TER 85
SQ SEQUENCE 85 AA; 9841 MW; 7B645627269165F8 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
|
|
|
|
|
|
DB 14 HHHHHH 19
RESULT 42
Q5TRG3 ANOGA PRELIMINARY; PRT; 86 AA.
ID Q5TRG3 ANOGA PRELIMINARY;
AC Q5TRG3
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE ENSANGP0000029435.
GN ORFNames=ENSANGG0000023751;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;

RG The Anopheles gambiae Sequence Committee;
 RA "Anopheles gambiae re-annotation."
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAAB01008960; EAL39901.1; -; Genomic DNA.
 SQ SEQUENCE 86 AA; 9902 MW; 7CFA192D4C8940FE CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 Db 30 HHHHHH 35
 RESULT 43
 ID 061311 CAEBR PRELIMINARY; PRT; 87 AA.
 AC 061311
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein CBG16337.
 GN Name=CBG16337;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditiidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C. briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAC01000076; CAB69948.1; -; Genomic DNA.
 KM Hypothetical protein.
 SQ SEQUENCE 87 AA; 9316 MW; F1B900A2DD0B89C4 CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 Db 52 HHHHHH 57
 RESULT 44
 ID 061HC6 DROME PRELIMINARY; PRT; 87 AA.
 AC 061HC6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE HDC02760.
 GN ORFNames=HDC02760;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CC NCI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 DR EMBL; AF101000175; DOI=10.1186/gb-2003-5-1-r3;
 RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;

RA Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,
 RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohnsels J.D.,
 RA Pato R.;
 RT "An integrated gene annotation and transcriptional profiling approach
 RT towards the full gene content of the Drosophila genome."
 RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK003490; DAA03689.1; -; Genomic DNA.
 SQ SEQUENCE 87 AA; 9474 MW; 6F2616FFB03B5E87 CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHHHHH 6
 Db 23 HHHHHH 28
 RESULT 45
 ID 0861J5 DICDI PRELIMINARY; PRT; 89 AA.
 AC 0861J5;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Similar to F22H10.2.p (Hypothetical protein).
 GN ORFNames=DD80168879;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 RA Gloeckner G., Eichinger L., Szifranski K., Pachebat J.A.,
 RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
 RA Abril J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A.,
 RA Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
 RL Nature 418:79-85(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Berriman M., Song J., Olsen R., Szifranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Fathrocher P., Desany B., Just E., Morio T., Rost R., Church C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Landay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Louised H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch B., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox B.C.,
 RA Chaholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrett B., Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum."
 RL Nature 0:0-0(2005).
 DR EMBL; AC117176; AA052096.1; -; Genomic DNA.
 DR EMBL; AAF101000022; EAL70996.1; -; Genomic DNA.
 KW Hypothetical protein.

SQ SEQUENCE 89 AA; 10155 MW; DF4C1349B9B8E82C CRC64;
 Query Match 100.0%; Score 48; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 6 HHHHHH 11

RESULT 46
 Q6EPJ7_ORYSA PRELIMINARY; PRT; 89 AA.

ID Q6EPJ7_ORYSA PRELIMINARY; PRT; 89 AA.
 AC Q6EPJ7;
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE Hypothetical protein OSUNBa003K18.14;
 GN Name=OSUNBa003K18.14;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AP005875; BAD29423.1; -; Genomic_DNA.
 DR Gramene; Q6EPJ7; -;
 KM Hypothetical protein.
 SQ SEQUENCE 89 AA; 10274 MW; A6C59326FB2BD786 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 68 HHHHHH 73

RESULT 47
 Q698K8_AGKHB PRELIMINARY; PRT; 89 AA.

ID Q698K8_AGKHB PRELIMINARY; PRT; 89 AA.
 AC Q698K8;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Adinbitor (Fragment).
 OS Agdistrodon halys brevicaudus (Korean slamosa snake) (Gloydus halys brevicaudus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OC NCBI_TaxID=259325;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA TISSUE=Venom gland;
 RC Wang J.H., Wu Y., Ren F., Zhao B.C.;
 RT "Cloning and characterization of adinbitor: a novel disintegrin from a snake venom."
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.

DR EMBL; AY551929; AAT76292.1; -; mRNA.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR001762; Disintegrin.
 DR Pfam; PF00200; Disintegrin; 1.
 DR PRINTS; PR00289; Disintegrin; 1.
 DR Prodom; PD000664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS00427; DISINTEGRIN_1; 1.

DR PROSITE; PS00214; DISINTEGRIN_2; 1.
 KW Cell adhesion.
 SQ SEQUENCE 89 AA; 9645 MW; 40BD95DCE2D7A313 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 84 HHHHHH 89

RESULT 48
 OS24U9_ORYSA PRELIMINARY; PRT; 91 AA.

ID OS24U9_ORYSA PRELIMINARY; PRT; 91 AA.
 AC OS24U9;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein P0545E05.30.
 CN Name=P0545E05.30;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa n1pbonate (GN3) genomic DNA, chromosome 6, PAC clone: P0545E05.30."
 RT Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AP005931; BAD54668.1; -; Genomic_DNA.
 KM Hypothetical protein.
 SQ SEQUENCE 91 AA; 10464 MW; E84483B6567E5342 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
 |||||
 DB 15 HHHHHH 20

RESULT 49
 Q18410_CAEEL PRELIMINARY; PRT; 92 AA.

ID Q18410_CAEEL PRELIMINARY; PRT; 92 AA.
 AC Q18410;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein C33H5.13.
 GN ORFNames=C33H5.13;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).

RA STRAIN=Bristol N2;
 RC MEDLINE=99069613; PubMed=9851916;
 RX The C. elegans sequencing consortium;
 RG "Genome sequence of the nematode C. elegans: a platform for investigating biology."
 RT Science 282:2012-2018 (1998).
 RL EMBL; U41007; AAA82273.1; -; Genomic_DNA.
 DR PIR; T34146; T34146.
 DR Ensembl; C33H5.13; Caenorhabditis elegans.
 DR Wormbase; WBGene0016379; C33H5.13.
 DR WormPep; C33H5.13; CE04156.

KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 92 AA; 9969 MW; C91B6555BA701A06 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 58 HHHHHH 63

RESULT 50

0861J4 DICDI
 ID 0861J4_DICDI PRELIMINARY; PRT; 93 AA.

AC 0861J4;
 DT 01-JUN-2003 (TRENBLREL. 24, Created)
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
 RA Gloeckner G., Richter U., Szafranski K., Pachdat J.A.,
 RA Bankier A.T., Dear P.H., Lehmann R., Baumgart C., Parra G.,
 RA Abriil J.F., Guigo R., Kumpf K., Tunggal B., Cox B., Quail M.A.,
 RA Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
 RL Nature 418:79-85(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC117176; A052097.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 93 AA; 10589 MW; 1A860E9A266A7637 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHHHHH 6
 |||||
 DB 3 HHHHHH 8

Search completed: March 21, 2006, 11:08:19
 Job time : 271 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:08:37 ; Search time 47 Seconds
(without alignments)
10.554 Million cell updates/sec

Title: US-10-719-523-5

Perfect score: 48

Sequence: 1 HHHHH 6

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/prodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/ECTUS_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/FE_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 48 | 100.0 | 6 | 1 | US-08-160-670A-6 |
| 2 | 48 | 100.0 | 6 | 1 | US-08-140-222-1 |
| 3 | 48 | 100.0 | 6 | 1 | US-08-131-365B-48 |
| 4 | 48 | 100.0 | 6 | 1 | US-08-469-486-47 |
| 5 | 48 | 100.0 | 6 | 1 | US-08-460-343B-51 |
| 6 | 48 | 100.0 | 6 | 1 | US-08-299-567-1 |
| 7 | 48 | 100.0 | 6 | 1 | US-08-398-028B-51 |
| 8 | 48 | 100.0 | 6 | 1 | US-08-660-626-4 |
| 9 | 48 | 100.0 | 6 | 1 | US-08-434-705B-17 |
| 10 | 48 | 100.0 | 6 | 1 | US-08-470-837-22 |
| 11 | 48 | 100.0 | 6 | 1 | US-08-472-244-14 |
| 12 | 48 | 100.0 | 6 | 1 | US-08-504-265B-51 |
| 13 | 48 | 100.0 | 6 | 1 | US-08-623-833B-16 |
| 14 | 48 | 100.0 | 6 | 1 | US-08-652-507-8 |
| 15 | 48 | 100.0 | 6 | 1 | US-08-668-123-48 |
| 16 | 48 | 100.0 | 6 | 1 | US-08-469-658-47 |
| 17 | 48 | 100.0 | 6 | 1 | US-09-086-201-17 |
| 18 | 48 | 100.0 | 6 | 1 | US-08-591-196-57 |
| 19 | 48 | 100.0 | 6 | 2 | US-08-996-139-18 |
| 20 | 48 | 100.0 | 6 | 2 | US-08-481-435-42 |
| 21 | 48 | 100.0 | 6 | 2 | US-08-772-440-28 |
| 22 | 48 | 100.0 | 6 | 2 | US-09-267-031-18 |
| 23 | 48 | 100.0 | 6 | 2 | US-09-398-341-1 |
| 24 | 48 | 100.0 | 6 | 2 | US-09-031-168-4 |
| 25 | 48 | 100.0 | 6 | 2 | US-08-789-333F-99 |
| 26 | 48 | 100.0 | 6 | 2 | US-08-995-659-18 |
| 27 | 48 | 100.0 | 6 | 2 | US-09-142-334-26 |

| | | | | | | |
|-----|----|-------|---|---|--------------------|-------------------|
| 28 | 48 | 100.0 | 6 | 2 | US-09-215-649A-18 | Sequence 18, App1 |
| 29 | 48 | 100.0 | 6 | 2 | US-09-140-084-7 | Sequence 7, App1 |
| 30 | 48 | 100.0 | 6 | 2 | US-09-382-950-4 | Sequence 4, App1 |
| 31 | 48 | 100.0 | 6 | 2 | US-09-382-736B-5 | Sequence 5, App1 |
| 32 | 48 | 100.0 | 6 | 2 | US-08-977-378-2 | Sequence 2, App1 |
| 33 | 48 | 100.0 | 6 | 2 | US-09-353-555-2 | Sequence 22, App1 |
| 34 | 48 | 100.0 | 6 | 2 | US-08-868-452-22 | Sequence 47, App1 |
| 35 | 48 | 100.0 | 6 | 2 | US-09-000-094-47 | Sequence 7, App1 |
| 36 | 48 | 100.0 | 6 | 2 | US-09-058-483-7 | Sequence 8, App1 |
| 37 | 48 | 100.0 | 6 | 2 | US-09-140-201-8 | Sequence 106, App |
| 38 | 48 | 100.0 | 6 | 2 | US-09-039-780A-106 | Sequence 14, App1 |
| 39 | 48 | 100.0 | 6 | 2 | US-09-291-170A-14 | Sequence 18, App1 |
| 40 | 48 | 100.0 | 6 | 2 | US-09-577-780-18 | Sequence 1, App1 |
| 41 | 48 | 100.0 | 6 | 2 | US-09-724-297-7 | Sequence 4, App1 |
| 42 | 48 | 100.0 | 6 | 2 | US-09-367-309A-4 | Sequence 14, App1 |
| 43 | 48 | 100.0 | 6 | 2 | US-09-724-884-14 | Sequence 6, App1 |
| 44 | 48 | 100.0 | 6 | 2 | US-09-529-279-6 | Sequence 1, App1 |
| 45 | 48 | 100.0 | 6 | 2 | US-09-313-942-1 | Sequence 6, App1 |
| 46 | 48 | 100.0 | 6 | 2 | US-09-353-215-6 | Sequence 18, App1 |
| 47 | 48 | 100.0 | 6 | 2 | US-09-577-800-18 | Sequence 7, App1 |
| 48 | 48 | 100.0 | 6 | 2 | US-09-667-422-7 | Sequence 81, App1 |
| 49 | 48 | 100.0 | 6 | 2 | US-09-315-926A-81 | Sequence 11, App1 |
| 50 | 48 | 100.0 | 6 | 2 | US-09-731-558-11 | Sequence 61, App1 |
| 51 | 48 | 100.0 | 6 | 2 | US-09-280-030-61 | Sequence 18, App1 |
| 52 | 48 | 100.0 | 6 | 2 | US-09-466-496-18 | Sequence 39, App1 |
| 53 | 48 | 100.0 | 6 | 2 | US-09-648-569A-39 | Sequence 18, App1 |
| 54 | 48 | 100.0 | 6 | 2 | US-09-871-856-18 | Sequence 6, App1 |
| 55 | 48 | 100.0 | 6 | 2 | US-10-158-895-6 | Sequence 9, App1 |
| 56 | 48 | 100.0 | 6 | 2 | US-09-904-196B-9 | Sequence 18, App1 |
| 57 | 48 | 100.0 | 6 | 2 | US-09-871-291-18 | Sequence 1, App1 |
| 58 | 48 | 100.0 | 6 | 2 | US-09-115-397-1 | Sequence 1, App1 |
| 59 | 48 | 100.0 | 6 | 2 | US-09-463-194-2 | Sequence 1, App1 |
| 60 | 48 | 100.0 | 6 | 2 | US-09-353-554-1 | Sequence 3, App1 |
| 61 | 48 | 100.0 | 6 | 2 | US-09-669-516C-4 | Sequence 2, App1 |
| 62 | 48 | 100.0 | 6 | 2 | US-09-051-994-3 | Sequence 9, App1 |
| 63 | 48 | 100.0 | 6 | 2 | US-09-951-265-2 | Sequence 2, App1 |
| 64 | 48 | 100.0 | 6 | 2 | US-09-546-013-9 | Sequence 9, App1 |
| 65 | 48 | 100.0 | 6 | 2 | US-09-640-958-13 | Sequence 13, App1 |
| 66 | 48 | 100.0 | 6 | 2 | US-09-570-363-6 | Sequence 9, App1 |
| 67 | 48 | 100.0 | 6 | 2 | US-09-760-008A-9 | Sequence 18, App1 |
| 68 | 48 | 100.0 | 6 | 2 | US-09-877-650-18 | Sequence 20, App1 |
| 69 | 48 | 100.0 | 6 | 2 | US-09-596-794-20 | Sequence 43, App1 |
| 70 | 48 | 100.0 | 6 | 2 | US-09-970-989A-43 | Sequence 6, App1 |
| 71 | 48 | 100.0 | 6 | 2 | US-09-272-960-6 | Sequence 7, App1 |
| 72 | 48 | 100.0 | 6 | 2 | US-09-724-108-7 | Sequence 7, App1 |
| 73 | 48 | 100.0 | 6 | 2 | US-09-009-388C-7 | Sequence 6, App1 |
| 74 | 48 | 100.0 | 6 | 2 | US-10-058-636-6 | Sequence 43, App1 |
| 75 | 48 | 100.0 | 6 | 2 | US-09-974-992B-43 | Sequence 47, App1 |
| 76 | 48 | 100.0 | 6 | 2 | US-10-011-749-47 | Sequence 19, App1 |
| 77 | 48 | 100.0 | 6 | 2 | US-09-821-726A-19 | Sequence 21, App1 |
| 78 | 48 | 100.0 | 6 | 2 | US-09-916-940-99 | Sequence 11, App1 |
| 79 | 48 | 100.0 | 6 | 2 | US-09-826-312A-21 | Sequence 11, App1 |
| 80 | 48 | 100.0 | 6 | 2 | US-09-865-363-18 | Sequence 11, App1 |
| 81 | 48 | 100.0 | 6 | 2 | US-09-809-517A-11 | Sequence 3, App1 |
| 82 | 48 | 100.0 | 6 | 2 | US-09-943-382-1 | Sequence 1, App1 |
| 83 | 48 | 100.0 | 6 | 2 | US-09-352-171-3 | Sequence 9, App1 |
| 84 | 48 | 100.0 | 6 | 2 | US-10-452-786-1 | Sequence 2, App1 |
| 85 | 48 | 100.0 | 6 | 2 | US-09-288-719B-9 | Sequence 13, App1 |
| 86 | 48 | 100.0 | 6 | 2 | US-10-387-335-2 | Sequence 16, App1 |
| 87 | 48 | 100.0 | 6 | 2 | US-09-901-187C-13 | Sequence 15, App1 |
| 88 | 48 | 100.0 | 6 | 2 | US-09-043-861-36 | Sequence 12, App1 |
| 89 | 48 | 100.0 | 6 | 2 | US-09-692-945-15 | Sequence 11, App1 |
| 90 | 48 | 100.0 | 6 | 2 | US-09-782-587B-12 | Sequence 11, App1 |
| 91 | 48 | 100.0 | 6 | 2 | US-09-391-606-11 | Sequence 11, App1 |
| 92 | 48 | 100.0 | 6 | 2 | US-09-612-852A-17 | Sequence 11, App1 |
| 93 | 48 | 100.0 | 6 | 2 | US-09-989-981A-11 | Sequence 26, App1 |
| 94 | 48 | 100.0 | 6 | 2 | US-09-763-397A-26 | Sequence 9, App1 |
| 95 | 48 | 100.0 | 6 | 2 | US-10-192-294-9 | Sequence 18, App1 |
| 96 | 48 | 100.0 | 6 | 2 | US-09-688-459-18 | Sequence 13, App1 |
| 97 | 48 | 100.0 | 6 | 2 | US-09-979-338A-13 | Sequence 698, App |
| 98 | 48 | 100.0 | 6 | 2 | US-09-801-676A-2 | Sequence 7, App1 |
| 99 | 48 | 100.0 | 6 | 2 | US-09-935-430-658 | |
| 100 | 48 | 100.0 | 6 | 2 | US-10-246-435-7 | |

| | | | | | | | | | | | | | |
|-----|----|-------|---|---|--------------------|-------------------|-----|----|-------|----|---|--------------------|-------------------|
| 101 | 48 | 100.0 | 6 | 2 | US-09-622-613C-43 | Sequence 43, Appl | 174 | 48 | 100.0 | 9 | 2 | US-09-149-727-17 | Sequence 17, Appl |
| 102 | 48 | 100.0 | 6 | 2 | US-09-673-222-14 | Sequence 14, Appl | 175 | 48 | 100.0 | 9 | 2 | US-09-422-375-8 | Sequence 8, Appl |
| 103 | 48 | 100.0 | 6 | 2 | US-09-813-197-5 | Sequence 5, Appl | 176 | 48 | 100.0 | 9 | 2 | US-09-270-957-56 | Sequence 56, Appl |
| 104 | 48 | 100.0 | 6 | 2 | US-09-962-756-1778 | Sequence 1778, Ap | 177 | 48 | 100.0 | 9 | 2 | US-09-498-134A-5 | Sequence 5, Appl |
| 105 | 48 | 100.0 | 6 | 2 | US-10-090-365-12 | Sequence 12, Appl | 178 | 48 | 100.0 | 9 | 2 | US-09-809-517A-9 | Sequence 9, Appl |
| 106 | 48 | 100.0 | 6 | 2 | US-10-093-248-10 | Sequence 10, Appl | 179 | 48 | 100.0 | 9 | 2 | US-09-612-852A-16 | Sequence 16, Appl |
| 107 | 48 | 100.0 | 6 | 2 | US-10-046-442-2 | Sequence 2, Appl | 180 | 48 | 100.0 | 9 | 2 | US-10-665-227A-6 | Sequence 6, Appl |
| 108 | 48 | 100.0 | 6 | 2 | US-09-728-911-12 | Sequence 12, Appl | 181 | 48 | 100.0 | 10 | 1 | US-07-807-529A-73 | Sequence 73, Appl |
| 109 | 48 | 100.0 | 6 | 2 | US-10-093-200A-10 | Sequence 10, Appl | 182 | 48 | 100.0 | 10 | 1 | US-08-340-812-16 | Sequence 16, Appl |
| 110 | 48 | 100.0 | 6 | 2 | US-10-665-227A-3 | Sequence 3, Appl | 183 | 48 | 100.0 | 10 | 1 | US-08-459-064B-16 | Sequence 16, Appl |
| 111 | 48 | 100.0 | 6 | 2 | US-10-282-162-1 | Sequence 1, Appl | 184 | 48 | 100.0 | 10 | 1 | US-08-737-757-10 | Sequence 10, Appl |
| 112 | 48 | 100.0 | 6 | 2 | US-09-997-623-41 | Sequence 41, Appl | 185 | 48 | 100.0 | 10 | 1 | US-08-628-665-14 | Sequence 14, Appl |
| 113 | 48 | 100.0 | 6 | 2 | US-10-346-658-1 | Sequence 1, Appl | 186 | 48 | 100.0 | 10 | 1 | US-08-524-757-30 | Sequence 30, Appl |
| 114 | 48 | 100.0 | 6 | 2 | US-10-317-252B-400 | Sequence 400, App | 187 | 48 | 100.0 | 10 | 1 | US-08-524-757-30 | Sequence 31, Appl |
| 115 | 48 | 100.0 | 6 | 2 | US-10-195-707B-35 | Sequence 35, Appl | 188 | 48 | 100.0 | 10 | 1 | US-08-482-142-150 | Sequence 150, App |
| 116 | 48 | 100.0 | 6 | 4 | PCR-US94-04361-55 | Sequence 55, Appl | 189 | 48 | 100.0 | 10 | 1 | US-08-460-421A-16 | Sequence 16, Appl |
| 117 | 48 | 100.0 | 7 | 1 | US-08-100-744-7 | Sequence 7, Appl | 190 | 48 | 100.0 | 10 | 1 | US-08-717-169-13 | Sequence 13, Appl |
| 118 | 48 | 100.0 | 7 | 1 | US-08-284-784-7 | Sequence 7, Appl | 191 | 48 | 100.0 | 10 | 1 | US-08-220-240A-3 | Sequence 3, Appl |
| 119 | 48 | 100.0 | 7 | 1 | US-08-854-811-7 | Sequence 7, Appl | 192 | 48 | 100.0 | 10 | 1 | US-08-478-572-150 | Sequence 150, App |
| 120 | 48 | 100.0 | 7 | 2 | US-08-865-468-9 | Sequence 9, Appl | 193 | 48 | 100.0 | 10 | 1 | US-08-792-553-24 | Sequence 24, Appl |
| 121 | 48 | 100.0 | 7 | 2 | US-09-216-430C-33 | Sequence 33, Appl | 194 | 48 | 100.0 | 10 | 2 | US-08-300-928C-88 | Sequence 88, Appl |
| 122 | 48 | 100.0 | 7 | 2 | US-09-809-517A-12 | Sequence 12, Appl | 195 | 48 | 100.0 | 10 | 2 | US-08-430-944D-88 | Sequence 88, Appl |
| 123 | 48 | 100.0 | 7 | 2 | US-09-809-517A-13 | Sequence 13, Appl | 196 | 48 | 100.0 | 10 | 2 | US-08-430-014-88 | Sequence 88, Appl |
| 124 | 48 | 100.0 | 7 | 2 | US-10-665-227A-4 | Sequence 4, Appl | 197 | 48 | 100.0 | 10 | 2 | US-08-431-184-88 | Sequence 88, Appl |
| 125 | 48 | 100.0 | 8 | 1 | US-08-762-433-6 | Sequence 6, Appl | 198 | 48 | 100.0 | 10 | 2 | US-08-163-919A-17 | Sequence 17, Appl |
| 126 | 48 | 100.0 | 8 | 1 | US-09-001-219-6 | Sequence 6, Appl | 199 | 48 | 100.0 | 10 | 2 | US-08-639-294-9 | Sequence 9, Appl |
| 127 | 48 | 100.0 | 8 | 1 | US-08-481-658B-22 | Sequence 22, Appl | 200 | 48 | 100.0 | 10 | 2 | US-08-556-978B-10 | Sequence 10, Appl |
| 128 | 48 | 100.0 | 8 | 1 | US-08-477-504A-22 | Sequence 22, Appl | 201 | 48 | 100.0 | 10 | 2 | US-08-484-296-150 | Sequence 150, App |
| 129 | 48 | 100.0 | 8 | 1 | US-08-486-756A-22 | Sequence 22, Appl | 202 | 48 | 100.0 | 10 | 2 | US-09-425-638A-129 | Sequence 129, App |
| 130 | 48 | 100.0 | 8 | 1 | US-08-485-862B-22 | Sequence 22, Appl | 203 | 48 | 100.0 | 10 | 2 | US-09-543-004-129 | Sequence 129, App |
| 131 | 48 | 100.0 | 8 | 1 | US-08-787-732A-22 | Sequence 22, Appl | 204 | 48 | 100.0 | 10 | 2 | US-09-039-780A-101 | Sequence 101, App |
| 132 | 48 | 100.0 | 8 | 2 | US-08-487-077A-22 | Sequence 22, Appl | 205 | 48 | 100.0 | 10 | 2 | US-09-099-053-27 | Sequence 27, Appl |
| 133 | 48 | 100.0 | 8 | 2 | US-08-816-977-11 | Sequence 11, Appl | 206 | 48 | 100.0 | 10 | 2 | US-09-228-901A-13 | Sequence 13, Appl |
| 134 | 48 | 100.0 | 8 | 2 | US-08-485-863A-22 | Sequence 22, Appl | 207 | 48 | 100.0 | 10 | 2 | US-08-981-490B-5 | Sequence 5, Appl |
| 135 | 48 | 100.0 | 8 | 2 | US-08-485-049D-22 | Sequence 22, Appl | 208 | 48 | 100.0 | 10 | 2 | US-09-861-034B-9 | Sequence 9, Appl |
| 136 | 48 | 100.0 | 8 | 2 | US-08-875-533-57 | Sequence 57, Appl | 209 | 48 | 100.0 | 10 | 2 | US-08-462-515-17 | Sequence 17, Appl |
| 137 | 48 | 100.0 | 8 | 2 | US-08-556-978B-13 | Sequence 13, Appl | 210 | 48 | 100.0 | 10 | 2 | US-09-809-517A-2 | Sequence 2, Appl |
| 138 | 48 | 100.0 | 8 | 2 | US-08-637-732A-40 | Sequence 40, Appl | 211 | 48 | 100.0 | 10 | 2 | US-09-015-399-13 | Sequence 13, Appl |
| 139 | 48 | 100.0 | 8 | 2 | US-08-817-787-31 | Sequence 31, Appl | 212 | 48 | 100.0 | 10 | 2 | US-09-015-399-11 | Sequence 11, Appl |
| 140 | 48 | 100.0 | 8 | 2 | US-09-178-115-22 | Sequence 22, Appl | 213 | 48 | 100.0 | 10 | 2 | US-08-594-575C-24 | Sequence 24, Appl |
| 141 | 48 | 100.0 | 8 | 2 | US-09-177-776-22 | Sequence 22, Appl | 214 | 48 | 100.0 | 10 | 2 | US-09-402-131-9 | Sequence 9, Appl |
| 142 | 48 | 100.0 | 8 | 2 | US-09-549-831-15 | Sequence 15, Appl | 215 | 48 | 100.0 | 10 | 2 | US-10-188-347-1 | Sequence 1, Appl |
| 143 | 48 | 100.0 | 8 | 2 | US-09-326-529-16 | Sequence 16, Appl | 216 | 48 | 100.0 | 10 | 2 | US-10-665-227A-7 | Sequence 7, Appl |
| 144 | 48 | 100.0 | 8 | 2 | US-09-464-152A-14 | Sequence 14, Appl | 217 | 48 | 100.0 | 10 | 2 | US-10-048-882C-3 | Sequence 3, Appl |
| 145 | 48 | 100.0 | 8 | 2 | US-09-648-569A-40 | Sequence 40, Appl | 218 | 48 | 100.0 | 10 | 4 | PCR-US93-00909-13 | Sequence 13, Appl |
| 146 | 48 | 100.0 | 8 | 2 | US-09-904-196B-10 | Sequence 10, Appl | 219 | 48 | 100.0 | 10 | 4 | PCR-US94-14073-17 | Sequence 17, Appl |
| 147 | 48 | 100.0 | 8 | 2 | US-09-760-008A-10 | Sequence 10, Appl | 220 | 48 | 100.0 | 10 | 4 | PCR-US95-04439-9 | Sequence 9, Appl |
| 148 | 48 | 100.0 | 8 | 2 | US-09-334-477-11 | Sequence 11, Appl | 221 | 48 | 100.0 | 11 | 1 | US-08-133-804-11 | Sequence 11, Appl |
| 149 | 48 | 100.0 | 8 | 2 | US-09-583-808-31 | Sequence 31, Appl | 222 | 48 | 100.0 | 11 | 1 | US-08-461-838-11 | Sequence 11, Appl |
| 150 | 48 | 100.0 | 8 | 2 | US-09-772-719B-22 | Sequence 22, Appl | 223 | 48 | 100.0 | 11 | 1 | US-08-737-757-4 | Sequence 4, Appl |
| 151 | 48 | 100.0 | 8 | 2 | US-08-260-190-22 | Sequence 22, Appl | 224 | 48 | 100.0 | 11 | 1 | US-08-461-386-11 | Sequence 11, Appl |
| 152 | 48 | 100.0 | 8 | 2 | US-09-786-442B-18 | Sequence 18, Appl | 225 | 48 | 100.0 | 11 | 2 | US-09-814-569-2 | Sequence 2, Appl |
| 153 | 48 | 100.0 | 8 | 2 | US-09-589-483-28 | Sequence 28, Appl | 226 | 48 | 100.0 | 11 | 2 | US-09-515-534A-8 | Sequence 8, Appl |
| 154 | 48 | 100.0 | 8 | 2 | US-09-782-587B-13 | Sequence 13, Appl | 227 | 48 | 100.0 | 11 | 2 | US-09-319-806-8 | Sequence 8, Appl |
| 155 | 48 | 100.0 | 8 | 2 | US-09-319-806-7 | Sequence 7, Appl | 228 | 48 | 100.0 | 11 | 2 | US-10-665-227A-8 | Sequence 8, Appl |
| 156 | 48 | 100.0 | 8 | 2 | US-10-192-294-10 | Sequence 10, Appl | 229 | 48 | 100.0 | 12 | 1 | US-08-100-744-11 | Sequence 11, Appl |
| 157 | 48 | 100.0 | 8 | 2 | US-09-244-984-2 | Sequence 2, Appl | 230 | 48 | 100.0 | 12 | 1 | US-08-284-784-11 | Sequence 11, Appl |
| 158 | 48 | 100.0 | 8 | 2 | US-09-589-777C-20 | Sequence 20, Appl | 231 | 48 | 100.0 | 12 | 1 | US-08-459-064B-35 | Sequence 35, Appl |
| 159 | 48 | 100.0 | 8 | 2 | US-10-665-227A-5 | Sequence 5, Appl | 232 | 48 | 100.0 | 12 | 1 | US-08-460-421A-35 | Sequence 35, Appl |
| 160 | 48 | 100.0 | 8 | 2 | US-09-997-623-42 | Sequence 42, Appl | 233 | 48 | 100.0 | 12 | 2 | US-08-854-811-11 | Sequence 11, Appl |
| 161 | 48 | 100.0 | 8 | 2 | US-10-195-707B-36 | Sequence 36, Appl | 234 | 48 | 100.0 | 12 | 2 | US-09-331-362-10 | Sequence 10, Appl |
| 162 | 48 | 100.0 | 9 | 1 | US-08-155-171B-4 | Sequence 4, Appl | 235 | 48 | 100.0 | 12 | 2 | US-08-327-874A-4 | Sequence 4, Appl |
| 163 | 48 | 100.0 | 9 | 1 | US-08-100-744-12 | Sequence 12, Appl | 236 | 48 | 100.0 | 12 | 2 | US-09-266-498-7 | Sequence 7, Appl |
| 164 | 48 | 100.0 | 9 | 1 | US-08-284-784-12 | Sequence 12, Appl | 237 | 48 | 100.0 | 12 | 2 | US-09-376-330-6 | Sequence 6, Appl |
| 165 | 48 | 100.0 | 9 | 1 | US-08-737-757-12 | Sequence 12, Appl | 238 | 48 | 100.0 | 12 | 2 | US-09-395-017B-36 | Sequence 36, Appl |
| 166 | 48 | 100.0 | 9 | 1 | US-08-854-811-12 | Sequence 12, Appl | 239 | 48 | 100.0 | 12 | 2 | US-09-643-657-43 | Sequence 43, Appl |
| 167 | 48 | 100.0 | 9 | 1 | US-08-435-998-4 | Sequence 4, Appl | 240 | 48 | 100.0 | 12 | 2 | US-09-601-040A-13 | Sequence 13, Appl |
| 168 | 48 | 100.0 | 9 | 2 | US-09-143-470-19 | Sequence 19, Appl | 241 | 48 | 100.0 | 12 | 2 | US-10-008-960-4 | Sequence 4, Appl |
| 169 | 48 | 100.0 | 9 | 2 | US-09-254-567-1 | Sequence 1, Appl | 242 | 48 | 100.0 | 12 | 2 | US-09-921-992-83 | Sequence 83, Appl |
| 170 | 48 | 100.0 | 9 | 2 | US-08-895-707-9 | Sequence 9, Appl | 243 | 48 | 100.0 | 12 | 2 | US-09-715-836A-10 | Sequence 10, Appl |
| 171 | 48 | 100.0 | 9 | 2 | US-08-875-533-36 | Sequence 36, Appl | 244 | 48 | 100.0 | 12 | 2 | US-09-568-470A-9 | Sequence 9, Appl |
| 172 | 48 | 100.0 | 9 | 2 | US-08-556-978B-102 | Sequence 102, App | 245 | 48 | 100.0 | 12 | 2 | US-10-665-227A-3 | Sequence 3, Appl |
| 173 | 48 | 100.0 | 9 | 2 | US-09-076-804-1 | Sequence 1, Appl | 246 | 48 | 100.0 | 12 | 2 | US-09-269-874A-8 | Sequence 8, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|----|---|--------------------|--------------------|-----|----|-------|----|---|--------------------|--------------------|
| 247 | 48 | 100.0 | 12 | 4 | PCT-US94-09700-4 | Sequence 4, Appl1 | 320 | 48 | 100.0 | 17 | 2 | US-09-809-517A-32 | Sequence 32, Appl1 |
| 248 | 48 | 100.0 | 13 | 1 | US-08-571-643A-4 | Sequence 4, Appl1 | 321 | 48 | 100.0 | 17 | 4 | PCT-US94-01176-19 | Sequence 19, Appl1 |
| 249 | 48 | 100.0 | 13 | 1 | US-08-439-747A-22 | Sequence 22, Appl1 | 322 | 48 | 100.0 | 18 | 1 | US-08-145-006C-6 | Sequence 6, Appl1 |
| 250 | 48 | 100.0 | 13 | 1 | US-08-482-577B-15 | Sequence 15, Appl1 | 323 | 48 | 100.0 | 18 | 1 | US-08-578-649-14 | Sequence 14, Appl1 |
| 251 | 48 | 100.0 | 13 | 1 | US-08-440-409B-22 | Sequence 22, Appl1 | 324 | 48 | 100.0 | 18 | 1 | US-08-356-060A-47 | Sequence 47, Appl1 |
| 252 | 48 | 100.0 | 13 | 2 | US-08-981-321-8 | Sequence 8, Appl1 | 325 | 48 | 100.0 | 18 | 1 | US-08-670-175-8 | Sequence 8, Appl1 |
| 253 | 48 | 100.0 | 13 | 2 | US-09-218-176-40 | Sequence 40, Appl1 | 326 | 48 | 100.0 | 18 | 2 | US-08-895-707-15 | Sequence 15, Appl1 |
| 254 | 48 | 100.0 | 13 | 2 | US-09-331-362-8 | Sequence 8, Appl1 | 327 | 48 | 100.0 | 18 | 2 | US-08-460-900C-47 | Sequence 47, Appl1 |
| 255 | 48 | 100.0 | 13 | 2 | US-08-556-978B-40 | Sequence 40, Appl1 | 328 | 48 | 100.0 | 18 | 2 | US-08-460-900C-61 | Sequence 61, Appl1 |
| 256 | 48 | 100.0 | 13 | 2 | US-09-147-805-7 | Sequence 7, Appl1 | 329 | 48 | 100.0 | 18 | 2 | US-08-674-509B-47 | Sequence 47, Appl1 |
| 257 | 48 | 100.0 | 13 | 2 | US-09-418-785-3 | Sequence 3, Appl1 | 330 | 48 | 100.0 | 18 | 2 | US-08-954-698-47 | Sequence 47, Appl1 |
| 258 | 48 | 100.0 | 13 | 2 | US-09-116-492A-32 | Sequence 32, Appl1 | 331 | 48 | 100.0 | 18 | 2 | US-08-957-874-47 | Sequence 47, Appl1 |
| 259 | 48 | 100.0 | 13 | 2 | US-09-863-859-20 | Sequence 20, Appl1 | 332 | 48 | 100.0 | 18 | 2 | US-09-400-816-1 | Sequence 1, Appl1 |
| 260 | 48 | 100.0 | 13 | 2 | US-09-823-266-2 | Sequence 2, Appl1 | 333 | 48 | 100.0 | 18 | 2 | US-09-429-370-45 | Sequence 45, Appl1 |
| 261 | 48 | 100.0 | 13 | 2 | US-09-823-266-3 | Sequence 3, Appl1 | 334 | 48 | 100.0 | 18 | 2 | US-09-639-695-47 | Sequence 47, Appl1 |
| 262 | 48 | 100.0 | 13 | 2 | US-09-823-266-4 | Sequence 4, Appl1 | 335 | 48 | 100.0 | 18 | 2 | US-09-639-695-61 | Sequence 61, Appl1 |
| 263 | 48 | 100.0 | 13 | 2 | US-09-823-266-5 | Sequence 5, Appl1 | 336 | 48 | 100.0 | 18 | 2 | US-09-448-188-47 | Sequence 47, Appl1 |
| 264 | 48 | 100.0 | 13 | 2 | US-10-188-602-1 | Sequence 1, Appl1 | 337 | 48 | 100.0 | 18 | 2 | US-08-954-128-47 | Sequence 47, Appl1 |
| 265 | 48 | 100.0 | 13 | 2 | US-10-155-419-2 | Sequence 2, Appl1 | 338 | 48 | 100.0 | 18 | 2 | US-08-954-740-47 | Sequence 47, Appl1 |
| 266 | 48 | 100.0 | 13 | 2 | US-10-155-419-3 | Sequence 3, Appl1 | 339 | 48 | 100.0 | 18 | 2 | US-09-395-017B-48 | Sequence 28, Appl1 |
| 267 | 48 | 100.0 | 13 | 2 | US-10-155-419-4 | Sequence 4, Appl1 | 340 | 48 | 100.0 | 18 | 2 | US-09-795-872-1 | Sequence 1, Appl1 |
| 268 | 48 | 100.0 | 13 | 2 | US-10-155-419-5 | Sequence 5, Appl1 | 341 | 48 | 100.0 | 18 | 2 | US-09-736-476-47 | Sequence 47, Appl1 |
| 269 | 48 | 100.0 | 14 | 1 | US-07-807-529A-76 | Sequence 76, Appl1 | 342 | 48 | 100.0 | 18 | 2 | US-09-809-517A-1 | Sequence 1, Appl1 |
| 270 | 48 | 100.0 | 14 | 1 | US-08-226-264-7 | Sequence 7, Appl1 | 343 | 48 | 100.0 | 18 | 4 | PCT-US94-00545-6 | Sequence 6, Appl1 |
| 271 | 48 | 100.0 | 14 | 1 | US-08-226-264-19 | Sequence 19, Appl1 | 344 | 48 | 100.0 | 19 | 2 | US-09-167-434-15 | Sequence 15, Appl1 |
| 272 | 48 | 100.0 | 14 | 1 | US-08-226-264-20 | Sequence 20, Appl1 | 345 | 48 | 100.0 | 19 | 2 | US-08-853-755-15 | Sequence 15, Appl1 |
| 273 | 48 | 100.0 | 14 | 1 | US-08-448-418-100 | Sequence 100, Appl | 346 | 48 | 100.0 | 19 | 2 | US-09-129-192C-72 | Sequence 72, Appl1 |
| 274 | 48 | 100.0 | 14 | 1 | US-08-467-603-58 | Sequence 58, Appl1 | 347 | 48 | 100.0 | 19 | 2 | US-09-933-999A-31 | Sequence 31, Appl1 |
| 275 | 48 | 100.0 | 14 | 1 | US-08-466-793-58 | Sequence 58, Appl1 | 348 | 48 | 100.0 | 20 | 1 | US-08-373-134D-3 | Sequence 3, Appl1 |
| 276 | 48 | 100.0 | 14 | 1 | US-08-491-861A-58 | Sequence 58, Appl1 | 349 | 48 | 100.0 | 20 | 1 | US-08-416-336-4 | Sequence 4, Appl1 |
| 277 | 48 | 100.0 | 14 | 2 | US-08-300-928C-91 | Sequence 91, Appl1 | 350 | 48 | 100.0 | 20 | 1 | US-08-543-020-12 | Sequence 12, Appl1 |
| 278 | 48 | 100.0 | 14 | 2 | US-08-430-944D-91 | Sequence 91, Appl1 | 351 | 48 | 100.0 | 20 | 1 | US-09-114-637-3 | Sequence 3, Appl1 |
| 279 | 48 | 100.0 | 14 | 2 | US-08-430-014-91 | Sequence 91, Appl1 | 352 | 48 | 100.0 | 20 | 2 | US-08-542-051-21 | Sequence 21, Appl1 |
| 280 | 48 | 100.0 | 14 | 2 | US-08-956-307B-3 | Sequence 3, Appl1 | 353 | 48 | 100.0 | 20 | 2 | US-08-485-942A-99 | Sequence 99, Appl1 |
| 281 | 48 | 100.0 | 14 | 2 | US-08-431-184-91 | Sequence 91, Appl1 | 354 | 48 | 100.0 | 20 | 2 | US-08-488-214A-99 | Sequence 99, Appl1 |
| 282 | 48 | 100.0 | 14 | 2 | US-09-374-671A-58 | Sequence 58, Appl1 | 355 | 48 | 100.0 | 20 | 2 | US-08-640-737-32 | Sequence 32, Appl1 |
| 283 | 48 | 100.0 | 14 | 2 | US-09-146-979-100 | Sequence 100, Appl | 356 | 48 | 100.0 | 20 | 2 | US-09-186-448-6 | Sequence 6, Appl1 |
| 284 | 48 | 100.0 | 14 | 2 | US-09-623-326-16 | Sequence 16, Appl1 | 357 | 48 | 100.0 | 20 | 2 | US-08-122-458D-7 | Sequence 7, Appl1 |
| 285 | 48 | 100.0 | 14 | 2 | US-09-823-266-1 | Sequence 1, Appl1 | 358 | 48 | 100.0 | 20 | 2 | US-08-438-431A-99 | Sequence 99, Appl1 |
| 286 | 48 | 100.0 | 14 | 2 | US-09-388-316C-30 | Sequence 30, Appl1 | 359 | 48 | 100.0 | 20 | 2 | US-09-638-202A-114 | Sequence 114, Appl |
| 287 | 48 | 100.0 | 14 | 2 | US-10-004-381-32 | Sequence 32, Appl1 | 360 | 48 | 100.0 | 20 | 2 | US-09-096-724B-34 | Sequence 34, Appl1 |
| 288 | 48 | 100.0 | 14 | 2 | US-10-155-419-1 | Sequence 1, Appl1 | 361 | 48 | 100.0 | 20 | 2 | US-09-674-677-34 | Sequence 34, Appl1 |
| 289 | 48 | 100.0 | 15 | 1 | US-08-469-486-48 | Sequence 48, Appl1 | 362 | 48 | 100.0 | 20 | 2 | US-10-043-665B-6 | Sequence 6, Appl1 |
| 290 | 48 | 100.0 | 15 | 1 | US-08-467-603-53 | Sequence 53, Appl1 | 363 | 48 | 100.0 | 20 | 2 | US-09-623-326-14 | Sequence 14, Appl1 |
| 291 | 48 | 100.0 | 15 | 1 | US-08-466-793-53 | Sequence 53, Appl1 | 364 | 48 | 100.0 | 20 | 2 | US-09-096-749A-114 | Sequence 114, Appl |
| 292 | 48 | 100.0 | 15 | 1 | US-08-469-658-48 | Sequence 48, Appl1 | 365 | 48 | 100.0 | 20 | 2 | US-09-637-614-114 | Sequence 114, Appl |
| 293 | 48 | 100.0 | 15 | 1 | US-08-491-861A-53 | Sequence 53, Appl1 | 366 | 48 | 100.0 | 20 | 2 | US-09-612-314A-48 | Sequence 48, Appl1 |
| 294 | 48 | 100.0 | 15 | 2 | US-09-374-671A-53 | Sequence 53, Appl1 | 367 | 48 | 100.0 | 20 | 2 | US-10-420-564-6 | Sequence 6, Appl1 |
| 295 | 48 | 100.0 | 15 | 2 | US-10-015-328-2 | Sequence 2, Appl1 | 368 | 48 | 100.0 | 20 | 2 | US-09-935-280B-19 | Sequence 19, Appl1 |
| 296 | 48 | 100.0 | 15 | 2 | US-09-728-653-2 | Sequence 2, Appl1 | 369 | 48 | 100.0 | 20 | 2 | US-09-486-480-5 | Sequence 5, Appl1 |
| 297 | 48 | 100.0 | 15 | 2 | US-09-921-992-85 | Sequence 85, Appl1 | 370 | 48 | 100.0 | 21 | 1 | US-08-432-871C-46 | Sequence 46, Appl1 |
| 298 | 48 | 100.0 | 15 | 2 | US-09-506-078-37 | Sequence 37, Appl1 | 371 | 48 | 100.0 | 21 | 1 | US-08-651-818A-21 | Sequence 21, Appl1 |
| 299 | 48 | 100.0 | 15 | 2 | US-10-221-655A-5 | Sequence 5, Appl1 | 372 | 48 | 100.0 | 21 | 1 | US-08-712-878-6 | Sequence 6, Appl1 |
| 300 | 48 | 100.0 | 16 | 1 | US-08-578-649-13 | Sequence 13, Appl1 | 373 | 48 | 100.0 | 21 | 2 | US-08-485-942A-98 | Sequence 98, Appl1 |
| 301 | 48 | 100.0 | 16 | 1 | US-08-226-264-8 | Sequence 8, Appl1 | 374 | 48 | 100.0 | 21 | 2 | US-08-488-214A-98 | Sequence 98, Appl1 |
| 302 | 48 | 100.0 | 16 | 1 | US-08-226-264-21 | Sequence 21, Appl1 | 375 | 48 | 100.0 | 21 | 2 | US-08-488-208A-98 | Sequence 98, Appl1 |
| 303 | 48 | 100.0 | 16 | 2 | US-08-706-945D-145 | Sequence 145, App | 376 | 48 | 100.0 | 21 | 2 | US-09-071-710-41 | Sequence 41, Appl1 |
| 304 | 48 | 100.0 | 16 | 2 | US-09-039-780A-103 | Sequence 103, App | 377 | 48 | 100.0 | 21 | 2 | US-08-912-276-25 | Sequence 25, Appl1 |
| 305 | 48 | 100.0 | 16 | 2 | US-09-039-780A-105 | Sequence 105, App | 378 | 48 | 100.0 | 21 | 2 | US-09-153-804-17 | Sequence 17, Appl1 |
| 306 | 48 | 100.0 | 16 | 2 | US-09-367-309A-3 | Sequence 3, Appl1 | 379 | 48 | 100.0 | 21 | 2 | US-08-944-483-76 | Sequence 76, Appl1 |
| 307 | 48 | 100.0 | 16 | 2 | US-09-506-768-15 | Sequence 15, Appl1 | 380 | 48 | 100.0 | 21 | 2 | US-09-184-886-21 | Sequence 21, Appl1 |
| 308 | 48 | 100.0 | 16 | 2 | US-09-822-765A-1 | Sequence 1, Appl1 | 381 | 48 | 100.0 | 21 | 2 | US-09-525-397-41 | Sequence 41, Appl1 |
| 309 | 48 | 100.0 | 16 | 2 | US-09-809-517A-4 | Sequence 4, Appl1 | 382 | 48 | 100.0 | 21 | 2 | US-08-483-231A-98 | Sequence 98, Appl1 |
| 310 | 48 | 100.0 | 16 | 2 | US-09-809-517A-29 | Sequence 29, Appl1 | 383 | 48 | 100.0 | 21 | 2 | US-09-566-876-16 | Sequence 16, Appl1 |
| 311 | 48 | 100.0 | 17 | 1 | US-09-645-415A-23 | Sequence 23, Appl1 | 384 | 48 | 100.0 | 21 | 2 | US-08-488-223A-98 | Sequence 98, Appl1 |
| 312 | 48 | 100.0 | 17 | 1 | US-08-021-603A-19 | Sequence 19, Appl1 | 385 | 48 | 100.0 | 21 | 2 | US-09-049-698-51 | Sequence 51, Appl1 |
| 313 | 48 | 100.0 | 17 | 1 | US-08-155-171B-37 | Sequence 37, Appl1 | 386 | 48 | 100.0 | 21 | 2 | US-09-065-383-33 | Sequence 33, Appl1 |
| 314 | 48 | 100.0 | 17 | 1 | US-08-435-998-37 | Sequence 37, Appl1 | 387 | 48 | 100.0 | 21 | 2 | US-08-438-431A-98 | Sequence 98, Appl1 |
| 315 | 48 | 100.0 | 17 | 1 | US-08-600-783-13 | Sequence 13, Appl1 | 388 | 48 | 100.0 | 21 | 2 | US-09-270-956-46 | Sequence 46, Appl1 |
| 316 | 48 | 100.0 | 17 | 2 | US-08-946-475-10 | Sequence 10, Appl1 | 389 | 48 | 100.0 | 21 | 2 | US-09-276-600-11 | Sequence 11, Appl1 |
| 317 | 48 | 100.0 | 17 | 2 | US-09-136-421-10 | Sequence 10, Appl1 | 390 | 48 | 100.0 | 21 | 2 | US-08-488-225A-98 | Sequence 98, Appl1 |
| 318 | 48 | 100.0 | 17 | 2 | US-09-340-479-10 | Sequence 10, Appl1 | 391 | 48 | 100.0 | 21 | 2 | US-09-193-881-29 | Sequence 29, Appl1 |
| 319 | 48 | 100.0 | 17 | 2 | US-09-230-846A-5 | Sequence 5, Appl1 | 392 | 48 | 100.0 | 21 | 2 | US-09-689-065B-104 | Sequence 104, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|----|---|--------------------|--------------------|-----|----|-------|----|---|--------------------|--------------------|
| 333 | 48 | 100.0 | 21 | 2 | US-09-050-516-49 | Sequence 49, Appl | 466 | 48 | 100.0 | 29 | 2 | US-09-419-381-47 | Sequence 47, Appl |
| 334 | 48 | 100.0 | 21 | 2 | US-09-939-126-8 | Sequence 8, Appl.i | 467 | 48 | 100.0 | 29 | 2 | US-09-419-381-48 | Sequence 48, Appl |
| 335 | 48 | 100.0 | 21 | 2 | US-09-939-126-9 | Sequence 9, Appl.i | 468 | 48 | 100.0 | 29 | 2 | US-09-880-901-2 | Sequence 2, Appl.i |
| 336 | 48 | 100.0 | 21 | 2 | US-09-939-126-10 | Sequence 10, Appl | 469 | 48 | 100.0 | 29 | 2 | US-09-962-756-2202 | Sequence 2202, Ap |
| 337 | 48 | 100.0 | 21 | 2 | US-09-939-126-11 | Sequence 11, Appl | 470 | 48 | 100.0 | 29 | 2 | US-09-486-480-7 | Sequence 7, Appl |
| 338 | 48 | 100.0 | 21 | 2 | US-09-939-126-12 | Sequence 12, Appl | 471 | 48 | 100.0 | 29 | 2 | PCT-US94-05150-37 | Sequence 37, Appl |
| 339 | 48 | 100.0 | 21 | 2 | US-10-278-547-49 | Sequence 49, Appl | 472 | 48 | 100.0 | 30 | 2 | US-09-039-780A-98 | Sequence 98, Appl |
| 340 | 48 | 100.0 | 21 | 2 | US-09-431-384B-31 | Sequence 31, Appl | 473 | 48 | 100.0 | 30 | 2 | US-09-039-780A-100 | Sequence 100, App |
| 401 | 48 | 100.0 | 21 | 2 | US-09-589-483-15 | Sequence 15, Appl | 474 | 48 | 100.0 | 30 | 2 | US-09-039-780A-104 | Sequence 104, App |
| 402 | 48 | 100.0 | 21 | 2 | US-09-589-483-29 | Sequence 29, Appl | 475 | 48 | 100.0 | 30 | 2 | US-09-150-867-11 | Sequence 11, Appl |
| 403 | 48 | 100.0 | 21 | 2 | US-09-832-464-21 | Sequence 21, Appl | 476 | 48 | 100.0 | 31 | 1 | US-08-662-2227-37 | Sequence 37, Appl |
| 404 | 48 | 100.0 | 21 | 2 | US-10-010-160-68 | Sequence 68, Appl | 477 | 48 | 100.0 | 31 | 2 | US-09-017-947-37 | Sequence 37, Appl |
| 405 | 48 | 100.0 | 21 | 2 | US-09-173-713-5 | Sequence 5, Appl.i | 478 | 48 | 100.0 | 31 | 2 | US-09-925-442-37 | Sequence 37, Appl |
| 406 | 48 | 100.0 | 21 | 2 | US-09-589-777C-7 | Sequence 7, Appl.i | 479 | 48 | 100.0 | 31 | 2 | US-09-897-776A-35 | Sequence 35, Appl |
| 407 | 48 | 100.0 | 21 | 2 | US-09-052-855A-10 | Sequence 10, Appl | 480 | 48 | 100.0 | 31 | 2 | US-09-962-756-2203 | Sequence 2203, Ap |
| 408 | 48 | 100.0 | 21 | 2 | US-09-080-140-31 | Sequence 31, Appl | 481 | 48 | 100.0 | 32 | 2 | US-08-737-336-1 | Sequence 1, Appl |
| 409 | 48 | 100.0 | 21 | 2 | US-09-092-297A-32 | Sequence 32, Appl | 482 | 48 | 100.0 | 33 | 2 | US-09-897-776A-28 | Sequence 28, Appl |
| 410 | 48 | 100.0 | 22 | 2 | US-09-039-780A-102 | Sequence 102, App | 483 | 48 | 100.0 | 33 | 2 | US-09-866-538-21 | Sequence 21, Appl |
| 411 | 48 | 100.0 | 22 | 2 | US-09-660-742-3 | Sequence 3, Appl.i | 484 | 48 | 100.0 | 33 | 2 | US-10-346-658-2 | Sequence 2, Appl |
| 412 | 48 | 100.0 | 23 | 1 | US-08-480-604A-24 | Sequence 24, Appl | 485 | 48 | 100.0 | 33 | 2 | US-09-839-577A-6 | Sequence 6, Appl.i |
| 413 | 48 | 100.0 | 23 | 1 | US-08-273-146-37 | Sequence 37, Appl | 486 | 48 | 100.0 | 33 | 2 | US-09-839-577A-7 | Sequence 7, Appl.i |
| 414 | 48 | 100.0 | 23 | 1 | US-08-405-496A-24 | Sequence 24, Appl | 487 | 48 | 100.0 | 35 | 2 | US-09-962-756-2204 | Sequence 2204, Ap |
| 415 | 48 | 100.0 | 23 | 1 | US-08-350-260A-42 | Sequence 42, Appl | 488 | 48 | 100.0 | 37 | 2 | US-09-507-333B-10 | Sequence 10, Appl |
| 416 | 48 | 100.0 | 23 | 2 | US-08-762-483-7 | Sequence 7, Appl.i | 489 | 48 | 100.0 | 37 | 2 | US-09-039-780A-97 | Sequence 97, Appl |
| 417 | 48 | 100.0 | 23 | 2 | US-08-913-136-24 | Sequence 24, Appl | 490 | 48 | 100.0 | 37 | 2 | US-09-575-847-5 | Sequence 5, Appl.i |
| 418 | 48 | 100.0 | 23 | 2 | US-09-660-742-5 | Sequence 5, Appl.i | 491 | 48 | 100.0 | 37 | 2 | US-09-084-303B-283 | Sequence 283, App |
| 419 | 48 | 100.0 | 23 | 2 | US-09-104-337A-42 | Sequence 42, Appl | 492 | 48 | 100.0 | 37 | 2 | US-10-094-944-15 | Sequence 15, Appl |
| 420 | 48 | 100.0 | 23 | 2 | US-09-084-517-24 | Sequence 24, Appl | 493 | 48 | 100.0 | 38 | 2 | US-09-962-756-2069 | Sequence 2069, Ap |
| 421 | 48 | 100.0 | 23 | 2 | US-09-939-126-7 | Sequence 7, Appl.i | 494 | 48 | 100.0 | 38 | 2 | US-09-839-577A-12 | Sequence 12, Appl |
| 422 | 48 | 100.0 | 23 | 2 | US-09-897-776A-31 | Sequence 31, Appl | 495 | 48 | 100.0 | 39 | 1 | US-08-679-865-39 | Sequence 39, Appl |
| 423 | 48 | 100.0 | 23 | 2 | US-09-589-483-30 | Sequence 30, Appl | 496 | 48 | 100.0 | 39 | 1 | US-08-680-876-39 | Sequence 39, Appl |
| 424 | 48 | 100.0 | 23 | 2 | US-09-589-483-30 | Sequence 30, Appl | 497 | 48 | 100.0 | 39 | 2 | US-09-263-975-39 | Sequence 39, Appl |
| 425 | 48 | 100.0 | 24 | 1 | US-08-021-603A-16 | Sequence 16, Appl | 498 | 48 | 100.0 | 39 | 2 | US-09-450-072-78 | Sequence 78, Appl |
| 426 | 48 | 100.0 | 24 | 2 | US-08-584-031-8 | Sequence 8, Appl.i | 499 | 48 | 100.0 | 39 | 2 | US-09-351-348-78 | Sequence 78, Appl |
| 427 | 48 | 100.0 | 24 | 2 | US-08-780-496-8 | Sequence 8, Appl.i | 500 | 48 | 100.0 | 40 | 1 | US-08-273-146-39 | Sequence 39, Appl |
| 428 | 48 | 100.0 | 24 | 2 | US-09-507-323B-9 | Sequence 9, Appl.i | 501 | 48 | 100.0 | 41 | 2 | US-09-129-192C-70 | Sequence 70, Appl |
| 429 | 48 | 100.0 | 24 | 2 | US-09-556-877-221 | Sequence 221, App | 502 | 48 | 100.0 | 42 | 1 | US-08-664-449-39 | Sequence 39, Appl |
| 430 | 48 | 100.0 | 24 | 2 | US-09-620-412C-221 | Sequence 221, App | 503 | 48 | 100.0 | 42 | 2 | US-09-309-382-12 | Sequence 12, Appl |
| 431 | 48 | 100.0 | 24 | 2 | US-09-292-858B-27 | Sequence 27, Appl | 504 | 48 | 100.0 | 42 | 2 | US-09-510-031A-3 | Sequence 3, Appl.i |
| 432 | 48 | 100.0 | 24 | 2 | US-08-928-069-9 | Sequence 9, Appl.i | 505 | 48 | 100.0 | 43 | 1 | US-08-273-146-41 | Sequence 41, Appl |
| 433 | 48 | 100.0 | 24 | 2 | US-09-598-419-221 | Sequence 221, App | 506 | 48 | 100.0 | 43 | 1 | US-08-652-816A-43 | Sequence 43, Appl |
| 434 | 48 | 100.0 | 24 | 2 | US-09-582-450-8 | Sequence 8, Appl.i | 507 | 48 | 100.0 | 43 | 1 | US-08-347-563A-12 | Sequence 12, Appl |
| 435 | 48 | 100.0 | 24 | 2 | US-09-934-465-8 | Sequence 8, Appl.i | 508 | 48 | 100.0 | 43 | 2 | US-08-485-942A-12 | Sequence 12, Appl |
| 436 | 48 | 100.0 | 24 | 2 | US-09-589-483-14 | Sequence 14, Appl | 509 | 48 | 100.0 | 43 | 2 | US-08-488-214A-12 | Sequence 12, Appl |
| 437 | 48 | 100.0 | 24 | 2 | US-09-589-777C-5 | Sequence 5, Appl.i | 510 | 48 | 100.0 | 43 | 2 | US-08-488-208A-12 | Sequence 12, Appl |
| 438 | 48 | 100.0 | 24 | 4 | PCT-US94-01176-16 | Sequence 16, Appl | 511 | 48 | 100.0 | 43 | 2 | US-08-483-211A-12 | Sequence 12, Appl |
| 439 | 48 | 100.0 | 25 | 2 | US-09-039-780A-96 | Sequence 96, Appl | 512 | 48 | 100.0 | 43 | 2 | US-08-488-223A-12 | Sequence 12, Appl |
| 440 | 48 | 100.0 | 25 | 2 | US-09-721-154-14 | Sequence 14, Appl | 513 | 48 | 100.0 | 43 | 2 | US-08-438-431A-12 | Sequence 12, Appl |
| 441 | 48 | 100.0 | 25 | 2 | US-09-897-776A-22 | Sequence 22, Appl | 514 | 48 | 100.0 | 43 | 2 | US-08-488-225A-12 | Sequence 12, Appl |
| 442 | 48 | 100.0 | 25 | 2 | US-10-381-846-5 | Sequence 5, Appl.i | 515 | 48 | 100.0 | 43 | 2 | US-09-686-647A-12 | Sequence 12, Appl |
| 443 | 48 | 100.0 | 26 | 1 | US-08-227-372-2 | Sequence 2, Appl.i | 516 | 48 | 100.0 | 43 | 2 | US-09-962-756-2111 | Sequence 2111, Ap |
| 444 | 48 | 100.0 | 26 | 1 | US-08-657-641-12 | Sequence 12, Appl | 517 | 48 | 100.0 | 43 | 2 | US-08-896-535-62 | Sequence 62, Appl |
| 445 | 48 | 100.0 | 26 | 2 | US-08-470-397-2 | Sequence 2, Appl.i | 518 | 48 | 100.0 | 44 | 1 | US-08-652-507-6 | Sequence 6, Appl |
| 446 | 48 | 100.0 | 26 | 2 | US-08-895-707-21 | Sequence 21, Appl | 519 | 48 | 100.0 | 44 | 2 | US-09-039-780A-99 | Sequence 99, Appl |
| 447 | 48 | 100.0 | 26 | 2 | US-09-897-776A-25 | Sequence 25, Appl | 520 | 48 | 100.0 | 44 | 2 | US-09-419-381-121 | Sequence 121, App |
| 448 | 48 | 100.0 | 26 | 2 | US-09-589-483-17 | Sequence 17, Appl | 521 | 48 | 100.0 | 44 | 2 | US-09-419-381-122 | Sequence 122, App |
| 449 | 48 | 100.0 | 26 | 2 | US-09-589-777C-13 | Sequence 13, Appl | 522 | 48 | 100.0 | 44 | 2 | US-10-317-252B-296 | Sequence 296, App |
| 450 | 48 | 100.0 | 26 | 2 | US-09-486-480-6 | Sequence 6, Appl.i | 523 | 48 | 100.0 | 45 | 2 | US-09-921-144-6 | Sequence 6, Appl.i |
| 451 | 48 | 100.0 | 26 | 4 | PCT-US94-07233-12 | Sequence 12, Appl | 524 | 48 | 100.0 | 45 | 2 | US-10-010-160-63 | Sequence 63, Appl |
| 452 | 48 | 100.0 | 27 | 2 | US-09-411-329C-32 | Sequence 32, Appl | 525 | 48 | 100.0 | 48 | 1 | US-08-457-245-21 | Sequence 21, Appl |
| 453 | 48 | 100.0 | 27 | 2 | US-09-411-329C-26 | Sequence 26, Appl | 526 | 48 | 100.0 | 48 | 2 | US-09-419-381-120 | Sequence 120, App |
| 454 | 48 | 100.0 | 27 | 2 | US-09-846-729A-22 | Sequence 22, Appl | 527 | 48 | 100.0 | 48 | 2 | US-09-921-144-8 | Sequence 8, Appl.i |
| 455 | 48 | 100.0 | 27 | 2 | US-09-846-729A-26 | Sequence 26, Appl | 528 | 48 | 100.0 | 48 | 2 | US-10-158-742A-15 | Sequence 15, Appl |
| 456 | 48 | 100.0 | 27 | 2 | US-09-898-461-9 | Sequence 9, Appl.i | 529 | 48 | 100.0 | 49 | 2 | US-09-979-338A-26 | Sequence 26, Appl |
| 457 | 48 | 100.0 | 28 | 2 | US-08-978-741-14 | Sequence 14, Appl | 530 | 48 | 100.0 | 49 | 2 | US-10-084-288-10 | Sequence 10, Appl |
| 458 | 48 | 100.0 | 28 | 2 | US-09-333-729A-14 | Sequence 14, Appl | 531 | 48 | 100.0 | 50 | 2 | US-09-507-333B-11 | Sequence 11, Appl |
| 459 | 48 | 100.0 | 28 | 2 | US-09-897-776A-20 | Sequence 20, Appl | 532 | 48 | 100.0 | 50 | 2 | US-09-360-237-53 | Sequence 53, Appl |
| 460 | 48 | 100.0 | 29 | 2 | US-09-419-381-41 | Sequence 41, Appl | 533 | 48 | 100.0 | 50 | 2 | US-10-010-160-64 | Sequence 64, Appl |
| 461 | 48 | 100.0 | 29 | 2 | US-09-419-381-42 | Sequence 42, Appl | 534 | 48 | 100.0 | 51 | 2 | US-10-158-742A-14 | Sequence 14, Appl |
| 462 | 48 | 100.0 | 29 | 2 | US-09-419-381-43 | Sequence 43, Appl | 535 | 48 | 100.0 | 52 | 2 | US-08-978-741-15 | Sequence 15, Appl |
| 463 | 48 | 100.0 | 29 | 2 | US-09-419-381-44 | Sequence 44, Appl | 536 | 48 | 100.0 | 52 | 2 | US-09-333-729A-15 | Sequence 15, Appl |
| 464 | 48 | 100.0 | 29 | 2 | US-09-419-381-45 | Sequence 45, Appl | 537 | 48 | 100.0 | 52 | 2 | US-10-158-742A-13 | Sequence 13, Appl |
| 465 | 48 | 100.0 | 29 | 2 | US-09-419-381-46 | Sequence 46, Appl | 538 | 48 | 100.0 | 53 | 1 | US-08-651-818A-19 | Sequence 19, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|----|---|----------------------|-------------------|-----|----|-------|-----|---|----------------------|-------------------|
| 539 | 48 | 100.0 | 53 | 2 | US-09-184-826-19 | Sequence 19, Appl | 612 | 48 | 100.0 | 95 | 2 | US-09-270-767-57350 | Sequence 57350, A |
| 540 | 48 | 100.0 | 53 | 1 | US-09-832-464-19 | Sequence 19, Appl | 613 | 48 | 100.0 | 95 | 2 | US-09-270-767-60865 | Sequence 60865, A |
| 541 | 48 | 100.0 | 54 | 2 | US-08-651-818A-23 | Sequence 23, Appl | 614 | 48 | 100.0 | 96 | 1 | US-07-807-529A-39 | Sequence 39, Appl |
| 542 | 48 | 100.0 | 54 | 2 | US-09-184-826-23 | Sequence 23, Appl | 615 | 48 | 100.0 | 96 | 2 | US-08-430-944D-103 | Sequence 103, App |
| 543 | 48 | 100.0 | 54 | 2 | US-09-832-464-23 | Sequence 23, Appl | 616 | 48 | 100.0 | 96 | 2 | US-08-431-184-103 | Sequence 103, App |
| 544 | 48 | 100.0 | 54 | 2 | US-10-158-742A-11 | Sequence 11, Appl | 617 | 48 | 100.0 | 96 | 2 | US-09-636-215-827 | Sequence 827, App |
| 545 | 48 | 100.0 | 54 | 2 | US-10-158-742A-12 | Sequence 12, Appl | 618 | 48 | 100.0 | 96 | 2 | US-09-685-166A-827 | Sequence 827, App |
| 546 | 48 | 100.0 | 54 | 1 | US-08-652-816A-41 | Sequence 41, Appl | 619 | 48 | 100.0 | 96 | 2 | US-09-679-426-827 | Sequence 827, App |
| 547 | 48 | 100.0 | 57 | 1 | US-08-958-201-18 | Sequence 18, Appl | 620 | 48 | 100.0 | 96 | 2 | US-09-759-143-827 | Sequence 827, App |
| 548 | 48 | 100.0 | 57 | 2 | US-09-979-338A-23 | Sequence 23, Appl | 621 | 48 | 100.0 | 96 | 2 | US-09-651-236-827 | Sequence 827, App |
| 549 | 48 | 100.0 | 57 | 2 | US-09-979-338A-29 | Sequence 29, Appl | 622 | 48 | 100.0 | 96 | 2 | US-09-657-278-827 | Sequence 827, App |
| 550 | 48 | 100.0 | 58 | 2 | US-10-158-742A-2 | Sequence 2, Appl1 | 623 | 48 | 100.0 | 96 | 2 | US-10-012-896-827 | Sequence 827, App |
| 551 | 48 | 100.0 | 60 | 1 | US-08-255-457-1 | Sequence 1, Appl1 | 624 | 48 | 100.0 | 97 | 2 | US-08-816-977-23 | Sequence 23, Appl |
| 552 | 48 | 100.0 | 60 | 1 | US-09-115-032-1 | Sequence 1, Appl1 | 625 | 48 | 100.0 | 97 | 2 | US-08-816-977-27 | Sequence 27, Appl |
| 553 | 48 | 100.0 | 60 | 2 | US-09-076-804-4 | Sequence 4, Appl1 | 626 | 48 | 100.0 | 97 | 2 | US-09-174-943-2 | Sequence 2, Appl1 |
| 554 | 48 | 100.0 | 60 | 4 | PCT-US95-05772-1 | Sequence 1, Appl1 | 627 | 48 | 100.0 | 97 | 2 | US-09-334-477-23 | Sequence 23, Appl |
| 555 | 48 | 100.0 | 62 | 2 | US-10-017-754-1880 | Sequence 1880, Ap | 628 | 48 | 100.0 | 97 | 2 | US-09-334-477-27 | Sequence 27, Appl |
| 556 | 48 | 100.0 | 64 | 2 | US-09-601-537-17 | Sequence 17, Appl | 629 | 48 | 100.0 | 99 | 2 | US-09-407-687-43 | Sequence 43, Appl |
| 557 | 48 | 100.0 | 67 | 1 | US-08-142-551B-9 | Sequence 9, Appl1 | 630 | 48 | 100.0 | 101 | 2 | US-10-263-103-31 | Sequence 31, Appl |
| 558 | 48 | 100.0 | 67 | 2 | US-09-268-070-3 | Sequence 3, Appl1 | 631 | 48 | 100.0 | 103 | 2 | US-10-263-103-29 | Sequence 29, Appl |
| 559 | 48 | 100.0 | 67 | 2 | US-09-921-144-10 | Sequence 10, Appl | 632 | 48 | 100.0 | 103 | 2 | US-10-263-103-32 | Sequence 32, Appl |
| 560 | 48 | 100.0 | 68 | 2 | US-09-268-070-1 | Sequence 1, Appl1 | 633 | 48 | 100.0 | 105 | 2 | US-10-263-103-28 | Sequence 28, Appl |
| 561 | 48 | 100.0 | 68 | 2 | US-09-174-943-6 | Sequence 6, Appl1 | 634 | 48 | 100.0 | 105 | 2 | US-10-263-103-30 | Sequence 30, Appl |
| 562 | 48 | 100.0 | 68 | 2 | US-09-979-338A-25 | Sequence 25, Appl | 635 | 48 | 100.0 | 108 | 2 | US-10-263-103-33 | Sequence 33, Appl |
| 563 | 48 | 100.0 | 69 | 1 | US-08-687-865A-21 | Sequence 21, Appl | 636 | 48 | 100.0 | 108 | 2 | US-09-473-551-15 | Sequence 15, Appl |
| 564 | 48 | 100.0 | 69 | 2 | US-09-268-070-2 | Sequence 2, Appl1 | 637 | 48 | 100.0 | 109 | 2 | US-09-407-687-41 | Sequence 41, Appl |
| 565 | 48 | 100.0 | 70 | 2 | US-09-043-711-21 | Sequence 21, Appl | 638 | 48 | 100.0 | 109 | 2 | US-09-979-338A-28 | Sequence 28, Appl |
| 566 | 48 | 100.0 | 70 | 2 | US-09-921-144-12 | Sequence 12, Appl | 639 | 48 | 100.0 | 109 | 2 | US-09-473-551-11 | Sequence 11, Appl |
| 567 | 48 | 100.0 | 71 | 2 | US-09-146-054-9 | Sequence 9, Appl1 | 640 | 48 | 100.0 | 109 | 2 | US-09-473-551-13 | Sequence 13, Appl |
| 568 | 48 | 100.0 | 71 | 2 | US-09-664-977A-9 | Sequence 9, Appl1 | 641 | 48 | 100.0 | 110 | 1 | US-08-434-705B-15 | Sequence 15, Appl |
| 569 | 48 | 100.0 | 72 | 2 | US-09-042-071-38 | Sequence 38, Appl | 642 | 48 | 100.0 | 110 | 1 | US-09-086-201-15 | Sequence 15, Appl |
| 570 | 48 | 100.0 | 72 | 2 | US-09-979-338A-30 | Sequence 30, Appl | 643 | 48 | 100.0 | 111 | 2 | US-09-622-613C-9 | Sequence 9, Appl1 |
| 571 | 48 | 100.0 | 74 | 2 | US-09-490-291-11 | Sequence 11, Appl | 644 | 48 | 100.0 | 112 | 2 | US-08-728-742A-56 | Sequence 56, Appl |
| 572 | 48 | 100.0 | 76 | 2 | US-08-956-307B-17 | Sequence 17, Appl | 645 | 48 | 100.0 | 113 | 2 | US-09-581-894A-11 | Sequence 11, Appl |
| 573 | 48 | 100.0 | 76 | 2 | US-08-356-307B-18 | Sequence 18, Appl | 646 | 48 | 100.0 | 114 | 2 | US-09-248-796A-23116 | Sequence 23116, A |
| 574 | 48 | 100.0 | 77 | 2 | US-09-643-597-361 | Sequence 361, App | 647 | 48 | 100.0 | 116 | 2 | US-09-270-767-36280 | Sequence 36280, A |
| 575 | 48 | 100.0 | 77 | 2 | US-09-630-940B-361 | Sequence 361, App | 648 | 48 | 100.0 | 116 | 2 | US-09-270-767-51497 | Sequence 51497, A |
| 576 | 48 | 100.0 | 77 | 2 | US-10-007-700-361 | Sequence 361, App | 649 | 48 | 100.0 | 117 | 2 | US-09-622-613C-22 | Sequence 22, Appl |
| 577 | 48 | 100.0 | 78 | 2 | US-09-248-796A-23216 | Sequence 23216, A | 650 | 48 | 100.0 | 117 | 2 | US-09-581-894A-12 | Sequence 12, Appl |
| 578 | 48 | 100.0 | 78 | 2 | US-09-248-796A-25811 | Sequence 25811, A | 651 | 48 | 100.0 | 118 | 2 | US-09-084-307B-9 | Sequence 9, Appl1 |
| 579 | 48 | 100.0 | 79 | 1 | US-08-448-418-97 | Sequence 97, Appl | 652 | 48 | 100.0 | 118 | 2 | US-09-205-658-120 | Sequence 120, App |
| 580 | 48 | 100.0 | 79 | 2 | US-09-146-979-97 | Sequence 97, Appl | 653 | 48 | 100.0 | 118 | 2 | US-09-581-894A-1 | Sequence 1, Appl1 |
| 581 | 48 | 100.0 | 79 | 2 | US-09-248-796A-27876 | Sequence 27876, A | 654 | 48 | 100.0 | 119 | 2 | US-09-581-894A-10 | Sequence 10, Appl |
| 582 | 48 | 100.0 | 80 | 2 | US-09-174-943-4 | Sequence 4, Appl1 | 655 | 48 | 100.0 | 119 | 2 | US-09-979-338A-32 | Sequence 32, Appl |
| 583 | 48 | 100.0 | 80 | 2 | US-09-084-303B-15 | Sequence 15, Appl | 656 | 48 | 100.0 | 120 | 2 | US-08-341-560B-2 | Sequence 2, Appl1 |
| 584 | 48 | 100.0 | 80 | 2 | US-09-248-796A-15929 | Sequence 15929, A | 657 | 48 | 100.0 | 120 | 2 | US-08-353-940-4 | Sequence 4, Appl1 |
| 585 | 48 | 100.0 | 81 | 1 | US-08-717-169-15 | Sequence 15, Appl | 658 | 48 | 100.0 | 120 | 2 | US-10-162-127-2 | Sequence 2, Appl1 |
| 586 | 48 | 100.0 | 81 | 2 | US-09-228-901A-15 | Sequence 15, Appl | 659 | 48 | 100.0 | 120 | 2 | US-09-581-894A-2 | Sequence 2, Appl1 |
| 587 | 48 | 100.0 | 82 | 2 | US-09-979-338A-27 | Sequence 27, Appl | 660 | 48 | 100.0 | 120 | 4 | PCT-US93-03895-2 | Sequence 2, Appl1 |
| 588 | 48 | 100.0 | 84 | 2 | US-09-270-767-57811 | Sequence 57811, A | 661 | 48 | 100.0 | 121 | 2 | US-08-341-560B-4 | Sequence 4, Appl1 |
| 589 | 48 | 100.0 | 85 | 2 | US-08-772-440-32 | Sequence 32, Appl | 662 | 48 | 100.0 | 121 | 2 | US-08-353-940-4 | Sequence 4, Appl1 |
| 590 | 48 | 100.0 | 85 | 2 | US-09-256-976-82 | Sequence 82, Appl | 663 | 48 | 100.0 | 121 | 2 | US-09-613-303-12 | Sequence 12, Appl |
| 591 | 48 | 100.0 | 85 | 2 | US-09-280-030-65 | Sequence 65, Appl | 664 | 48 | 100.0 | 121 | 2 | US-10-162-127-4 | Sequence 4, Appl1 |
| 592 | 48 | 100.0 | 87 | 1 | US-08-160-670A-7 | Sequence 7, Appl1 | 665 | 48 | 100.0 | 121 | 2 | US-10-267-311-12 | Sequence 12, Appl |
| 593 | 48 | 100.0 | 89 | 1 | US-08-340-812-13 | Sequence 13, Appl | 666 | 48 | 100.0 | 121 | 2 | US-08-931-855B-16 | Sequence 16, Appl |
| 594 | 48 | 100.0 | 89 | 1 | US-08-459-064B-13 | Sequence 13, Appl | 667 | 48 | 100.0 | 121 | 2 | US-09-581-894A-3 | Sequence 3, Appl1 |
| 595 | 48 | 100.0 | 89 | 1 | US-08-460-421A-13 | Sequence 13, Appl | 668 | 48 | 100.0 | 121 | 4 | PCT-US93-03895-4 | Sequence 4, Appl1 |
| 596 | 48 | 100.0 | 89 | 1 | US-08-717-169-7 | Sequence 7, Appl1 | 669 | 48 | 100.0 | 122 | 2 | US-08-956-307B-19 | Sequence 19, Appl |
| 597 | 48 | 100.0 | 89 | 2 | US-09-507-323B-12 | Sequence 12, Appl | 670 | 48 | 100.0 | 122 | 2 | US-09-270-767-42087 | Sequence 42087, A |
| 598 | 48 | 100.0 | 89 | 2 | US-09-228-901A-7 | Sequence 7, Appl1 | 671 | 48 | 100.0 | 124 | 1 | US-08-434-705B-16 | Sequence 16, Appl |
| 599 | 48 | 100.0 | 89 | 2 | US-09-545-894-29 | Sequence 29, Appl | 672 | 48 | 100.0 | 124 | 1 | US-09-086-201-16 | Sequence 16, Appl |
| 600 | 48 | 100.0 | 90 | 2 | US-09-175-713-12 | Sequence 12, Appl | 673 | 48 | 100.0 | 124 | 2 | US-09-042-071-39 | Sequence 39, Appl |
| 601 | 48 | 100.0 | 91 | 2 | US-09-509-391-16 | Sequence 16, Appl | 674 | 48 | 100.0 | 124 | 2 | US-09-270-767-61747 | Sequence 61747, A |
| 602 | 48 | 100.0 | 91 | 2 | US-10-148-306-18 | Sequence 18, Appl | 675 | 48 | 100.0 | 126 | 1 | US-08-268-346A-12 | Sequence 12, Appl |
| 603 | 48 | 100.0 | 92 | 2 | US-09-979-338A-31 | Sequence 31, Appl | 676 | 48 | 100.0 | 127 | 2 | US-08-467-023-188 | Sequence 188, App |
| 604 | 48 | 100.0 | 93 | 2 | US-09-248-796A-24094 | Sequence 24094, A | 677 | 48 | 100.0 | 127 | 2 | US-08-467-023-189 | Sequence 189, App |
| 605 | 48 | 100.0 | 93 | 2 | US-09-509-391-17 | Sequence 17, Appl | 678 | 48 | 100.0 | 127 | 2 | US-08-467-023-190 | Sequence 190, App |
| 606 | 48 | 100.0 | 94 | 2 | US-09-256-976-95 | Sequence 95, Appl | 679 | 48 | 100.0 | 127 | 2 | US-09-481-620A-72 | Sequence 72, Appl |
| 607 | 48 | 100.0 | 94 | 2 | US-09-556-877-89 | Sequence 89, Appl | 680 | 48 | 100.0 | 127 | 2 | US-09-481-620A-72 | Sequence 72, Appl |
| 608 | 48 | 100.0 | 94 | 2 | US-09-620-412C-89 | Sequence 89, Appl | 681 | 48 | 100.0 | 128 | 2 | US-08-467-023-187 | Sequence 187, App |
| 609 | 48 | 100.0 | 94 | 2 | US-09-410-568-89 | Sequence 89, Appl | 682 | 48 | 100.0 | 128 | 2 | US-09-012-097A-42 | Sequence 22, Appl |
| 610 | 48 | 100.0 | 94 | 2 | US-09-598-419-89 | Sequence 89, Appl | 683 | 48 | 100.0 | 128 | 2 | US-09-742-373-9 | Sequence 9, Appl1 |
| 611 | 48 | 100.0 | 94 | 2 | US-09-175-713-13 | Sequence 13, Appl | 684 | 48 | 100.0 | 128 | 2 | US-09-781-804-21 | Sequence 21, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|----------------------|--------------------|-----|----|-------|-----|---|----------------------|--------------------|
| 665 | 48 | 100.0 | 128 | 2 | US-10-394-058-9 | Sequence 9, Appl1 | 758 | 48 | 100.0 | 166 | 2 | US-10-012-896-838 | Sequence 838, App |
| 666 | 48 | 100.0 | 129 | 2 | US-09-556-877-91 | Sequence 91, Appl1 | 759 | 48 | 100.0 | 166 | 2 | US-10-089-019-10 | Sequence 10, Appl1 |
| 667 | 48 | 100.0 | 129 | 2 | US-09-620-412C-91 | Sequence 91, Appl1 | 760 | 48 | 100.0 | 167 | 2 | US-09-507-323B-13 | Sequence 13, Appl1 |
| 668 | 48 | 100.0 | 129 | 2 | US-09-410-568-91 | Sequence 91, Appl1 | 761 | 48 | 100.0 | 167 | 2 | US-09-741-243C-4 | Sequence 4, Appl1 |
| 669 | 48 | 100.0 | 129 | 2 | US-09-598-419-91 | Sequence 91, Appl1 | 762 | 48 | 100.0 | 167 | 2 | US-09-675-922-8 | Sequence 8, Appl1 |
| 680 | 48 | 100.0 | 130 | 2 | US-09-280-030-62 | Sequence 62, Appl1 | 763 | 48 | 100.0 | 167 | 2 | US-10-017-754-1921 | Sequence 1921, Ap |
| 681 | 48 | 100.0 | 130 | 2 | US-09-270-767-39206 | Sequence 39206, A | 764 | 48 | 100.0 | 167 | 2 | US-09-563-768A-30 | Sequence 30, Appl1 |
| 682 | 48 | 100.0 | 130 | 2 | US-09-370-767-54423 | Sequence 54423, A | 765 | 48 | 100.0 | 167 | 2 | US-09-798-338B-10 | Sequence 20, Appl1 |
| 683 | 48 | 100.0 | 131 | 2 | US-09-367-309A-2 | Sequence 2, Appl1 | 766 | 48 | 100.0 | 168 | 2 | US-09-468-647A-27 | Sequence 27, Appl1 |
| 684 | 48 | 100.0 | 132 | 2 | US-09-771-161A-158 | Sequence 158, App | 767 | 48 | 100.0 | 168 | 2 | US-09-468-647A-126 | Sequence 126, App |
| 685 | 48 | 100.0 | 133 | 1 | US-08-268-348A-8 | Sequence 8, Appl1 | 768 | 48 | 100.0 | 170 | 2 | US-09-896-580B-6 | Sequence 6, Appl1 |
| 686 | 48 | 100.0 | 133 | 1 | US-08-268-348A-10 | Sequence 10, Appl1 | 769 | 48 | 100.0 | 170 | 2 | US-10-068-059-4 | Sequence 4, Appl1 |
| 687 | 48 | 100.0 | 133 | 1 | US-09-556-877-304 | Sequence 304, App | 770 | 48 | 100.0 | 171 | 2 | US-09-646-028-9 | Sequence 9, Appl1 |
| 688 | 48 | 100.0 | 133 | 2 | US-09-620-412C-304 | Sequence 304, App | 771 | 48 | 100.0 | 172 | 2 | US-08-860-165-12 | Sequence 12, Appl1 |
| 689 | 48 | 100.0 | 133 | 2 | US-09-598-419-304 | Sequence 304, App | 772 | 48 | 100.0 | 172 | 2 | US-08-860-165-14 | Sequence 14, Appl1 |
| 700 | 48 | 100.0 | 139 | 2 | US-08-856-253-8 | Sequence 8, Appl1 | 773 | 48 | 100.0 | 172 | 2 | US-09-359-382-12 | Sequence 12, Appl1 |
| 701 | 48 | 100.0 | 140 | 2 | US-09-280-030-64 | Sequence 64, Appl1 | 774 | 48 | 100.0 | 172 | 2 | US-09-359-382-14 | Sequence 14, Appl1 |
| 702 | 48 | 100.0 | 140 | 2 | US-09-645-415A-60 | Sequence 60, Appl1 | 775 | 48 | 100.0 | 175 | 2 | US-09-248-796A-16887 | Sequence 16887, A |
| 703 | 48 | 100.0 | 143 | 2 | US-09-674-183-16 | Sequence 16, Appl1 | 776 | 48 | 100.0 | 177 | 2 | US-09-058-483-4 | Sequence 4, Appl1 |
| 704 | 48 | 100.0 | 144 | 2 | US-09-230-421-3 | Sequence 3, Appl1 | 777 | 48 | 100.0 | 177 | 2 | US-09-695-437A-59 | Sequence 59, Appl1 |
| 705 | 48 | 100.0 | 145 | 2 | US-09-640-211A-794 | Sequence 794, App | 778 | 48 | 100.0 | 178 | 2 | US-09-042-071-42 | Sequence 42, Appl1 |
| 706 | 48 | 100.0 | 146 | 2 | US-09-554-765-11 | Sequence 11, Appl1 | 779 | 48 | 100.0 | 178 | 2 | US-09-183-841-2 | Sequence 2, Appl1 |
| 707 | 48 | 100.0 | 146 | 2 | US-09-923-304-9 | Sequence 9, Appl1 | 780 | 48 | 100.0 | 178 | 2 | US-09-409-096-8 | Sequence 8, Appl1 |
| 708 | 48 | 100.0 | 147 | 2 | US-08-122-458D-9 | Sequence 9, Appl1 | 781 | 48 | 100.0 | 178 | 2 | US-09-813-718-6 | Sequence 6, Appl1 |
| 709 | 48 | 100.0 | 147 | 2 | US-09-554-765-10 | Sequence 10, Appl1 | 782 | 48 | 100.0 | 180 | 2 | US-08-772-440-31 | Sequence 31, Appl1 |
| 710 | 48 | 100.0 | 148 | 2 | US-09-828-523A-94 | Sequence 94, Appl1 | 783 | 48 | 100.0 | 180 | 2 | US-09-230-078A-4 | Sequence 4, Appl1 |
| 711 | 48 | 100.0 | 149 | 2 | US-09-646-028-6 | Sequence 6, Appl1 | 784 | 48 | 100.0 | 183 | 2 | US-09-832-659A-4 | Sequence 4, Appl1 |
| 712 | 48 | 100.0 | 149 | 2 | US-09-270-767-38212 | Sequence 38212, A | 785 | 48 | 100.0 | 183 | 2 | US-09-832-658A-2 | Sequence 2, Appl1 |
| 713 | 48 | 100.0 | 149 | 2 | US-09-270-767-53429 | Sequence 53429, A | 786 | 48 | 100.0 | 184 | 2 | US-09-023-082A-10 | Sequence 30, Appl1 |
| 714 | 48 | 100.0 | 149 | 2 | US-09-468-647A-124 | Sequence 124, App | 787 | 48 | 100.0 | 184 | 2 | US-09-248-998-30 | Sequence 30, Appl1 |
| 715 | 48 | 100.0 | 151 | 2 | US-09-646-028-7 | Sequence 7, Appl1 | 788 | 48 | 100.0 | 184 | 2 | US-09-610-651-30 | Sequence 30, Appl1 |
| 716 | 48 | 100.0 | 152 | 2 | US-09-646-028-8 | Sequence 8, Appl1 | 789 | 48 | 100.0 | 184 | 2 | US-09-248-796A-24480 | Sequence 24480, A |
| 717 | 48 | 100.0 | 152 | 2 | US-09-927-738-22 | Sequence 22, Appl1 | 790 | 48 | 100.0 | 184 | 2 | US-09-921-174-20 | Sequence 20, Appl1 |
| 718 | 48 | 100.0 | 153 | 2 | US-09-675-922-2 | Sequence 2, Appl1 | 791 | 48 | 100.0 | 184 | 2 | US-09-345-373-30 | Sequence 30, Appl1 |
| 719 | 48 | 100.0 | 153 | 2 | US-09-563-760A-32 | Sequence 32, Appl1 | 792 | 48 | 100.0 | 184 | 2 | US-10-075-446-30 | Sequence 30, Appl1 |
| 720 | 48 | 100.0 | 153 | 2 | US-09-798-338B-14 | Sequence 14, Appl1 | 793 | 48 | 100.0 | 185 | 2 | US-09-058-483-10 | Sequence 10, Appl1 |
| 721 | 48 | 100.0 | 155 | 2 | US-10-237-551-181 | Sequence 181, App | 794 | 48 | 100.0 | 185 | 2 | US-09-921-144-18 | Sequence 18, Appl1 |
| 722 | 48 | 100.0 | 156 | 2 | US-09-270-767-40443 | Sequence 40443, A | 795 | 48 | 100.0 | 186 | 2 | US-09-270-767-38819 | Sequence 38819, A |
| 723 | 48 | 100.0 | 156 | 2 | US-09-270-767-55659 | Sequence 55659, A | 796 | 48 | 100.0 | 186 | 2 | US-09-828-523A-58 | Sequence 58, Appl1 |
| 724 | 48 | 100.0 | 156 | 2 | US-09-586-937-69 | Sequence 69, Appl1 | 797 | 48 | 100.0 | 188 | 2 | US-09-561-500-13 | Sequence 13, Appl1 |
| 725 | 48 | 100.0 | 157 | 2 | US-08-875-533-46 | Sequence 46, Appl1 | 798 | 48 | 100.0 | 191 | 2 | US-09-561-528-13 | Sequence 13, Appl1 |
| 726 | 48 | 100.0 | 157 | 2 | US-09-675-922-4 | Sequence 4, Appl1 | 799 | 48 | 100.0 | 191 | 2 | US-09-561-528-13 | Sequence 13, Appl1 |
| 727 | 48 | 100.0 | 157 | 2 | US-09-563-760A-34 | Sequence 34, Appl1 | 800 | 48 | 100.0 | 191 | 2 | US-09-561-528-13 | Sequence 13, Appl1 |
| 728 | 48 | 100.0 | 157 | 2 | US-09-798-338B-16 | Sequence 16, Appl1 | 801 | 48 | 100.0 | 191 | 2 | US-09-561-528-13 | Sequence 13, Appl1 |
| 729 | 48 | 100.0 | 158 | 2 | US-08-875-533-47 | Sequence 47, Appl1 | 802 | 48 | 100.0 | 191 | 2 | US-09-998-831-13 | Sequence 13, Appl1 |
| 730 | 48 | 100.0 | 159 | 2 | US-08-991-890-4 | Sequence 4, Appl1 | 803 | 48 | 100.0 | 191 | 2 | US-09-561-005-13 | Sequence 13, Appl1 |
| 731 | 48 | 100.0 | 159 | 2 | US-08-856-253-2 | Sequence 2, Appl1 | 804 | 48 | 100.0 | 191 | 2 | US-09-562-245-13 | Sequence 13, Appl1 |
| 732 | 48 | 100.0 | 159 | 2 | US-09-166-966E-8 | Sequence 8, Appl1 | 805 | 48 | 100.0 | 191 | 2 | US-10-148-306-19 | Sequence 19, Appl1 |
| 733 | 48 | 100.0 | 159 | 2 | US-09-518-842-4 | Sequence 4, Appl1 | 806 | 48 | 100.0 | 192 | 2 | US-09-771-161A-159 | Sequence 159, App |
| 734 | 48 | 100.0 | 160 | 2 | US-09-355-700-59 | Sequence 59, Appl1 | 807 | 48 | 100.0 | 193 | 2 | US-09-874-923-119 | Sequence 119, App |
| 735 | 48 | 100.0 | 160 | 2 | US-09-534-376A-59 | Sequence 59, Appl1 | 808 | 48 | 100.0 | 195 | 2 | US-09-042-071-40 | Sequence 40, Appl1 |
| 736 | 48 | 100.0 | 160 | 2 | US-10-089-019-18 | Sequence 18, Appl1 | 809 | 48 | 100.0 | 195 | 2 | US-08-849-634B-3 | Sequence 3, Appl1 |
| 737 | 48 | 100.0 | 161 | 2 | US-09-636-215-846 | Sequence 846, App | 810 | 48 | 100.0 | 195 | 2 | US-09-546-04-5 | Sequence 5, Appl1 |
| 738 | 48 | 100.0 | 161 | 2 | US-09-685-166A-846 | Sequence 846, App | 811 | 48 | 100.0 | 197 | 2 | US-09-248-796A-23752 | Sequence 23752, A |
| 739 | 48 | 100.0 | 161 | 2 | US-09-679-426-846 | Sequence 846, App | 812 | 48 | 100.0 | 198 | 1 | US-08-642-253-111 | Sequence 111, App |
| 740 | 48 | 100.0 | 161 | 2 | US-09-759-143-846 | Sequence 846, App | 813 | 48 | 100.0 | 198 | 1 | US-08-397-633A-91 | Sequence 91, Appl1 |
| 741 | 48 | 100.0 | 161 | 2 | US-09-651-236-846 | Sequence 846, App | 814 | 48 | 100.0 | 198 | 1 | US-08-397-633A-52 | Sequence 52, Appl1 |
| 742 | 48 | 100.0 | 161 | 2 | US-09-657-279-846 | Sequence 846, App | 815 | 48 | 100.0 | 198 | 1 | US-09-248-796A-17554 | Sequence 17554, A |
| 743 | 48 | 100.0 | 161 | 2 | US-10-012-896-846 | Sequence 846, App | 816 | 48 | 100.0 | 201 | 2 | US-09-695-437A-61 | Sequence 61, Appl1 |
| 744 | 48 | 100.0 | 161 | 2 | US-10-007-700-423 | Sequence 423, App | 817 | 48 | 100.0 | 202 | 2 | US-09-556-877-92 | Sequence 92, Appl1 |
| 745 | 48 | 100.0 | 162 | 2 | US-09-921-144-16 | Sequence 16, Appl1 | 818 | 48 | 100.0 | 202 | 2 | US-09-620-412C-92 | Sequence 92, Appl1 |
| 746 | 48 | 100.0 | 163 | 2 | US-09-675-922-6 | Sequence 6, Appl1 | 819 | 48 | 100.0 | 202 | 2 | US-09-410-568-92 | Sequence 92, Appl1 |
| 747 | 48 | 100.0 | 163 | 2 | US-09-248-796A-22113 | Sequence 22113, A | 820 | 48 | 100.0 | 202 | 2 | US-09-598-419-92 | Sequence 92, Appl1 |
| 748 | 48 | 100.0 | 163 | 2 | US-09-921-144-14 | Sequence 14, Appl1 | 821 | 48 | 100.0 | 203 | 2 | US-09-270-767-35326 | Sequence 35326, A |
| 749 | 48 | 100.0 | 163 | 2 | US-09-563-760A-24 | Sequence 24, Appl1 | 822 | 48 | 100.0 | 203 | 2 | US-09-270-767-50543 | Sequence 50543, A |
| 750 | 48 | 100.0 | 163 | 2 | US-09-798-338B-18 | Sequence 18, Appl1 | 823 | 48 | 100.0 | 206 | 2 | US-09-183-861-26 | Sequence 26, Appl1 |
| 751 | 48 | 100.0 | 166 | 2 | US-09-646-028-5 | Sequence 5, Appl1 | 824 | 48 | 100.0 | 206 | 2 | US-09-022-765-26 | Sequence 26, Appl1 |
| 752 | 48 | 100.0 | 166 | 2 | US-09-636-215-838 | Sequence 838, App | 825 | 48 | 100.0 | 206 | 2 | US-09-551-974A-26 | Sequence 26, Appl1 |
| 753 | 48 | 100.0 | 166 | 2 | US-09-685-166A-838 | Sequence 838, App | 826 | 48 | 100.0 | 206 | 2 | US-09-565-501A-26 | Sequence 26, Appl1 |
| 754 | 48 | 100.0 | 166 | 2 | US-09-679-426-838 | Sequence 838, App | 827 | 48 | 100.0 | 206 | 2 | US-09-639-206A-26 | Sequence 26, Appl1 |
| 755 | 48 | 100.0 | 166 | 2 | US-09-759-143-838 | Sequence 838, App | 828 | 48 | 100.0 | 206 | 2 | US-09-874-923-26 | Sequence 26, Appl1 |
| 756 | 48 | 100.0 | 166 | 2 | US-09-651-236-838 | Sequence 838, App | 829 | 48 | 100.0 | 206 | 2 | US-09-270-767-558211 | Sequence 58211, A |
| 757 | 48 | 100.0 | 166 | 2 | US-09-657-279-838 | Sequence 838, App | 830 | 48 | 100.0 | 206 | 2 | US-08-798-841-26 | Sequence 26, Appl1 |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|---------------------|-------------------|-----|----|-------|-----|---|----------------------|--------------------|
| 831 | 48 | 100.0 | 207 | 2 | US-09-702-705-1667 | Sequence 1667, Ap | 904 | 48 | 100.0 | 225 | 2 | US-09-456-090A-98 | Sequence 98, Appl |
| 832 | 48 | 100.0 | 207 | 2 | US-09-736-457-1667 | Sequence 1667, Ap | 905 | 48 | 100.0 | 225 | 2 | US-09-456-090A-100 | Sequence 100, App |
| 833 | 48 | 100.0 | 207 | 2 | US-09-614-124B-1667 | Sequence 1667, Ap | 906 | 48 | 100.0 | 225 | 2 | US-09-456-090A-102 | Sequence 102, App |
| 834 | 48 | 100.0 | 207 | 2 | US-09-671-325-1667 | Sequence 1667, Ap | 907 | 48 | 100.0 | 225 | 2 | US-09-456-090A-106 | Sequence 106, App |
| 835 | 48 | 100.0 | 207 | 2 | US-09-658-824-1667 | Sequence 1667, Ap | 908 | 48 | 100.0 | 225 | 2 | US-09-456-090A-108 | Sequence 108, App |
| 836 | 48 | 100.0 | 207 | 2 | US-10-017-754-1667 | Sequence 1667, Ap | 909 | 48 | 100.0 | 225 | 2 | US-09-456-090A-110 | Sequence 110, App |
| 837 | 48 | 100.0 | 207 | 2 | US-10-017-754-1913 | Sequence 1913, Ap | 910 | 48 | 100.0 | 225 | 2 | US-09-453-234-54 | Sequence 54, Appl |
| 838 | 48 | 100.0 | 207 | 2 | US-09-651-563-1667 | Sequence 1667, Ap | 911 | 48 | 100.0 | 225 | 2 | US-09-453-234-56 | Sequence 56, Appl |
| 839 | 48 | 100.0 | 207 | 2 | US-09-771-161A-160 | Sequence 160, App | 912 | 48 | 100.0 | 225 | 2 | US-09-453-234-58 | Sequence 58, Appl |
| 840 | 48 | 100.0 | 209 | 2 | US-09-166-966B-11 | Sequence 11, Appl | 913 | 48 | 100.0 | 225 | 2 | US-09-453-234-60 | Sequence 60, Appl |
| 841 | 48 | 100.0 | 210 | 1 | US-08-234-783-2 | Sequence 2, Appl | 914 | 48 | 100.0 | 225 | 2 | US-09-453-234-62 | Sequence 62, Appl |
| 842 | 48 | 100.0 | 210 | 1 | US-08-456-907-2 | Sequence 28, Appl | 915 | 48 | 100.0 | 225 | 2 | US-09-453-234-66 | Sequence 66, Appl |
| 843 | 48 | 100.0 | 210 | 1 | US-08-612-973-28 | Sequence 28, Appl | 916 | 48 | 100.0 | 225 | 2 | US-09-453-234-68 | Sequence 68, Appl |
| 844 | 48 | 100.0 | 210 | 2 | US-08-927-597-28 | Sequence 28, Appl | 917 | 48 | 100.0 | 225 | 2 | US-09-453-234-70 | Sequence 70, Appl |
| 845 | 48 | 100.0 | 210 | 2 | US-08-928-757-28 | Sequence 28, Appl | 918 | 48 | 100.0 | 225 | 2 | US-09-453-234-92 | Sequence 92, Appl |
| 846 | 48 | 100.0 | 210 | 4 | PCT-US95-05523-2 | Sequence 2, Appl | 919 | 48 | 100.0 | 225 | 2 | US-09-453-234-94 | Sequence 94, Appl |
| 847 | 48 | 100.0 | 211 | 2 | US-08-856-253-4 | Sequence 4, Appl | 920 | 48 | 100.0 | 225 | 2 | US-09-453-234-96 | Sequence 96, Appl |
| 848 | 48 | 100.0 | 211 | 2 | US-09-612-314A-46 | Sequence 46, Appl | 921 | 48 | 100.0 | 225 | 2 | US-09-453-234-98 | Sequence 98, Appl |
| 849 | 48 | 100.0 | 214 | 2 | US-09-632-553-1 | Sequence 1, Appl | 922 | 48 | 100.0 | 225 | 2 | US-09-453-234-100 | Sequence 100, App |
| 850 | 48 | 100.0 | 214 | 2 | US-09-693-156A-1 | Sequence 46, Appl | 923 | 48 | 100.0 | 225 | 2 | US-09-453-234-102 | Sequence 102, App |
| 851 | 48 | 100.0 | 215 | 2 | US-09-198-723A-46 | Sequence 46, Appl | 924 | 48 | 100.0 | 225 | 2 | US-09-453-234-106 | Sequence 106, App |
| 852 | 48 | 100.0 | 215 | 2 | US-09-198-723A-50 | Sequence 50, Appl | 925 | 48 | 100.0 | 225 | 2 | US-09-453-234-108 | Sequence 108, App |
| 853 | 48 | 100.0 | 215 | 2 | US-09-198-723A-53 | Sequence 53, Appl | 926 | 48 | 100.0 | 225 | 2 | US-09-453-234-110 | Sequence 110, App |
| 854 | 48 | 100.0 | 215 | 2 | US-09-198-723A-57 | Sequence 57, Appl | 927 | 48 | 100.0 | 226 | 2 | US-08-865-468-1 | Sequence 1, Appl |
| 855 | 48 | 100.0 | 215 | 2 | US-09-684-881-46 | Sequence 46, Appl | 928 | 48 | 100.0 | 226 | 2 | US-08-898-649-1 | Sequence 1, Appl |
| 856 | 48 | 100.0 | 215 | 2 | US-09-684-881-50 | Sequence 50, Appl | 929 | 48 | 100.0 | 227 | 2 | US-09-485-885-16 | Sequence 16, Appl |
| 857 | 48 | 100.0 | 215 | 2 | US-09-684-881-53 | Sequence 53, Appl | 930 | 48 | 100.0 | 227 | 2 | US-09-485-885-19 | Sequence 19, Appl |
| 858 | 48 | 100.0 | 215 | 2 | US-09-684-881-57 | Sequence 57, Appl | 931 | 48 | 100.0 | 228 | 2 | US-09-248-796A-15127 | Sequence 15127, A |
| 859 | 48 | 100.0 | 215 | 2 | US-09-949-016-6554 | Sequence 6554, Ap | 932 | 48 | 100.0 | 229 | 2 | US-09-546-043-8 | Sequence 8, Appl |
| 860 | 48 | 100.0 | 216 | 2 | US-09-198-723A-1 | Sequence 1, Appl | 933 | 48 | 100.0 | 230 | 2 | US-09-485-737B-102 | Sequence 102, Appl |
| 861 | 48 | 100.0 | 216 | 2 | US-09-198-723A-2 | Sequence 2, Appl | 934 | 48 | 100.0 | 230 | 2 | US-09-248-796A-21362 | Sequence 21362, A |
| 862 | 48 | 100.0 | 216 | 2 | US-09-198-723A-3 | Sequence 3, Appl | 935 | 48 | 100.0 | 230 | 2 | US-10-071-485-102 | Sequence 102, App |
| 863 | 48 | 100.0 | 216 | 2 | US-09-198-723A-4 | Sequence 4, Appl | 936 | 48 | 100.0 | 231 | 2 | US-09-287-849-28 | Sequence 28, Appl |
| 864 | 48 | 100.0 | 216 | 2 | US-09-198-723A-5 | Sequence 5, Appl | 937 | 48 | 100.0 | 231 | 2 | US-09-324-258-20 | Sequence 20, Appl |
| 865 | 48 | 100.0 | 216 | 2 | US-09-198-723A-6 | Sequence 6, Appl | 938 | 48 | 100.0 | 233 | 1 | US-08-480-753-2 | Sequence 2, Appl |
| 866 | 48 | 100.0 | 216 | 2 | US-09-198-723A-7 | Sequence 7, Appl | 939 | 48 | 100.0 | 233 | 2 | US-09-041-889-9 | Sequence 9, Appl |
| 867 | 48 | 100.0 | 216 | 2 | US-09-198-723A-8 | Sequence 8, Appl | 940 | 48 | 100.0 | 233 | 2 | US-08-837-058-9 | Sequence 9, Appl |
| 868 | 48 | 100.0 | 216 | 2 | US-09-198-723A-9 | Sequence 9, Appl | 941 | 48 | 100.0 | 233 | 2 | US-09-417-264-9 | Sequence 9, Appl |
| 869 | 48 | 100.0 | 216 | 2 | US-09-198-723A-10 | Sequence 10, Appl | 942 | 48 | 100.0 | 233 | 2 | US-09-324-258-16 | Sequence 16, Appl |
| 870 | 48 | 100.0 | 216 | 2 | US-09-684-881-1 | Sequence 1, Appl | 943 | 48 | 100.0 | 234 | 2 | US-09-009-217-2 | Sequence 2, Appl |
| 871 | 48 | 100.0 | 216 | 2 | US-09-684-881-2 | Sequence 2, Appl | 944 | 48 | 100.0 | 234 | 2 | US-09-009-217-3 | Sequence 3, Appl |
| 872 | 48 | 100.0 | 216 | 2 | US-09-684-881-3 | Sequence 3, Appl | 945 | 48 | 100.0 | 234 | 2 | US-09-009-656-2 | Sequence 2, Appl |
| 873 | 48 | 100.0 | 216 | 2 | US-09-684-881-4 | Sequence 4, Appl | 946 | 48 | 100.0 | 234 | 2 | US-09-009-656-3 | Sequence 3, Appl |
| 874 | 48 | 100.0 | 216 | 2 | US-09-684-881-5 | Sequence 5, Appl | 947 | 48 | 100.0 | 235 | 2 | US-09-009-217-6 | Sequence 6, Appl |
| 875 | 48 | 100.0 | 216 | 2 | US-09-684-881-6 | Sequence 6, Appl | 948 | 48 | 100.0 | 235 | 2 | US-09-009-656-6 | Sequence 6, Appl |
| 876 | 48 | 100.0 | 216 | 2 | US-09-684-881-7 | Sequence 7, Appl | 949 | 48 | 100.0 | 235 | 2 | US-09-485-737B-93 | Sequence 93, Appl |
| 877 | 48 | 100.0 | 216 | 2 | US-09-684-881-8 | Sequence 8, Appl | 950 | 48 | 100.0 | 235 | 2 | US-10-071-485-93 | Sequence 93, Appl |
| 878 | 48 | 100.0 | 216 | 2 | US-09-684-881-9 | Sequence 9, Appl | 951 | 48 | 100.0 | 236 | 2 | US-09-009-217-7 | Sequence 7, Appl |
| 879 | 48 | 100.0 | 216 | 2 | US-09-684-881-10 | Sequence 10, Appl | 952 | 48 | 100.0 | 236 | 2 | US-09-009-656-7 | Sequence 7, Appl |
| 880 | 48 | 100.0 | 219 | 2 | US-09-674-183-14 | Sequence 14, Appl | 953 | 48 | 100.0 | 236 | 2 | US-09-456-090A-64 | Sequence 64, Appl |
| 881 | 48 | 100.0 | 219 | 1 | US-08-621-081A-16 | Sequence 16, Appl | 954 | 48 | 100.0 | 236 | 2 | US-09-456-090A-104 | Sequence 104, App |
| 882 | 48 | 100.0 | 220 | 2 | US-09-485-885-1 | Sequence 1, Appl | 955 | 48 | 100.0 | 236 | 2 | US-09-453-234-64 | Sequence 64, App |
| 883 | 48 | 100.0 | 220 | 2 | US-09-485-885-8 | Sequence 8, Appl | 956 | 48 | 100.0 | 236 | 2 | US-09-453-234-104 | Sequence 104, App |
| 884 | 48 | 100.0 | 220 | 2 | US-09-270-767-61056 | Sequence 61056, A | 957 | 48 | 100.0 | 238 | 2 | US-10-358-790-2 | Sequence 2, Appl |
| 885 | 48 | 100.0 | 221 | 1 | US-08-621-081A-19 | Sequence 19, Appl | 958 | 48 | 100.0 | 238 | 2 | US-10-197-720-124 | Sequence 124, App |
| 886 | 48 | 100.0 | 224 | 2 | US-09-636-215-825 | Sequence 825, App | 959 | 48 | 100.0 | 239 | 2 | US-09-485-885-12 | Sequence 12, Appl |
| 887 | 48 | 100.0 | 224 | 2 | US-09-685-166A-825 | Sequence 825, App | 960 | 48 | 100.0 | 240 | 2 | US-09-485-737B-91 | Sequence 91, Appl |
| 888 | 48 | 100.0 | 224 | 2 | US-09-679-426-825 | Sequence 825, App | 961 | 48 | 100.0 | 240 | 2 | US-09-435-054A-10 | Sequence 10, Appl |
| 889 | 48 | 100.0 | 224 | 2 | US-09-759-143-825 | Sequence 825, App | 962 | 48 | 100.0 | 240 | 2 | US-10-071-485-91 | Sequence 91, Appl |
| 890 | 48 | 100.0 | 224 | 2 | US-09-651-236-825 | Sequence 825, App | 963 | 48 | 100.0 | 241 | 2 | US-09-651-236-842 | Sequence 842, App |
| 891 | 48 | 100.0 | 224 | 2 | US-09-657-279-825 | Sequence 825, App | 964 | 48 | 100.0 | 241 | 2 | US-09-657-279-842 | Sequence 842, App |
| 892 | 48 | 100.0 | 224 | 2 | US-10-012-896-825 | Sequence 825, App | 965 | 48 | 100.0 | 241 | 2 | US-10-012-896-842 | Sequence 842, App |
| 893 | 48 | 100.0 | 225 | 2 | US-09-456-090A-54 | Sequence 54, App | 966 | 48 | 100.0 | 241 | 2 | US-09-679-426-842 | Sequence 842, App |
| 894 | 48 | 100.0 | 225 | 2 | US-09-456-090A-56 | Sequence 56, App | 967 | 48 | 100.0 | 241 | 2 | US-09-759-143-842 | Sequence 842, App |
| 895 | 48 | 100.0 | 225 | 2 | US-09-456-090A-58 | Sequence 58, App | 968 | 48 | 100.0 | 241 | 2 | US-09-651-236-842 | Sequence 842, App |
| 896 | 48 | 100.0 | 225 | 2 | US-09-456-090A-60 | Sequence 60, App | 969 | 48 | 100.0 | 241 | 2 | US-09-657-279-842 | Sequence 842, App |
| 897 | 48 | 100.0 | 225 | 2 | US-09-456-090A-62 | Sequence 62, App | 970 | 48 | 100.0 | 242 | 2 | US-10-012-896-842 | Sequence 842, App |
| 898 | 48 | 100.0 | 225 | 2 | US-09-456-090A-66 | Sequence 66, App | 971 | 48 | 100.0 | 242 | 2 | US-09-167-434-8 | Sequence 8, Appl |
| 899 | 48 | 100.0 | 225 | 2 | US-09-456-090A-68 | Sequence 68, App | 972 | 48 | 100.0 | 242 | 2 | US-08-853-755-8 | Sequence 8, Appl |
| 900 | 48 | 100.0 | 225 | 2 | US-09-456-090A-70 | Sequence 70, App | 973 | 48 | 100.0 | 243 | 2 | US-09-167-434-9 | Sequence 9, Appl |
| 901 | 48 | 100.0 | 225 | 2 | US-09-456-090A-92 | Sequence 92, App | 974 | 48 | 100.0 | 243 | 2 | US-08-853-755-9 | Sequence 9, Appl |
| 902 | 48 | 100.0 | 225 | 2 | US-09-456-090A-94 | Sequence 94, App | 975 | 48 | 100.0 | 243 | 2 | US-09-828-523A-50 | Sequence 50, Appl |
| 903 | 48 | 100.0 | 225 | 2 | US-09-456-090A-96 | Sequence 96, App | 976 | 48 | 100.0 | 244 | 1 | US-08-480-755-4 | Sequence 4, Appl |

977 48 100.0 246 2 US-09-167-434-11 Sequence 11, Appl
978 48 100.0 246 2 US-08-853-755-11 Sequence 11, Appl
979 48 100.0 246 2 US-09-546-043-6 Sequence 6, Appl
980 48 100.0 246 2 US-09-248-796A-16241 Sequence 16241, A
981 48 100.0 248 2 US-08-341-560B-8 Sequence 8, Appl
982 48 100.0 248 2 US-08-353-940-8 Sequence 8, Appl
983 48 100.0 248 2 US-09-649-063-23 Sequence 23, Appl
984 48 100.0 248 2 US-10-162-127-8 Sequence 8, Appl
985 48 100.0 248 4 PCT-US93-03895-8 Sequence 8, Appl
986 48 100.0 249 1 US-08-155-171B-32 Sequence 32, Appl
987 48 100.0 249 1 US-08-435-998-17 Sequence 32, Appl
988 48 100.0 249 2 US-09-324-258-17 Sequence 17, Appl
989 48 100.0 250 2 US-08-341-560B-6 Sequence 6, Appl
990 48 100.0 250 2 US-08-353-940-6 Sequence 6, Appl
991 48 100.0 250 2 US-10-162-127-6 Sequence 6, Appl
992 48 100.0 250 1 PCT-US93-03895-6 Sequence 6, Appl
993 48 100.0 251 1 US-08-397-633A-74 Sequence 74, Appl
994 48 100.0 253 2 US-09-270-767-42427 Sequence 42427, A
995 48 100.0 254 1 US-08-792-824-4 Sequence 4, Appl
996 48 100.0 254 1 US-08-792-824-7 Sequence 7, Appl
997 48 100.0 254 1 US-08-792-824-10 Sequence 10, Appl
998 48 100.0 254 1 US-08-792-824-13 Sequence 13, Appl
999 48 100.0 254 2 US-09-167-434-7 Sequence 7, Appl
1000 48 100.0 254 2 US-08-853-755-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-160-670A-6
; Sequence 6, Application US/08160670A
; Patent No. 5449758
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Protein Size Marker Ladder
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,670A
; FILING DATE: 12/2/93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bismond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.2580000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: both
US-08-160-670A-6

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||

Db 1 HHHHHH 6

RESULT 2
US-08-140-222-1
; Sequence 1, Application US/08140222
; Patent No. 5470952
; GENERAL INFORMATION:
; APPLICANT: Stahl, et al.
; TITLE OF INVENTION: CNF Family Antagonists
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,222
; FILING DATE: 20-OCT-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempner Ph.D., Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-347-2113
; TELEFAX: 914-347-2113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-140-222-1

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||

Db 1 HHHHHH 6

RESULT 3
US-08-131-365B-48
; Sequence 48, Application US/08131365B
; Patent No. 5527690
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Briggs, Michael R.
; APPLICANT: Wang, Xisodong
; APPLICANT: Goldstein, Joseph L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
; TO STEROL AND REGULATORY ELEMENT BINDING
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
; COMPUTER READABLE FORM:

```
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/131,365B
/ FILING DATE: 01-OCT-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parker, David L.
/ REGISTRATION NUMBER: 32,165
/ REFERENCE/DOCKET NUMBER: UTSD:372/PAR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (512) 474-7577
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-131-365B-48

Query Match          100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6

RESULT 4
US-08-469-486-47
/ Sequence 47, Application US/08469486
/ Patent No. 5739281
/ GENERAL INFORMATION:
/ APPLICANT: Thoenes, Hans Christian
/ APPLICANT: Holter, Thor Las
/ APPLICANT: Etzerodt, Michael
/ TITLE OF INVENTION: Improved method for the refolding of
/ TITLE OF INVENTION: proteins
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flinn & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version
/ SOFTWARE: #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/469,486
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/192,060
/ FILING DATE: February 4, 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paul T. Clark
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 06363/002001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617 542 5070
/ TELEFAX: 617 542 8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 47:
```

```
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-469-486-47

Query Match          100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6

RESULT 5
US-08-460-343B-51
/ Sequence 51, Application US/08460343B
/ Patent No. 5741664
/ GENERAL INFORMATION:
/ APPLICANT: Marcus D. Ballinger and James A. Wells
/ TITLE OF INVENTION: SUBSTITUTED VARIANTS OF CLEAVING
/ TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
/ NUMBER OF SEQUENCES: 74
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/460,343B
/ FILING DATE: 01-Jun-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/398028
/ FILING DATE: 03-mar-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Kuflinec, Jeffrey S.
/ REGISTRATION NUMBER: 36,575
/ REFERENCE/DOCKET NUMBER: P0936C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-8228
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: linear
US-08-460-343B-51

Query Match          100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6

RESULT 6
US-08-299-567-1
/ Sequence 1, Application US/08299567
/ Patent No. 5747033
/ GENERAL INFORMATION:
```

APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
TITLE OF INVENTION: ACTIVITY OF BPH FAMILY LIGANDS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,567
FILING DATE: 01-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kempster, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-299-567-1

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 7
US-08-398-028B-51
Sequence 51, Application US/08398028B
Patent No. 5780285
GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,028B
FILING DATE: 03-Mar-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kudinec, Jeffrey S.
REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0936
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8228
TELEFAX: 650/952-9891
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-028B-51

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 8
US-08-660-626-4
Sequence 4, Application US/08660626
Patent No. 5789655
GENERAL INFORMATION:
APPLICANT: Stanley B. Frusiner
APPLICANT: Glenn C. Telling
APPLICANT: Fred E. Cohen
APPLICANT: Michael R. Scott
TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
TITLE OF INVENTION: EPTROPE-TAGGED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Asciii
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,626
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Valeta Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07532/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-660-626-4

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
DB 1 HHHHH 6

RESULT 9

US-08-434-705B-17
; Sequence 17, Application US/08434705B
; Patent No. 5798258
; GENERAL INFORMATION:
; APPLICANT: Douglas Ph.D., James
; TITLE OF INVENTION: CART PROTEIN AND DNA ENCODING THEREFOR
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis K. Shelton
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,705B
; FILING DATE: May 4, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: OHSU18446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-434-705B-17

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 10
US-08-470-837-22
; Sequence 22, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimmi, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 1150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-837-22

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 11
US-08-472-244-14
; Sequence 14, Application US/08472244
; Patent No. 5821088
; GENERAL INFORMATION:
; APPLICANT: Darzins, Aldis
; APPLICANT: Whitehead, Stephen
; APPLICANT: Hruby, Dennis E.
; TITLE OF INVENTION: Use of Gram-Positive Bacteria to Express
; TITLE OF INVENTION: Recombinant Proteins
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,244
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 016921-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-472-244-14

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
| | | | |
DB 1 HHHHH 6

RESULT 12

US-08-504-265B-51
; Sequence 51, Application US/08504265B
; Patent No. 5837516
; GENERAL INFORMATION:
; APPLICANT: Marcue D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
; TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/504,265B
; FILING DATE: 19-Jul-1995
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398028
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0936P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8228
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ. ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-504-265B-51
Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
| | | | |
DB 1 HHHHH 6

RESULT 13

US-08-623-833B-16
; Sequence 16, Application US/08623833B
; Patent No. 5866683

; GENERAL INFORMATION:
; APPLICANT: SHIMURA, Kiyohito
; APPLICANT: KASAI, Kenichi
; APPLICANT: MATSUMOTO, Hiroyuki
; APPLICANT: TAKAMOTO, Hiroyoshi
; TITLE OF INVENTION: ISOELECTRIC POINT MARKERS FOR
; TITLE OF INVENTION: ISOELECTRIC FOCUSING WITH FLUORESCENCE DETECTION
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Suto, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/623,833B
; FILING DATE: 29-MAR-1996
; CLASSIFICATION: 530

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 076863/1995
; FILING DATE: 31-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 271196/1995
; FILING DATE: 19-OCT-1995

INFORMATION FOR SEQ. ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acid
; TYPE: amino acid
; TOPOLOGY: linear

US-08-623-833B-16
MOLECULE TYPE: peptide

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
| | | | |
DB 1 HHHHH 6

RESULT 14
US-08-652-507-8
; Sequence 8, Application US/08652507
; Patent No. 5876691

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 5876691th Glebe Road, 8th floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,507
; FILING DATE: 02-Jul-1996
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 117-211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ. ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-507-8

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
1 HHHHH 6

RESULT 15
US-08-668-123-48
Sequence 48, Application US/08668123
Patent No. 5891631

GENERAL INFORMATION:
APPLICANT: Brown, Michael S.
APPLICANT: Briggs, Michael R.
APPLICANT: Wang, Xiaodong
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TO STEROL REGULATORY ELEMENT BINDING
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,123
CLASSIFICATION: 435
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/131,365
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSD:372/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-668-123-48

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
1 HHHHH 6

RESULT 16
US-08-469-658-47

Sequence 47, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Th egeren, Hans Christian
APPLICANT: Holter, Thor Lae
APPLICANT: Etzeid, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOOLDING OF
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-469-658-47

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
1 HHHHH 6

RESULT 17
US-09-086-201-17
Sequence 17, Application US/09086201
Patent No. 5969103
GENERAL INFORMATION:
APPLICANT: Douglas Ph. D., James
TITLE OF INVENTION: CART PROTEIN AND DNA ENCODING THEREFOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis K. Shelton
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,201
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,705
FILING DATE: May 4, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: OHSU18446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-09-086-201-17

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 18
US-08-591-196-57
Sequence 57, Application US/08591196
Patent No. 5977316
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,196
FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-591-196-57

Query Match 100.0%; Score 48; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 19
US-08-996-139-18
Sequence 18, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-18

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 20
US-08-481-435-42
; Sequence 42, Application US/08481435
; Patent No. 6027906
; GENERAL INFORMATION:
; APPLICANT: Baiganesh, Tanjore S
; APPLICANT: Town, Christine
; TITLE OF INVENTION: No. 6027906el Polypeptides
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,435
; FILING DATE: 10-JUL-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IN 580/MMS/94
; FILING DATE: 01-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9404072-2
; FILING DATE: 24-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 354-8113
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-481-435-42

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 21
US-08-772-440-28
; Sequence 28, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Arizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas

COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-772-440-28

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 22
US-09-267-031-18
; Sequence 18, Application US/09267031
; Patent No. 6137031
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yuelin
; APPLICANT: Kinkema, Mark
; APPLICANT: Dong, Ximian
; APPLICANT: Ronald, Pamela
; APPLICANT: Chern, Mawsheng
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: DNA Binding Proteins That Interact With NPRI
; FILE REFERENCE: 023070-092500US
; CURRENT APPLICATION NUMBER: US/09/267,031
; CURRENT FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: (His)6-tag
US-09-267-031-18

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 23
US-09-398-341-1
; Sequence 1, Application US/09398341

Patent No. 6146842
GENERAL INFORMATION:
APPLICANT: Josiah, Serene
APPLICANT: Boischall, Michael
TITLE OF INVENTION: High-Throughput Screening Assays Utilizing Metal-
TITLE OF INVENTION: Chelate Capture
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: ONE POST OFFICE SQUARE
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,341
FILING DATE: 17-SEP-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-116.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-398-341-1

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
Db 1 HHHHHH 6

RESULT 24
US-09-031-168-4
Sequence 4, Application US/09031168
Patent No. 6150583
GENERAL INFORMATION:
APPLICANT: Stanley B. Prusiner
APPLICANT: Glenn C. Telling
APPLICANT: Fred E. Cohen
APPLICANT: Michael R. Scott
TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING
TITLE OF INVENTION: EPIPOPE-TAGGED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascliti
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,168

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,626
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Valecia Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07532/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-031-168-4

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
Db 1 HHHHHH 6

RESULT 25
US-08-789-333F-99
Sequence 99, Application US/08789333F
Patent No. 6153380
GENERAL INFORMATION:
APPLICANT: Rothenberg, S. M.
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
FILE REFERENCE: A642601DJBMSDS
CURRENT APPLICATION NUMBER: US/08/789,333F
CURRENT FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: 08/589,108
PRIOR FILING DATE: 1996-01-23
PRIOR APPLICATION NUMBER: 08/589,911
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 99
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: histidine tag
US-08-789-333F-99

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||||
Db 1 HHHHHH 6

RESULT 26
US-08-995-659-18
Sequence 18, Application US/0895659
Patent No. 6242213
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Marabkovsky, Eugene

```
/ TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Immunex Corporation, Law Department
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Power Macintosh
/ OPERATING SYSTEM: Apple Operating System 7.5.5
/ SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/995,659
/ FILING DATE: 22 DECEMBER 1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US95/064,671
/ FILING DATE: 14 OCTOBER 1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US95/08/813,509
/ FILING DATE: 07 MARCH 1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US95/08/772,330
/ FILING DATE: 23 DECEMBER 1996
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2852-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-995-659-18

Query Match          100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 27
US-09-142-334-26
/ Sequence 26; Application US/09142334
/ Patent No. 6268485
/ GENERAL INFORMATION:
/ APPLICANT: Faries, Timothy C.
/ APPLICANT: Harrison, Richard A.
/ TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
/ FILE REFERENCE: 4-30443/A/IRU/PCT
/ CURRENT APPLICATION NUMBER: US/09/142,334
/ CURRENT FILING DATE: 1999-04-15
/ EARLIER APPLICATION NUMBER: PCT/GB97/00603
/ EARLIER FILING DATE: 1997-03-04
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: amino acid
/ OTHER INFORMATION: insertion
/ US-09-142-334-26

Query Match          100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 28
US-09-215-649A-18
/ Sequence 18; Application US/09215649A
/ Patent No. 6271349
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, Dirk M.
/ Galibert, Laurent
/ Maraskovsky, Eugene
/ TITLE OF INVENTION: Receptor Activator of NF-kappaB
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Immunex Corporation, Law Department
/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Power Macintosh
/ OPERATING SYSTEM: Apple Operating System 7.5.5
/ SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/215,649A
/ FILING DATE: 17-Dec-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/996,139
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US95/08/813,509
/ FILING DATE: 07 MARCH 1997
/ APPLICATION NUMBER: US95/08/772,330
/ FILING DATE: 23 DECEMBER 1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,693
/ REFERENCE/DOCKET NUMBER: 2851-A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)587-0430
/ TELEFAX: (206)233-0644
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-215-649A-18

Query Match          100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 29
```

US-09-140-084-7
; Sequence 7, Application US/09140084A
; Patent No. 6300065
; GENERAL INFORMATION:
; APPLICANT: Kieke, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: D6061CIP2
; CURRENT APPLICATION NUMBER: US/09/140,084A
; CURRENT FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Epitope Tag
US-09-140-084-7

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 30
US-09-382-950-4
; Sequence 4, Application US/09382950
; Patent No. 6303337
; GENERAL INFORMATION:
; APPLICANT: Rotbschild, Kenneth
; APPLICANT: Gite, Sadanand
; APPLICANT: Olejnik, Jerzy
; TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins
; FILE REFERENCE: AMBER-03879
; CURRENT APPLICATION NUMBER: US/09/382,950
; CURRENT FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial/Unknown
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: ().()
; OTHER INFORMATION: Synthetic
US-09-382-950-4

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 31
US-09-382-736B-5
; Sequence 5, Application US/09382736B
; Patent No. 6306628
; GENERAL INFORMATION:
; APPLICANT: Rotbschild, Kenneth
; APPLICANT: Gite, Sadanand
; APPLICANT: Olejnik, Jerzy
; TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Pro
; FILE REFERENCE: AMBER-03951
; CURRENT APPLICATION NUMBER: US/09/382,736B
; CURRENT FILING DATE: 1999-08-25

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-382-736B-5

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 32
US-08-977-378-2
; Sequence 2, Application US/08977378
; Patent No. 6309842
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Gates, Christopher M.
; Heinkel, Gregory L.
; Lalonde, Guy
; Matheakis, Larry C.
; Paddon, Christopher J.
; Schatz, Peter J.
; TITLE OF INVENTION: Use of Modified Tethers in Screening
; Compound Libraries
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977,378
; FILING DATE: 24-No. 6309842-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,307
; FILING DATE: 03-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16528A-018010US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-977-378-2
Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 33
US-09-353-555-2
; Sequence 2, Application US/09353555
; Patent No. 6329209
; GENERAL INFORMATION:
; APPLICANT: Wagner, Peter
; APPLICANT: No. 6329209K, Steffen
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Ilin, Christian
; TITLE OF INVENTION: Arrays of Protein-Capture Agents and Methods of Use
; FILE REFERENCE: 24406-0006
; CURRENT APPLICATION NUMBER: US/09/353,555
; CURRENT FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: US 09/115,455
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: histidine tag
US-09-353-555-2

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 34
US-08-868-452-22
; Sequence 22, Application US/08868452C
; Patent No. 6352972
; GENERAL INFORMATION:
; APPLICANT: Marcel E. Nimmi
; APPLICANT: Frederick L. Hall
; APPLICANT: Lingtao Wu
; APPLICANT: Bo Han
; APPLICANT: Edwin Shore
; TITLE OF INVENTION: BONE MORPHOGENETIC PROTEINS AND THEIR
; FILE REFERENCE: 17972-11
; CURRENT APPLICATION NUMBER: US/08/868,452C
; CURRENT FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Human
US-08-868-452-22

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 35
US-09-000-094-47
; Sequence 47, Application US/09000094
; Patent No. 6365160
; GENERAL INFORMATION:
; APPLICANT: WEBB, Elizabeth Ann
; MARGERTS, Mary Brigid
; COX, John Cooper
; FRAZER, Ian
; MCMILLAN, Nigel Alan John
; WILLIAMS, Mark Philip
; MOLONER, Margaret Bridget
; Holland
; EDWARDS, Stirling John
; TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,094
; FILING DATE: 21-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU96/00473
; FILING DATE: 26-JUL-1996
; APPLICATION NUMBER: AU PN 4439/95
; FILING DATE: 27-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 017227/0137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-000-094-47

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 36
US-09-058-483-7
; Sequence 7, Application US/09058483A
; Patent No. 6365347
; GENERAL INFORMATION:
; APPLICANT: Murray, Andrew W.
; APPLICANT: Smith, Dana L.
; APPLICANT: Sorger, Peter K.
; APPLICANT: No. 6365347man, Thea C.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING DISRUPTORS OF BIOLOGICAL

1 TITLE OF INVENTION: PATHWAYS USING GENETIC SELECTION
2 FILE REFERENCE: 30432.1US11
3 CURRENT APPLICATION NUMBER: US/09/058,483A
4 CURRENT FILING DATE: 1998-04-10
5 EARLIER APPLICATION NUMBER: 08/835,727
6 EARLIER FILING DATE: 1997-04-11
7 NUMBER OF SEQ ID NOS: 18
8 SOFTWARE: Patentin Ver. 2.0
9 SEQ ID NO: 7
10 LENGTH: 6
11 TYPE: PRT
12 ORGANISM: amino acid sequence of Staphylococcus aureus nuclease protei
13 US-09-058-483-7

Query Match 100.0%; Score 48; DB 2; length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 37
US-09-140-201-8
1 Sequence 8, Application US/09140201
2 Patent No. 6372425
3 GENERAL INFORMATION:
4 APPLICANT: KELLER, P.
5 TITLE OF INVENTION: LARGE SCALE AFFINITY CHROMATOGRAPHY OF
6 TITLE OF INVENTION: MACROMOLECULES
7 NUMBER OF SEQUENCES: 17
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: JACK TRIBBLE
10 STREET: P O BOX 2000, 126 E. LINCOLN AVENUE
11 CITY: RAHWAY
12 STATE: NJ
13 COUNTRY: USA
14 ZIP: 07065
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patentin Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/09/140,201
22 FILING DATE:
23 CLASSIFICATION:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/329,749
26 FILING DATE:
27 ATTORNEY/AGENT INFORMATION:
28 NAME: TRIBBLE, JACK
29 REGISTRATION NUMBER: 32,633
30 REFERENCE/DOCKET NUMBER: 18780
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (908) 594-5321
33 TELEFAX: (908) 594-4720
34 INFORMATION FOR SEQ ID NO: 8:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 6 amino acids
37 TYPE: amino acid
38 STRANDEDNESS: single
39 TOPOLOGY: linear
40 MOLECULE TYPE: peptide
41 US-09-140-201-8

Query Match 100.0%; Score 48; DB 2; length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
1 HHHHHH 6
Db 1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 38
US-09-039-780A-106
1 Sequence 106, Application US/09039780A
2 Patent No. 6376248
3 GENERAL INFORMATION:
4 APPLICANT: HAWLEY-NELSON, PAMELA
5 LAN, JIANQING
6 SHIH, POJEN
7 JESSE, JOEL A.
8 SCHIFFERLI, KEVIN P.
9 GEBREYERHU, GULIAT
10 TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
11 NUMBER OF SEQUENCES: 120
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: GREENLEE, WINNER & SULLIVAN
14 STREET: 5370 MANHATTAN CIRCLE, SUITE 201
15 CITY: BOULDER
16 STATE: CO
17 COUNTRY: US
18 ZIP: 80303
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patentin Release #1.0, Version #1.30
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/09/039,780A
26 FILING DATE: 16-Mar-1998
27 CLASSIFICATION: <Unknown>
28 ATTORNEY/AGENT INFORMATION:
29 NAME: SULLIVAN, SALLY A.
30 REGISTRATION NUMBER: 32,064
31 REFERENCE/DOCKET NUMBER: 32-95C
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (303)499-8080
34 TELEFAX: (303)499-8089
35 INFORMATION FOR SEQ ID NO: 106:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 6 amino acids
38 TYPE: amino acid
39 STRANDEDNESS: not relevant
40 TOPOLOGY: linear
41 MOLECULE TYPE: peptide
42 HYPOTHETICAL: NO
43 ANTI-SENSE: NO
44 SEQUENCE DESCRIPTION: SEQ ID NO: 106:
45 US-09-039-780A-106

Query Match 100.0%; Score 48; DB 2; length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 39
US-09-291-170A-14
1 Sequence 14, Application US/09291170A
2 Patent No. 6410687
3 GENERAL INFORMATION:
4 APPLICANT: Vale, Ronald D.
5 APPLICANT: Hartman, James J.
6 TITLE OF INVENTION: The Regents of the University of California
7 TITLE OF INVENTION: Assays for the Detection of Microtubule
8 FILE REFERENCE: 18557B-000510US
9 CURRENT APPLICATION NUMBER: US/09/291,170A
10 CURRENT FILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 60/081,734
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: (His)6 or 6xHis
US-09-291-170A-14

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 40
US-09-577-780-18
Sequence 18, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/577,780
FILING DATE: 24-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-577-780-18

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 41
US-09-724-297-7
Sequence 7, Application US/09724297
Patent No. 642538
GENERAL INFORMATION:
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: Wiltrop, et al.
TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
FILE REFERENCE: 97-99C
CURRENT APPLICATION NUMBER: US/09/724,297
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/009,388
PRIOR FILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 6
TYPE: PRT
ORGANISM: unknown
FEATURE:
NAME/KEY: misc.feature
LOCATION: ()..()
OTHER INFORMATION: Epitope tag
US-09-724-297-7

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 42
US-09-367-309A-4
Sequence 4, Application US/09367309A
Patent No. 6428807
GENERAL INFORMATION:
APPLICANT: MACFARLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: 6-His tag
US-09-367-309A-4

Query Match
Best Local Similarity 100.0%; Score 48; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
Db 1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 43

US-09-724-884-14
; Sequence 14, Application US/09724884
; Patent No. 6429304
; GENERAL INFORMATION:
; APPLICANT: Vale, Ronald D.
; APPLICANT: Hartman, James J.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Assays for the Detection of Microtubule
; FILE REFERENCE: 18557B-00051005
; CURRENT APPLICATION NUMBER: US/09/724,884
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/291,170
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: (His)6 or 6xHis
US-09-724-884-14

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 44

US-09-529-279-6
; Sequence 6, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-529-279-6

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 45

US-09-313-942-1
; Sequence 1, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tag sequence
US-09-313-942-1

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 46

US-09-353-215-6
; Sequence 6, Application US/09353215
; Patent No. 6475808
; GENERAL INFORMATION:
; APPLICANT: Wagner, Peter
; APPLICANT: Ault-Riche, Dana
; APPLICANT: No. 6475808k, Steffen
; APPLICANT: Icin, Christian
; TITLE OF INVENTION: Arrays of Proteins and Methods of Use Thereof
; FILE REFERENCE: 24406-0004P1
; CURRENT APPLICATION NUMBER: US/09/353,215
; PRIOR FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: US 09/115,455
; CURRENT FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: histidine tag
US-09-353-215-6

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 47

US-09-577-800-18
; Sequence 18, Application US/09577800
; Patent No. 6479635

```

; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,800
; FILING DATE: 24-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/996,139
; FILING DATE: 22 DECEMBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-577-800-18

Query Match      100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6

RESULT 48
US-09-667-422-7
; Sequence 7, Application US/09667422
; Patent No. 6482611
; GENERAL INFORMATION:
; APPLICANT: Cortright, Daniel
; APPLICANT: Krause, James
; TITLE OF INVENTION: Human Capsaicin Receptor and Uses Thereof
; FILE REFERENCE: HCR
; CURRENT APPLICATION NUMBER: US/09/667,422
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 6
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: H16x epitope
; US-09-667-422-7

Query Match      100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6

RESULT 49
US-09-315-926A-81
; Sequence 81, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO-81
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(6)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
; US-09-315-926A-81

Query Match      100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6

RESULT 50
US-09-731-558-11
; Sequence 11, Application US/09731558
; Patent No. 6503717
; GENERAL INFORMATION:
; APPLICANT: Case, Casey Christopher
; APPLICANT: Liu, Qiang
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
; FILE REFERENCE: 019496-003210US
; CURRENT APPLICATION NUMBER: US/09/731,558
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 09/456,100
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
```

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:6xHis tag
US-09-731-558-11

Query Match 100.0%; Score 48; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||
Db 1 HHHHHH 6

Search completed: March 21, 2006, 11:09:39
Job time : 55 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:09:01 ; Search time 165 Seconds
(without alignments)
15.194 Million cell updates/sec

Title: US-10-719-523-5
Perfect score: 48
Sequence: 1 HHHHHH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : Published Applications_AA_Main:**
1: /cgn2_6/prodata/1/pubppaa/us07_PUBCOMB.pep:**
2: /cgn2_6/prodata/1/pubppaa/us08_PUBCOMB.pep:**
3: /cgn2_6/prodata/1/pubppaa/us09_PUBCOMB.pep:**
4: /cgn2_6/prodata/1/pubppaa/us10a_PUBCOMB.pep:**
5: /cgn2_6/prodata/1/pubppaa/us10b_PUBCOMB.pep:**
6: /cgn2_6/prodata/1/pubppaa/us11_PUBCOMB.pep:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|-------------------|--------------------|
| 1 | 48 | 100.0 | 6 | 3 | US-09-280-030-61 | Sequence 61, Appl |
| 2 | 48 | 100.0 | 6 | 3 | US-09-771-956-11 | Sequence 11, Appl |
| 3 | 48 | 100.0 | 6 | 3 | US-09-822-485-30 | Sequence 30, Appl |
| 4 | 48 | 100.0 | 6 | 3 | US-09-760-008A-9 | Sequence 9, Appl |
| 5 | 48 | 100.0 | 6 | 3 | US-09-728-911-12 | Sequence 12, Appl |
| 6 | 48 | 100.0 | 6 | 3 | US-09-313-942-1 | Sequence 1, Appl |
| 7 | 48 | 100.0 | 6 | 3 | US-09-809-517A-11 | Sequence 11, Appl |
| 8 | 48 | 100.0 | 6 | 3 | US-09-211-691-14 | Sequence 14, Appl |
| 9 | 48 | 100.0 | 6 | 3 | US-09-808-037-33 | Sequence 33, Appl |
| 10 | 48 | 100.0 | 6 | 3 | US-09-888-615-149 | Sequence 149, Appl |
| 11 | 48 | 100.0 | 6 | 3 | US-09-875-519A-26 | Sequence 26, Appl |
| 12 | 48 | 100.0 | 6 | 3 | US-09-367-309A-4 | Sequence 4, Appl |
| 13 | 48 | 100.0 | 6 | 3 | US-09-837-992-44 | Sequence 44, Appl |
| 14 | 48 | 100.0 | 6 | 3 | US-09-871-856-18 | Sequence 18, Appl |
| 15 | 48 | 100.0 | 6 | 3 | US-09-801-968-22 | Sequence 22, Appl |
| 16 | 48 | 100.0 | 6 | 3 | US-09-865-363-18 | Sequence 18, Appl |
| 17 | 48 | 100.0 | 6 | 3 | US-09-871-291-18 | Sequence 18, Appl |
| 18 | 48 | 100.0 | 6 | 3 | US-09-875-338-93 | Sequence 93, Appl |
| 19 | 48 | 100.0 | 6 | 3 | US-09-988-899-5 | Sequence 5, Appl |
| 20 | 48 | 100.0 | 6 | 3 | US-09-798-884-16 | Sequence 16, Appl |
| 21 | 48 | 100.0 | 6 | 3 | US-09-817-764-9 | Sequence 9, Appl |
| 22 | 48 | 100.0 | 6 | 3 | US-09-943-382-1 | Sequence 1, Appl |
| 23 | 48 | 100.0 | 6 | 3 | US-09-951-265-2 | Sequence 2, Appl |
| 24 | 48 | 100.0 | 6 | 3 | US-09-801-676A-2 | Sequence 99, Appl |
| 25 | 48 | 100.0 | 6 | 3 | US-09-916-940-99 | Sequence 14, Appl |
| 26 | 48 | 100.0 | 6 | 3 | US-09-780-933-14 | Sequence 15, Appl |
| 27 | 48 | 100.0 | 6 | 3 | US-09-900-530A-15 | |

| | | | | | | |
|-----|----|-------|---|---|--------------------|---------------------|
| 28 | 48 | 100.0 | 6 | 3 | US-09-973-145-4 | Sequence 4, Appl |
| 29 | 48 | 100.0 | 6 | 3 | US-09-731-558-11 | Sequence 11, Appl |
| 30 | 48 | 100.0 | 6 | 3 | US-09-822-698A-22 | Sequence 22, Appl |
| 31 | 48 | 100.0 | 6 | 3 | US-09-144-886-5 | Sequence 5, Appl |
| 32 | 48 | 100.0 | 6 | 3 | US-09-935-868-1 | Sequence 1, Appl |
| 33 | 48 | 100.0 | 6 | 3 | US-09-877-650-18 | Sequence 18, Appl |
| 34 | 48 | 100.0 | 6 | 3 | US-09-814-604-9 | Sequence 9, Appl |
| 35 | 48 | 100.0 | 6 | 3 | US-09-939-769-94 | Sequence 94, Appl |
| 36 | 48 | 100.0 | 6 | 3 | US-09-935-430-698 | Sequence 698, Appl |
| 37 | 48 | 100.0 | 6 | 3 | US-09-821-726-19 | Sequence 19, Appl |
| 38 | 48 | 100.0 | 6 | 3 | US-09-945-248B-3 | Sequence 3, Appl |
| 39 | 48 | 100.0 | 6 | 3 | US-09-997-623-41 | Sequence 41, Appl |
| 40 | 48 | 100.0 | 6 | 3 | US-09-978-917A-41 | Sequence 41, Appl |
| 41 | 48 | 100.0 | 6 | 3 | US-09-948-391A-43 | Sequence 43, Appl |
| 42 | 48 | 100.0 | 6 | 3 | US-09-989-981A-11 | Sequence 11, Appl |
| 43 | 48 | 100.0 | 6 | 3 | US-09-904-196B-9 | Sequence 9, Appl |
| 44 | 48 | 100.0 | 6 | 3 | US-09-911-569-106 | Sequence 106, Appl |
| 45 | 48 | 100.0 | 6 | 3 | US-09-922-226-43 | Sequence 43, Appl |
| 46 | 48 | 100.0 | 6 | 3 | US-09-906-311C-15 | Sequence 15, Appl |
| 47 | 48 | 100.0 | 6 | 3 | US-09-782-587B-12 | Sequence 12, Appl |
| 48 | 48 | 100.0 | 6 | 3 | US-09-802-154-22 | Sequence 22, Appl |
| 49 | 48 | 100.0 | 6 | 3 | US-09-961-400-43 | Sequence 43, Appl |
| 50 | 48 | 100.0 | 6 | 3 | US-09-932-165-1480 | Sequence 1480, Appl |
| 51 | 48 | 100.0 | 6 | 3 | US-09-834-597-32 | Sequence 32, Appl |
| 52 | 48 | 100.0 | 6 | 3 | US-09-874-907A-2 | Sequence 2, Appl |
| 53 | 48 | 100.0 | 6 | 3 | US-09-925-055D-13 | Sequence 13, Appl |
| 54 | 48 | 100.0 | 6 | 3 | US-09-870-353A-30 | Sequence 30, Appl |
| 55 | 48 | 100.0 | 6 | 3 | US-09-949-039-4 | Sequence 4, Appl |
| 56 | 48 | 100.0 | 6 | 3 | US-09-935-384-780 | Sequence 780, Appl |
| 57 | 48 | 100.0 | 6 | 3 | US-09-942-052-709 | Sequence 709, Appl |
| 58 | 48 | 100.0 | 6 | 3 | US-09-962-756-1778 | Sequence 1778, Appl |
| 59 | 48 | 100.0 | 6 | 3 | US-09-807-742-12 | Sequence 12, Appl |
| 60 | 48 | 100.0 | 6 | 3 | US-09-784-553C-61 | Sequence 61, Appl |
| 61 | 48 | 100.0 | 6 | 3 | US-09-796-076-1 | Sequence 1, Appl |
| 62 | 48 | 100.0 | 6 | 3 | US-09-813-197-5 | Sequence 5, Appl |
| 63 | 48 | 100.0 | 6 | 4 | US-10-046-442-2 | Sequence 2, Appl |
| 64 | 48 | 100.0 | 6 | 4 | US-10-003-496-9 | Sequence 9, Appl |
| 65 | 48 | 100.0 | 6 | 4 | US-10-005-646-16 | Sequence 16, Appl |
| 66 | 48 | 100.0 | 6 | 4 | US-10-158-895-6 | Sequence 6, Appl |
| 67 | 48 | 100.0 | 6 | 4 | US-10-029-009-17 | Sequence 17, Appl |
| 68 | 48 | 100.0 | 6 | 4 | US-10-093-200A-10 | Sequence 10, Appl |
| 69 | 48 | 100.0 | 6 | 4 | US-10-116-273-35 | Sequence 35, Appl |
| 70 | 48 | 100.0 | 6 | 4 | US-10-061-395-68 | Sequence 68, Appl |
| 71 | 48 | 100.0 | 6 | 4 | US-10-147-087-6 | Sequence 6, Appl |
| 72 | 48 | 100.0 | 6 | 4 | US-10-151-071-6 | Sequence 6, Appl |
| 73 | 48 | 100.0 | 6 | 4 | US-10-166-232A-6 | Sequence 6, Appl |
| 74 | 48 | 100.0 | 6 | 4 | US-10-083-815-1 | Sequence 1, Appl |
| 75 | 48 | 100.0 | 6 | 4 | US-10-077-023-93 | Sequence 93, Appl |
| 76 | 48 | 100.0 | 6 | 4 | US-10-015-979-12 | Sequence 12, Appl |
| 77 | 48 | 100.0 | 6 | 4 | US-10-071-838-13 | Sequence 13, Appl |
| 78 | 48 | 100.0 | 6 | 4 | US-10-058-636-6 | Sequence 6, Appl |
| 79 | 48 | 100.0 | 6 | 4 | US-10-035-045-24 | Sequence 24, Appl |
| 80 | 48 | 100.0 | 6 | 4 | US-10-092-934-11 | Sequence 11, Appl |
| 81 | 48 | 100.0 | 6 | 4 | US-10-047-991-12 | Sequence 12, Appl |
| 82 | 48 | 100.0 | 6 | 4 | US-10-090-365-12 | Sequence 12, Appl |
| 83 | 48 | 100.0 | 6 | 4 | US-10-059-261-286 | Sequence 286, Appl |
| 84 | 48 | 100.0 | 6 | 4 | US-10-059-271-80 | Sequence 80, Appl |
| 85 | 48 | 100.0 | 6 | 4 | US-10-001-469-1402 | Sequence 1402, Appl |
| 86 | 48 | 100.0 | 6 | 4 | US-10-259-460-2 | Sequence 2, Appl |
| 87 | 48 | 100.0 | 6 | 4 | US-10-174-368A-4 | Sequence 4, Appl |
| 88 | 48 | 100.0 | 6 | 4 | US-10-222-952A-13 | Sequence 13, Appl |
| 89 | 48 | 100.0 | 6 | 4 | US-10-093-248-10 | Sequence 10, Appl |
| 90 | 48 | 100.0 | 6 | 4 | US-10-119-235-2 | Sequence 2, Appl |
| 91 | 48 | 100.0 | 6 | 4 | US-10-104-919-12 | Sequence 12, Appl |
| 92 | 48 | 100.0 | 6 | 4 | US-10-153-882-10 | Sequence 10, Appl |
| 93 | 48 | 100.0 | 6 | 4 | US-10-287-035-1 | Sequence 1, Appl |
| 94 | 48 | 100.0 | 6 | 4 | US-10-128-590-63 | Sequence 63, Appl |
| 95 | 48 | 100.0 | 6 | 4 | US-10-322-142-17 | Sequence 17, Appl |
| 96 | 48 | 100.0 | 6 | 4 | US-10-370-071-2 | Sequence 2, Appl |
| 97 | 48 | 100.0 | 6 | 4 | US-10-134-643-25 | Sequence 25, Appl |
| 98 | 48 | 100.0 | 6 | 4 | US-10-309-513-3 | Sequence 3, Appl |
| 99 | 48 | 100.0 | 6 | 4 | US-10-192-294-9 | Sequence 9, Appl |
| 100 | 48 | 100.0 | 6 | 4 | US-10-195-707B-35 | Sequence 35, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|---|---|----------------------|--------------------|-----|----|-------|---|---|--------------------|-------------------|
| 101 | 48 | 100.0 | 6 | 4 | US-10-037-243-46 | Sequence 46, App1 | 174 | 48 | 100.0 | 6 | 4 | US-10-058-270A-139 | Sequence 139, App |
| 102 | 48 | 100.0 | 6 | 4 | US-10-032-214-299 | Sequence 299, App | 175 | 48 | 100.0 | 6 | 4 | US-10-449-831A-164 | Sequence 164, App |
| 103 | 48 | 100.0 | 6 | 4 | US-10-066-965A-9 | Sequence 9, App1 | 176 | 48 | 100.0 | 6 | 4 | US-10-211-462-230 | Sequence 230, App |
| 104 | 48 | 100.0 | 6 | 4 | US-10-282-162-1 | Sequence 1, App1 | 177 | 48 | 100.0 | 6 | 4 | US-10-668-778-5 | Sequence 5, App1 |
| 105 | 48 | 100.0 | 6 | 4 | US-10-200-879-106 | Sequence 106, App | 178 | 48 | 100.0 | 6 | 4 | US-10-667-494-43 | Sequence 43, App1 |
| 106 | 48 | 100.0 | 6 | 4 | US-10-256-705-13 | Sequence 13, App1 | 179 | 48 | 100.0 | 6 | 4 | US-10-181-937-78 | Sequence 78, App1 |
| 107 | 48 | 100.0 | 6 | 4 | US-10-942-103-9 | Sequence 9, App1 | 180 | 48 | 100.0 | 6 | 4 | US-10-147-239A-33 | Sequence 33, App1 |
| 108 | 48 | 100.0 | 6 | 4 | US-10-270-073-20 | Sequence 20, App1 | 181 | 48 | 100.0 | 6 | 4 | US-10-253-286-357 | Sequence 357, App |
| 109 | 48 | 100.0 | 6 | 4 | US-10-291-990-13 | Sequence .13, App1 | 182 | 48 | 100.0 | 6 | 4 | US-10-275-107-71 | Sequence 71, App1 |
| 110 | 48 | 100.0 | 6 | 4 | US-10-315-964A-400 | Sequence 400, App | 183 | 48 | 100.0 | 6 | 4 | US-10-459-199-23 | Sequence 23, App1 |
| 111 | 48 | 100.0 | 6 | 4 | US-10-317-251A-400 | Sequence 400, App | 184 | 48 | 100.0 | 6 | 4 | US-10-339-744-6 | Sequence 6, App1 |
| 112 | 48 | 100.0 | 6 | 4 | US-10-317-252A-400 | Sequence 400, App | 185 | 48 | 100.0 | 6 | 4 | US-10-188-832-207 | Sequence 207, App |
| 113 | 48 | 100.0 | 6 | 4 | US-10-021-660-135 | Sequence 135, App | 186 | 48 | 100.0 | 6 | 4 | US-10-280-133-17 | Sequence 17, App1 |
| 114 | 48 | 100.0 | 6 | 4 | US-10-128-587A-63 | Sequence 63, App1 | 187 | 48 | 100.0 | 6 | 4 | US-10-667-462-43 | Sequence 43, App1 |
| 115 | 48 | 100.0 | 6 | 4 | US-10-340-860A-41 | Sequence 41, App1 | 188 | 48 | 100.0 | 6 | 4 | US-10-667-464-43 | Sequence 43, App1 |
| 116 | 48 | 100.0 | 6 | 4 | US-10-227-617A-6 | Sequence 6, App1 | 189 | 48 | 100.0 | 6 | 4 | US-10-644-055-1 | Sequence 1, App1 |
| 117 | 48 | 100.0 | 6 | 4 | US-10-168-080-22 | Sequence 22, App1 | 190 | 48 | 100.0 | 6 | 4 | US-10-665-227-3 | Sequence 3, App1 |
| 118 | 48 | 100.0 | 6 | 4 | US-10-318-966-9 | Sequence 9, App1 | 191 | 48 | 100.0 | 6 | 4 | US-10-627-473-42 | Sequence 42, App1 |
| 119 | 48 | 100.0 | 6 | 4 | US-10-181-804A-13 | Sequence 13, App1 | 192 | 48 | 100.0 | 6 | 4 | US-10-691-383-20 | Sequence 20, App1 |
| 120 | 48 | 100.0 | 6 | 4 | US-10-384-743-6 | Sequence 6, App1 | 193 | 48 | 100.0 | 6 | 4 | US-10-372-966-9 | Sequence 9, App1 |
| 121 | 48 | 100.0 | 6 | 4 | US-10-190-414-16 | Sequence 16, App1 | 194 | 48 | 100.0 | 6 | 4 | US-10-676-299-13 | Sequence 13, App1 |
| 122 | 48 | 100.0 | 6 | 4 | US-10-328-190-16 | Sequence 16, App1 | 195 | 48 | 100.0 | 6 | 4 | US-10-676-296-13 | Sequence 13, App1 |
| 123 | 48 | 100.0 | 6 | 4 | US-10-235-175-81 | Sequence 81, App1 | 196 | 48 | 100.0 | 6 | 4 | US-10-662-906-2 | Sequence 2, App1 |
| 124 | 48 | 100.0 | 6 | 4 | US-10-126-764-3 | Sequence 3, App1 | 197 | 48 | 100.0 | 6 | 4 | US-10-626-905-53 | Sequence 53, App1 |
| 125 | 48 | 100.0 | 6 | 4 | US-10-084-706-49 | Sequence 49, App1 | 198 | 48 | 100.0 | 6 | 4 | US-10-363-552-76 | Sequence 76, App1 |
| 126 | 48 | 100.0 | 6 | 4 | US-10-374-207-30 | Sequence 30, App1 | 199 | 48 | 100.0 | 6 | 4 | US-10-612-410-20 | Sequence 20, App1 |
| 127 | 48 | 100.0 | 6 | 4 | US-10-325-720-39 | Sequence 39, App1 | 200 | 48 | 100.0 | 6 | 4 | US-10-656-624-4 | Sequence 4, App1 |
| 128 | 48 | 100.0 | 6 | 4 | US-10-351-189-39 | Sequence 39, App1 | 201 | 48 | 100.0 | 6 | 4 | US-10-467-243-27 | Sequence 27, App1 |
| 129 | 48 | 100.0 | 6 | 4 | US-10-405-878A-18 | Sequence 18, App1 | 202 | 48 | 100.0 | 6 | 4 | US-10-441-799C-21 | Sequence 21, App1 |
| 130 | 48 | 100.0 | 6 | 4 | US-10-325-717-72 | Sequence 72, App1 | 203 | 48 | 100.0 | 6 | 4 | US-10-628-432-23 | Sequence 23, App1 |
| 131 | 48 | 100.0 | 6 | 4 | US-10-321-558-4 | Sequence 4, App1 | 204 | 48 | 100.0 | 6 | 4 | US-10-664-421-167 | Sequence 167, App |
| 132 | 48 | 100.0 | 6 | 4 | US-10-317-773-14 | Sequence 14, App1 | 205 | 48 | 100.0 | 6 | 4 | US-10-346-658-1 | Sequence 1, App1 |
| 133 | 48 | 100.0 | 6 | 4 | US-10-203-531-3 | Sequence 3, App1 | 206 | 48 | 100.0 | 6 | 4 | US-10-738-454-7 | Sequence 7, App1 |
| 134 | 48 | 100.0 | 6 | 4 | US-10-317-428A-14 | Sequence 14, App1 | 207 | 48 | 100.0 | 6 | 4 | US-10-799-016-6 | Sequence 6, App1 |
| 135 | 48 | 100.0 | 6 | 4 | US-10-321-204-53 | Sequence 53, App1 | 208 | 48 | 100.0 | 6 | 4 | US-10-344-607-1 | Sequence 1, App1 |
| 136 | 48 | 100.0 | 6 | 4 | US-10-264-127-5 | Sequence 5, App1 | 209 | 48 | 100.0 | 6 | 4 | US-10-761-781-14 | Sequence 14, App1 |
| 137 | 48 | 100.0 | 6 | 4 | US-10-277-292-698 | Sequence 698, App | 210 | 48 | 100.0 | 6 | 4 | US-10-159-257A-207 | Sequence 207, App |
| 138 | 48 | 100.0 | 6 | 4 | US-10-168-447-22 | Sequence 22, App1 | 211 | 48 | 100.0 | 6 | 4 | US-10-651-674-7 | Sequence 7, App1 |
| 139 | 48 | 100.0 | 6 | 4 | US-10-167-634-66 | Sequence 66, App1 | 212 | 48 | 100.0 | 6 | 4 | US-10-377-268-34 | Sequence 34, App1 |
| 140 | 48 | 100.0 | 6 | 4 | US-10-280-340-698 | Sequence 698, App | 213 | 48 | 100.0 | 6 | 4 | US-10-701-913-11 | Sequence 11, App1 |
| 141 | 48 | 100.0 | 6 | 4 | US-10-187-967-1 | Sequence 1, App1 | 214 | 48 | 100.0 | 6 | 4 | US-10-472-724-20 | Sequence 20, App1 |
| 142 | 48 | 100.0 | 6 | 4 | US-10-292-088A-145 | Sequence 145, App | 215 | 48 | 100.0 | 6 | 4 | US-10-693-057-358 | Sequence 358, App |
| 143 | 48 | 100.0 | 6 | 4 | US-10-128-578B-63 | Sequence 63, App1 | 216 | 48 | 100.0 | 6 | 4 | US-10-821-274-2 | Sequence 2, App1 |
| 144 | 48 | 100.0 | 6 | 4 | US-10-417-924A-3 | Sequence 3, App1 | 217 | 48 | 100.0 | 6 | 4 | US-10-821-583-30 | Sequence 30, App1 |
| 145 | 48 | 100.0 | 6 | 4 | US-10-336-840-39 | Sequence 39, App1 | 218 | 48 | 100.0 | 6 | 4 | US-10-699-550-20 | Sequence 20, App1 |
| 146 | 48 | 100.0 | 6 | 4 | US-10-366-493-101 | Sequence 101, App | 219 | 48 | 100.0 | 6 | 4 | US-10-618-941-138 | Sequence 138, App |
| 147 | 48 | 100.0 | 6 | 4 | US-10-273-180-30 | Sequence 30, App1 | 220 | 48 | 100.0 | 6 | 4 | US-10-409-814A-19 | Sequence 19, App1 |
| 148 | 48 | 100.0 | 6 | 4 | US-10-013-312-2990 | Sequence 2990, App | 221 | 48 | 100.0 | 6 | 4 | US-10-725-276-24 | Sequence 24, App1 |
| 149 | 48 | 100.0 | 6 | 4 | US-10-256-851-7 | Sequence 7, App1 | 222 | 48 | 100.0 | 6 | 4 | US-10-677-641-10 | Sequence 10, App1 |
| 150 | 48 | 100.0 | 6 | 4 | US-10-045-674-12 | Sequence 12, App1 | 223 | 48 | 100.0 | 6 | 4 | US-10-627-592-38 | Sequence 38, App1 |
| 151 | 48 | 100.0 | 6 | 4 | US-10-295-027-1382 | Sequence 1382, App | 224 | 48 | 100.0 | 6 | 4 | US-10-768-976-20 | Sequence 20, App1 |
| 152 | 48 | 100.0 | 6 | 4 | US-10-245-871-357 | Sequence 357, App | 225 | 48 | 100.0 | 6 | 5 | US-10-622-088-50 | Sequence 50, App1 |
| 153 | 48 | 100.0 | 6 | 4 | US-10-175-689-32 | Sequence 32, App1 | 226 | 48 | 100.0 | 6 | 5 | US-10-470-987-17 | Sequence 17, App1 |
| 154 | 48 | 100.0 | 6 | 4 | US-10-253-471-1778 | Sequence 1778, App | 227 | 48 | 100.0 | 6 | 5 | US-10-627-582-47 | Sequence 47, App1 |
| 155 | 48 | 100.0 | 6 | 4 | US-10-336-041A-4 | Sequence 4, App1 | 228 | 48 | 100.0 | 6 | 5 | US-10-706-328-1 | Sequence 1, App1 |
| 156 | 48 | 100.0 | 6 | 4 | US-10-057-475B-10979 | Sequence 10979, A | 229 | 48 | 100.0 | 6 | 5 | US-10-810-262-33 | Sequence 33, App1 |
| 157 | 48 | 100.0 | 6 | 4 | US-10-422-523-23 | Sequence 23, App1 | 230 | 48 | 100.0 | 6 | 5 | US-10-759-762-1 | Sequence 1, App1 |
| 158 | 48 | 100.0 | 6 | 4 | US-10-277-216-32 | Sequence 32, App1 | 231 | 48 | 100.0 | 6 | 5 | US-10-705-745-9 | Sequence 9, App1 |
| 159 | 48 | 100.0 | 6 | 4 | US-10-452-786-1 | Sequence 1, App1 | 232 | 48 | 100.0 | 6 | 5 | US-10-416-456A-30 | Sequence 30, App1 |
| 160 | 48 | 100.0 | 6 | 4 | US-10-173-999-161 | Sequence 161, App | 233 | 48 | 100.0 | 6 | 5 | US-10-131-998A-42 | Sequence 42, App1 |
| 161 | 48 | 100.0 | 6 | 4 | US-10-374-726-52 | Sequence 52, App1 | 234 | 48 | 100.0 | 6 | 5 | US-10-627-649-286 | Sequence 286, App |
| 162 | 48 | 100.0 | 6 | 4 | US-10-387-355-2 | Sequence 2, App1 | 235 | 48 | 100.0 | 6 | 5 | US-10-475-706-5 | Sequence 5, App1 |
| 163 | 48 | 100.0 | 6 | 4 | US-10-423-847-43 | Sequence 43, App1 | 236 | 48 | 100.0 | 6 | 5 | US-10-786-505-54 | Sequence 54, App1 |
| 164 | 48 | 100.0 | 6 | 4 | US-10-355-218-7 | Sequence 7, App1 | 237 | 48 | 100.0 | 6 | 5 | US-10-802-133-18 | Sequence 18, App1 |
| 165 | 48 | 100.0 | 6 | 4 | US-10-609-296-49 | Sequence 49, App1 | 238 | 48 | 100.0 | 6 | 5 | US-10-829-388-20 | Sequence 20, App1 |
| 166 | 48 | 100.0 | 6 | 4 | US-10-384-788-33 | Sequence 33, App1 | 239 | 48 | 100.0 | 6 | 5 | US-10-769-308-16 | Sequence 16, App1 |
| 167 | 48 | 100.0 | 6 | 4 | US-10-339-712-5 | Sequence 5, App1 | 240 | 48 | 100.0 | 6 | 5 | US-10-859-739-16 | Sequence 16, App1 |
| 168 | 48 | 100.0 | 6 | 4 | US-10-339-712-61 | Sequence 61, App1 | 241 | 48 | 100.0 | 6 | 5 | US-10-883-472-9 | Sequence 9, App1 |
| 169 | 48 | 100.0 | 6 | 4 | US-10-373-238-5 | Sequence 5, App1 | 242 | 48 | 100.0 | 6 | 5 | US-10-863-729-14 | Sequence 14, App1 |
| 170 | 48 | 100.0 | 6 | 4 | US-10-385-415-91 | Sequence 91, App1 | 243 | 48 | 100.0 | 6 | 5 | US-10-622-893A-15 | Sequence 15, App1 |
| 171 | 48 | 100.0 | 6 | 4 | US-10-444-691-5 | Sequence 5, App1 | 244 | 48 | 100.0 | 6 | 5 | US-10-884-783-3 | Sequence 3, App1 |
| 172 | 48 | 100.0 | 6 | 4 | US-10-126-022-32 | Sequence 32, App1 | 245 | 48 | 100.0 | 6 | 5 | US-10-926-225-11 | Sequence 11, App1 |
| 173 | 48 | 100.0 | 6 | 4 | US-10-253-493-1778 | Sequence 1778, App | 246 | 48 | 100.0 | 6 | 5 | US-10-865-146-34 | Sequence 34, App1 |

| | | | | | | | | | | | | | |
|-----|----|-------|---|---|--------------------|--------------------|-----|----|-------|---|---|-------------------|--------------------|
| 247 | 48 | 100.0 | 6 | 5 | US-10-842-054-24 | Sequence 24, Appl | 320 | 48 | 100.0 | 6 | 5 | US-10-839-793-1 | Sequence 1, Appl1 |
| 248 | 48 | 100.0 | 6 | 5 | US-10-946-786-3 | Sequence 3, Appl1 | 321 | 48 | 100.0 | 6 | 5 | US-10-503-050A-10 | Sequence 10, Appl1 |
| 249 | 48 | 100.0 | 6 | 5 | US-10-842-989-16 | Sequence 16, Appl1 | 322 | 48 | 100.0 | 6 | 5 | US-10-981-141-18 | Sequence 18, Appl1 |
| 250 | 48 | 100.0 | 6 | 5 | US-10-719-523-5 | Sequence 5, Appl1 | 323 | 48 | 100.0 | 6 | 5 | US-10-994-824-93 | Sequence 93, Appl1 |
| 251 | 48 | 100.0 | 6 | 5 | US-10-835-096-21 | Sequence 21, Appl1 | 324 | 48 | 100.0 | 6 | 5 | US-10-982-543-1 | Sequence 1, Appl1 |
| 252 | 48 | 100.0 | 6 | 5 | US-10-725-284-24 | Sequence 24, Appl1 | 325 | 48 | 100.0 | 6 | 5 | US-10-981-998-12 | Sequence 12, Appl1 |
| 253 | 48 | 100.0 | 6 | 5 | US-10-857-673-19 | Sequence 19, Appl1 | 326 | 48 | 100.0 | 6 | 5 | US-10-806-062-325 | Sequence 325, App |
| 254 | 48 | 100.0 | 6 | 5 | US-10-754-485-49 | Sequence 49, Appl1 | 327 | 48 | 100.0 | 6 | 5 | US-10-961-826-41 | Sequence 41, Appl1 |
| 255 | 48 | 100.0 | 6 | 5 | US-10-831-063-43 | Sequence 43, Appl1 | 328 | 48 | 100.0 | 6 | 5 | US-10-969-245-90 | Sequence 90, Appl1 |
| 256 | 48 | 100.0 | 6 | 5 | US-10-854-735-28 | Sequence 28, Appl1 | 329 | 48 | 100.0 | 6 | 5 | US-10-965-006-15 | Sequence 15, Appl1 |
| 257 | 48 | 100.0 | 6 | 5 | US-10-839-615-4 | Sequence 4, Appl1 | 330 | 48 | 100.0 | 6 | 5 | US-10-756-813-16 | Sequence 16, Appl1 |
| 258 | 48 | 100.0 | 6 | 5 | US-10-693-056-358 | Sequence 358, App | 331 | 48 | 100.0 | 6 | 5 | US-10-971-736-474 | Sequence 474, App |
| 259 | 48 | 100.0 | 6 | 5 | US-10-771-833-7 | Sequence 7, Appl1 | 332 | 48 | 100.0 | 6 | 5 | US-10-990-137-698 | Sequence 698, App |
| 260 | 48 | 100.0 | 6 | 5 | US-10-833-951-54 | Sequence 54, Appl1 | 333 | 48 | 100.0 | 6 | 5 | US-10-980-974-7 | Sequence 7, Appl1 |
| 261 | 48 | 100.0 | 6 | 5 | US-10-840-723-358 | Sequence 358, App | 334 | 48 | 100.0 | 6 | 5 | US-10-804-687-63 | Sequence 63, Appl1 |
| 262 | 48 | 100.0 | 6 | 5 | US-10-473-571-16 | Sequence 16, Appl1 | 335 | 48 | 100.0 | 6 | 5 | US-10-871-606-5 | Sequence 5, Appl1 |
| 263 | 48 | 100.0 | 6 | 5 | US-10-497-003A-16 | Sequence 16, Appl1 | 336 | 48 | 100.0 | 6 | 6 | US-11-004-111-41 | Sequence 41, Appl1 |
| 264 | 48 | 100.0 | 6 | 5 | US-10-883-144-85 | Sequence 85, Appl1 | 337 | 48 | 100.0 | 6 | 6 | US-11-004-461-9 | Sequence 9, Appl1 |
| 265 | 48 | 100.0 | 6 | 5 | US-10-661-366-12 | Sequence 12, Appl1 | 338 | 48 | 100.0 | 6 | 6 | US-11-045-944-12 | Sequence 12, Appl1 |
| 266 | 48 | 100.0 | 6 | 5 | US-10-628-004-28 | Sequence 28, Appl1 | 339 | 48 | 100.0 | 6 | 6 | US-11-053-228-9 | Sequence 9, Appl1 |
| 267 | 48 | 100.0 | 6 | 5 | US-10-658-752-11 | Sequence 11, Appl1 | 340 | 48 | 100.0 | 6 | 6 | US-11-093-103-110 | Sequence 110, App |
| 268 | 48 | 100.0 | 6 | 5 | US-10-769-074-16 | Sequence 16, Appl1 | 341 | 48 | 100.0 | 6 | 6 | US-11-112-137-10 | Sequence 10, App |
| 269 | 48 | 100.0 | 6 | 5 | US-10-835-533-28 | Sequence 28, Appl1 | 342 | 48 | 100.0 | 6 | 6 | US-11-115-906-35 | Sequence 35, Appl1 |
| 270 | 48 | 100.0 | 6 | 5 | US-10-484-218-28 | Sequence 28, Appl1 | 343 | 48 | 100.0 | 6 | 6 | US-11-035-623-40 | Sequence 40, Appl1 |
| 271 | 48 | 100.0 | 6 | 5 | US-10-363-870A-11 | Sequence 11, Appl1 | 344 | 48 | 100.0 | 6 | 6 | US-11-128-026-44 | Sequence 44, Appl1 |
| 272 | 48 | 100.0 | 6 | 5 | US-10-899-551-50 | Sequence 50, Appl1 | 345 | 48 | 100.0 | 6 | 6 | US-11-003-306-5 | Sequence 5, Appl1 |
| 273 | 48 | 100.0 | 6 | 5 | US-10-826-572-20 | Sequence 20, Appl1 | 346 | 48 | 100.0 | 6 | 6 | US-11-029-242-11 | Sequence 11, Appl1 |
| 274 | 48 | 100.0 | 6 | 5 | US-10-937-372-11 | Sequence 11, Appl1 | 347 | 48 | 100.0 | 6 | 6 | US-11-134-114-11 | Sequence 1, Appl1 |
| 275 | 48 | 100.0 | 6 | 5 | US-10-968-432-12 | Sequence 12, Appl1 | 348 | 48 | 100.0 | 6 | 6 | US-11-010-558-10 | Sequence 10, Appl1 |
| 276 | 48 | 100.0 | 6 | 5 | US-10-473-524-16 | Sequence 16, Appl1 | 349 | 48 | 100.0 | 6 | 6 | US-11-047-365-23 | Sequence 23, Appl1 |
| 277 | 48 | 100.0 | 6 | 5 | US-10-897-387-72 | Sequence 72, Appl1 | 350 | 48 | 100.0 | 7 | 3 | US-09-809-517A-12 | Sequence 12, Appl1 |
| 278 | 48 | 100.0 | 6 | 5 | US-10-880-922-63 | Sequence 63, Appl1 | 351 | 48 | 100.0 | 7 | 3 | US-09-809-517A-13 | Sequence 13, Appl1 |
| 279 | 48 | 100.0 | 6 | 5 | US-10-886-949-7 | Sequence 7, Appl1 | 352 | 48 | 100.0 | 7 | 3 | US-09-963-761B-5 | Sequence 5, Appl1 |
| 280 | 48 | 100.0 | 6 | 5 | US-10-495-885-1 | Sequence 1, Appl1 | 353 | 48 | 100.0 | 7 | 4 | US-10-343-766-7 | Sequence 7, Appl1 |
| 281 | 48 | 100.0 | 6 | 5 | US-10-871-602-358 | Sequence 358, App | 354 | 48 | 100.0 | 7 | 4 | US-10-665-227-4 | Sequence 4, Appl1 |
| 282 | 48 | 100.0 | 6 | 5 | US-10-944-496-17 | Sequence 17, Appl1 | 355 | 48 | 100.0 | 7 | 5 | US-10-622-088-165 | Sequence 165, App |
| 283 | 48 | 100.0 | 6 | 5 | US-10-805-684-161 | Sequence 161, App | 356 | 48 | 100.0 | 7 | 5 | US-10-946-786-4 | Sequence 4, Appl1 |
| 284 | 48 | 100.0 | 6 | 5 | US-10-917-844-95 | Sequence 95, Appl1 | 357 | 48 | 100.0 | 7 | 5 | US-10-658-752-12 | Sequence 12, Appl1 |
| 285 | 48 | 100.0 | 6 | 5 | US-10-872-859-59 | Sequence 59, Appl1 | 358 | 48 | 100.0 | 7 | 5 | US-10-658-752-13 | Sequence 13, Appl1 |
| 286 | 48 | 100.0 | 6 | 5 | US-10-931-916-69 | Sequence 69, Appl1 | 359 | 48 | 100.0 | 7 | 5 | US-10-501-071-9 | Sequence 9, Appl1 |
| 287 | 48 | 100.0 | 6 | 5 | US-10-966-097A-4 | Sequence 4, Appl1 | 360 | 48 | 100.0 | 7 | 5 | US-10-965-227-3 | Sequence 3, Appl1 |
| 288 | 48 | 100.0 | 6 | 5 | US-10-966-097A-18 | Sequence 18, Appl1 | 361 | 48 | 100.0 | 7 | 5 | US-10-963-994-12 | Sequence 12, Appl1 |
| 289 | 48 | 100.0 | 6 | 5 | US-10-703-817-254 | Sequence 254, App | 362 | 48 | 100.0 | 8 | 3 | US-09-760-008A-10 | Sequence 10, Appl1 |
| 290 | 48 | 100.0 | 6 | 5 | US-10-729-475-13 | Sequence 13, Appl1 | 363 | 48 | 100.0 | 8 | 3 | US-09-334-477-11 | Sequence 11, Appl1 |
| 291 | 48 | 100.0 | 6 | 5 | US-10-505-486-17 | Sequence 17, Appl1 | 364 | 48 | 100.0 | 8 | 3 | US-09-244-984-2 | Sequence 2, Appl1 |
| 292 | 48 | 100.0 | 6 | 5 | US-10-984-958A-8 | Sequence 8, Appl1 | 365 | 48 | 100.0 | 8 | 3 | US-09-780-933-15 | Sequence 15, Appl1 |
| 293 | 48 | 100.0 | 6 | 5 | US-10-922-339-43 | Sequence 43, Appl1 | 366 | 48 | 100.0 | 8 | 3 | US-09-772-719-22 | Sequence 22, Appl1 |
| 294 | 48 | 100.0 | 6 | 5 | US-10-501-071-8 | Sequence 8, Appl1 | 367 | 48 | 100.0 | 8 | 3 | US-09-597-623-42 | Sequence 42, Appl1 |
| 295 | 48 | 100.0 | 6 | 5 | US-10-921-676-6 | Sequence 6, Appl1 | 368 | 48 | 100.0 | 8 | 3 | US-09-978-917A-42 | Sequence 42, App |
| 296 | 48 | 100.0 | 6 | 5 | US-10-877-467A-6 | Sequence 6, Appl1 | 369 | 48 | 100.0 | 8 | 3 | US-09-967-237-22 | Sequence 22, Appl1 |
| 297 | 48 | 100.0 | 6 | 5 | US-10-959-600-5 | Sequence 5, Appl1 | 370 | 48 | 100.0 | 8 | 3 | US-09-904-196B-10 | Sequence 10, Appl1 |
| 298 | 48 | 100.0 | 6 | 5 | US-10-959-600-5 | Sequence 5, Appl1 | 371 | 48 | 100.0 | 8 | 3 | US-09-782-587B-13 | Sequence 13, Appl1 |
| 299 | 48 | 100.0 | 6 | 5 | US-10-665-883-10 | Sequence 10, Appl1 | 372 | 48 | 100.0 | 8 | 4 | US-10-003-496-10 | Sequence 10, Appl1 |
| 300 | 48 | 100.0 | 6 | 5 | US-10-898-775-19 | Sequence 19, Appl1 | 373 | 48 | 100.0 | 8 | 4 | US-10-116-273-36 | Sequence 36, Appl1 |
| 301 | 48 | 100.0 | 6 | 5 | US-10-881-405-27 | Sequence 27, Appl1 | 374 | 48 | 100.0 | 8 | 4 | US-10-057-321-2 | Sequence 2, Appl1 |
| 302 | 48 | 100.0 | 6 | 5 | US-10-957-433-2 | Sequence 2, Appl1 | 375 | 48 | 100.0 | 8 | 4 | US-10-156-634A-16 | Sequence 16, Appl1 |
| 303 | 48 | 100.0 | 6 | 5 | US-10-479-901-299 | Sequence 299, App | 376 | 48 | 100.0 | 8 | 4 | US-10-191-879-15 | Sequence 15, Appl1 |
| 304 | 48 | 100.0 | 6 | 5 | US-10-820-474A-269 | Sequence 269, App | 377 | 48 | 100.0 | 8 | 4 | US-10-194-728-5 | Sequence 5, Appl1 |
| 305 | 48 | 100.0 | 6 | 5 | US-10-871-369-13 | Sequence 13, Appl1 | 378 | 48 | 100.0 | 8 | 4 | US-10-193-858-5 | Sequence 5, Appl1 |
| 306 | 48 | 100.0 | 6 | 5 | US-10-900-930-26 | Sequence 26, Appl1 | 379 | 48 | 100.0 | 8 | 4 | US-10-192-294-10 | Sequence 10, Appl1 |
| 307 | 48 | 100.0 | 6 | 5 | US-10-927-588-14 | Sequence 14, Appl1 | 380 | 48 | 100.0 | 8 | 4 | US-10-195-707B-36 | Sequence 36, Appl1 |
| 308 | 48 | 100.0 | 6 | 5 | US-10-941-635-167 | Sequence 167, App | 381 | 48 | 100.0 | 8 | 4 | US-10-318-966-10 | Sequence 10, Appl1 |
| 309 | 48 | 100.0 | 6 | 5 | US-10-971-679-358 | Sequence 358, App | 382 | 48 | 100.0 | 8 | 4 | US-10-190-414-17 | Sequence 17, Appl1 |
| 310 | 48 | 100.0 | 6 | 5 | US-10-764-212-81 | Sequence 81, Appl1 | 383 | 48 | 100.0 | 8 | 4 | US-10-356-088-63 | Sequence 63, Appl1 |
| 311 | 48 | 100.0 | 6 | 5 | US-10-872-770-13 | Sequence 13, Appl1 | 384 | 48 | 100.0 | 8 | 4 | US-10-084-706-50 | Sequence 50, Appl1 |
| 312 | 48 | 100.0 | 6 | 5 | US-10-903-476-13 | Sequence 13, Appl1 | 385 | 48 | 100.0 | 8 | 4 | US-10-325-720-40 | Sequence 40, Appl1 |
| 313 | 48 | 100.0 | 6 | 5 | US-10-965-227-4 | Sequence 4, Appl1 | 386 | 48 | 100.0 | 8 | 4 | US-10-351-189-40 | Sequence 40, Appl1 |
| 314 | 48 | 100.0 | 6 | 5 | US-10-789-818-22 | Sequence 22, Appl1 | 387 | 48 | 100.0 | 8 | 4 | US-10-325-717-73 | Sequence 73, Appl1 |
| 315 | 48 | 100.0 | 6 | 5 | US-10-704-513-774 | Sequence 774, App | 388 | 48 | 100.0 | 8 | 4 | US-10-303-531-4 | Sequence 4, Appl1 |
| 316 | 48 | 100.0 | 6 | 5 | US-10-805-075-9 | Sequence 9, Appl1 | 389 | 48 | 100.0 | 8 | 4 | US-10-366-493-102 | Sequence 102, App |
| 317 | 48 | 100.0 | 6 | 5 | US-10-922-802-20 | Sequence 20, Appl1 | 390 | 48 | 100.0 | 8 | 4 | US-10-609-296-50 | Sequence 50, Appl1 |
| 318 | 48 | 100.0 | 6 | 5 | US-10-716-095A-14 | Sequence 14, Appl1 | 391 | 48 | 100.0 | 8 | 4 | US-10-444-691-6 | Sequence 6, Appl1 |
| 319 | 48 | 100.0 | 6 | 5 | US-10-911-160-55 | Sequence 55, Appl1 | 392 | 48 | 100.0 | 8 | 4 | US-10-351-891-120 | Sequence 120, App |

| | | | | | | | | | | | | | |
|-----|----|-------|----|---|-------------------|-------------------|-----|----|-------|----|---|-------------------|-------------------|
| 393 | 48 | 100.0 | 8 | 4 | US-10-381-870-16 | Sequence 16, Appl | 466 | 48 | 100.0 | 10 | 2 | US-08-464-363-73 | Sequence 73, Appl |
| 394 | 48 | 100.0 | 8 | 4 | US-10-665-227-5 | Sequence 5, Appl1 | 467 | 48 | 100.0 | 10 | 3 | US-09-809-517A-2 | Sequence 2, Appl1 |
| 395 | 48 | 100.0 | 8 | 4 | US-10-296-733-16 | Sequence 16, Appl | 468 | 48 | 100.0 | 10 | 3 | US-09-402-131-9 | Sequence 9, Appl1 |
| 396 | 48 | 100.0 | 8 | 4 | US-10-467-243-28 | Sequence 28, Appl | 469 | 48 | 100.0 | 10 | 3 | US-09-981-636-2 | Sequence 2, Appl1 |
| 397 | 48 | 100.0 | 8 | 4 | US-10-741-204-36 | Sequence 36, Appl | 470 | 48 | 100.0 | 10 | 3 | US-09-981-636-3 | Sequence 3, Appl1 |
| 398 | 48 | 100.0 | 8 | 4 | US-10-741-205-23 | Sequence 23, Appl | 471 | 48 | 100.0 | 10 | 3 | US-09-911-568-101 | Sequence 101, App |
| 399 | 48 | 100.0 | 8 | 4 | US-10-741-208-36 | Sequence 36, Appl | 472 | 48 | 100.0 | 10 | 3 | US-09-976-935-31 | Sequence 31, Appl |
| 400 | 48 | 100.0 | 8 | 4 | US-10-377-268-35 | Sequence 35, Appl | 473 | 48 | 100.0 | 10 | 3 | US-09-933-780C-24 | Sequence 24, Appl |
| 401 | 48 | 100.0 | 8 | 4 | US-10-799-326-63 | Sequence 63, Appl | 474 | 48 | 100.0 | 10 | 4 | US-10-029-009-18 | Sequence 18, Appl |
| 402 | 48 | 100.0 | 8 | 5 | US-10-699-113-25 | Sequence 25, Appl | 475 | 48 | 100.0 | 10 | 4 | US-10-057-505-24 | Sequence 24, Appl |
| 403 | 48 | 100.0 | 8 | 5 | US-10-705-743-10 | Sequence 10, Appl | 476 | 48 | 100.0 | 10 | 4 | US-10-022-832-77 | Sequence 77, Appl |
| 404 | 48 | 100.0 | 8 | 5 | US-10-795-933-22 | Sequence 22, Appl | 477 | 48 | 100.0 | 10 | 4 | US-10-047-991-10 | Sequence 10, Appl |
| 405 | 48 | 100.0 | 8 | 5 | US-10-784-300-2 | Sequence 2, Appl1 | 478 | 48 | 100.0 | 10 | 4 | US-10-174-410-6 | Sequence 6, Appl1 |
| 406 | 48 | 100.0 | 8 | 5 | US-10-888-694-22 | Sequence 22, Appl | 479 | 48 | 100.0 | 10 | 4 | US-10-174-410-11 | Sequence 11, Appl |
| 407 | 48 | 100.0 | 8 | 5 | US-10-946-786-5 | Sequence 5, Appl1 | 480 | 48 | 100.0 | 10 | 4 | US-10-188-343-1 | Sequence 1, Appl1 |
| 408 | 48 | 100.0 | 8 | 5 | US-10-854-735-29 | Sequence 29, Appl | 481 | 48 | 100.0 | 10 | 4 | US-10-104-919-60 | Sequence 60, Appl |
| 409 | 48 | 100.0 | 8 | 5 | US-10-835-533-29 | Sequence 29, Appl | 482 | 48 | 100.0 | 10 | 4 | US-10-286-421-7 | Sequence 7, Appl1 |
| 410 | 48 | 100.0 | 8 | 5 | US-10-898-616-10 | Sequence 10, Appl | 483 | 48 | 100.0 | 10 | 4 | US-10-286-421-13 | Sequence 13, Appl |
| 411 | 48 | 100.0 | 8 | 5 | US-10-612-358-7 | Sequence 7, Appl1 | 484 | 48 | 100.0 | 10 | 4 | US-10-200-879-101 | Sequence 101, App |
| 412 | 48 | 100.0 | 8 | 5 | US-10-851-918B-17 | Sequence 17, Appl | 485 | 48 | 100.0 | 10 | 4 | US-10-168-080-23 | Sequence 23, Appl |
| 413 | 48 | 100.0 | 8 | 5 | US-10-851-918B-24 | Sequence 24, Appl | 486 | 48 | 100.0 | 10 | 4 | US-10-291-851-7 | Sequence 7, Appl1 |
| 414 | 48 | 100.0 | 8 | 5 | US-10-851-918B-29 | Sequence 29, Appl | 487 | 48 | 100.0 | 10 | 4 | US-10-181-804A-14 | Sequence 14, Appl |
| 415 | 48 | 100.0 | 8 | 5 | US-10-851-918B-45 | Sequence 45, Appl | 488 | 48 | 100.0 | 10 | 4 | US-10-291-190-58 | Sequence 58, Appl |
| 416 | 48 | 100.0 | 8 | 5 | US-10-851-918B-50 | Sequence 50, Appl | 489 | 48 | 100.0 | 10 | 4 | US-10-319-799-7 | Sequence 7, Appl1 |
| 417 | 48 | 100.0 | 8 | 5 | US-10-501-071-10 | Sequence 10, Appl | 490 | 48 | 100.0 | 10 | 4 | US-10-319-799-13 | Sequence 13, Appl |
| 418 | 48 | 100.0 | 8 | 5 | US-10-501-071-17 | Sequence 17, Appl | 491 | 48 | 100.0 | 10 | 4 | US-10-306-762-6 | Sequence 6, Appl1 |
| 419 | 48 | 100.0 | 8 | 5 | US-10-756-813-17 | Sequence 17, Appl | 492 | 48 | 100.0 | 10 | 4 | US-10-351-157-72 | Sequence 72, Appl |
| 420 | 48 | 100.0 | 8 | 5 | US-10-980-597-3 | Sequence 3, Appl1 | 493 | 48 | 100.0 | 10 | 4 | US-10-408-167A-9 | Sequence 9, Appl1 |
| 421 | 48 | 100.0 | 8 | 6 | US-11-004-111-42 | Sequence 42, Appl | 494 | 48 | 100.0 | 10 | 4 | US-10-352-554-72 | Sequence 72, Appl |
| 422 | 48 | 100.0 | 8 | 6 | US-11-004-461-10 | Sequence 10, Appl | 495 | 48 | 100.0 | 10 | 4 | US-10-385-415-78 | Sequence 78, Appl |
| 423 | 48 | 100.0 | 8 | 6 | US-11-053-228-10 | Sequence 10, Appl | 496 | 48 | 100.0 | 10 | 4 | US-10-395-741B-61 | Sequence 61, App |
| 424 | 48 | 100.0 | 8 | 6 | US-11-032-090-3 | Sequence 3, Appl1 | 497 | 48 | 100.0 | 10 | 4 | US-10-398-248-7 | Sequence 73, Appl |
| 425 | 48 | 100.0 | 8 | 6 | US-11-015-730-3 | Sequence 3, Appl1 | 498 | 48 | 100.0 | 10 | 4 | US-10-463-113-73 | Sequence 73, Appl |
| 426 | 48 | 100.0 | 8 | 6 | US-11-016-126-20 | Sequence 20, Appl | 499 | 48 | 100.0 | 10 | 4 | US-10-463-619-4 | Sequence 4, Appl1 |
| 427 | 48 | 100.0 | 8 | 6 | US-11-115-906-36 | Sequence 36, Appl | 500 | 48 | 100.0 | 10 | 4 | US-10-126-962-27 | Sequence 27, Appl |
| 428 | 48 | 100.0 | 9 | 3 | US-09-884-663A-25 | Sequence 25, Appl | 501 | 48 | 100.0 | 10 | 4 | US-10-665-227-7 | Sequence 7, Appl1 |
| 429 | 48 | 100.0 | 9 | 3 | US-09-809-517A-5 | Sequence 5, Appl1 | 502 | 48 | 100.0 | 10 | 4 | US-10-720-460-8 | Sequence 8, Appl1 |
| 430 | 48 | 100.0 | 9 | 3 | US-09-854-280-18 | Sequence 18, Appl | 503 | 48 | 100.0 | 10 | 4 | US-10-723-933-55 | Sequence 55, Appl |
| 431 | 48 | 100.0 | 9 | 3 | US-09-821-883-15 | Sequence 15, Appl | 504 | 48 | 100.0 | 10 | 4 | US-10-723-933-68 | Sequence 68, Appl |
| 432 | 48 | 100.0 | 9 | 3 | US-09-854-208-18 | Sequence 18, Appl | 505 | 48 | 100.0 | 10 | 4 | US-10-763-619-4 | Sequence 4, Appl1 |
| 433 | 48 | 100.0 | 9 | 4 | US-10-171-417-8 | Sequence 8, Appl1 | 506 | 48 | 100.0 | 10 | 5 | US-10-681-381B-47 | Sequence 47, Appl |
| 434 | 48 | 100.0 | 9 | 4 | US-10-246-837-8 | Sequence 8, Appl1 | 507 | 48 | 100.0 | 10 | 5 | US-10-482-793-9 | Sequence 9, Appl1 |
| 435 | 48 | 100.0 | 9 | 4 | US-10-120-145-17 | Sequence 17, Appl | 508 | 48 | 100.0 | 10 | 5 | US-10-416-456A-29 | Sequence 29, Appl |
| 436 | 48 | 100.0 | 9 | 4 | US-10-203-013-27 | Sequence 27, Appl | 509 | 48 | 100.0 | 10 | 5 | US-10-683-451-13 | Sequence 13, Appl |
| 437 | 48 | 100.0 | 9 | 4 | US-10-203-013-29 | Sequence 29, Appl | 510 | 48 | 100.0 | 10 | 5 | US-10-946-786-7 | Sequence 7, Appl1 |
| 438 | 48 | 100.0 | 9 | 4 | US-10-287-841-8 | Sequence 8, Appl1 | 511 | 48 | 100.0 | 10 | 5 | US-10-854-735-30 | Sequence 30, Appl |
| 439 | 48 | 100.0 | 9 | 4 | US-10-136-187-27 | Sequence 27, Appl | 512 | 48 | 100.0 | 10 | 5 | US-10-658-752-2 | Sequence 2, Appl1 |
| 440 | 48 | 100.0 | 9 | 4 | US-10-354-774-32 | Sequence 32, Appl | 513 | 48 | 100.0 | 10 | 5 | US-10-835-533-30 | Sequence 30, Appl |
| 441 | 48 | 100.0 | 9 | 4 | US-10-271-012-32 | Sequence 32, Appl | 514 | 48 | 100.0 | 10 | 5 | US-10-968-432-60 | Sequence 60, Appl |
| 442 | 48 | 100.0 | 9 | 4 | US-10-364-649-56 | Sequence 56, Appl | 515 | 48 | 100.0 | 10 | 5 | US-10-949-685-1 | Sequence 1, Appl1 |
| 443 | 48 | 100.0 | 9 | 4 | US-10-665-227-6 | Sequence 6, Appl1 | 516 | 48 | 100.0 | 10 | 5 | US-10-917-844-108 | Sequence 108, App |
| 444 | 48 | 100.0 | 9 | 4 | US-10-350-682-7 | Sequence 7, Appl1 | 517 | 48 | 100.0 | 10 | 5 | US-10-846-341-17 | Sequence 17, Appl |
| 445 | 48 | 100.0 | 9 | 4 | US-10-729-122-32 | Sequence 32, Appl | 518 | 48 | 100.0 | 10 | 5 | US-10-990-207-9 | Sequence 9, Appl1 |
| 446 | 48 | 100.0 | 9 | 4 | US-10-729-039-32 | Sequence 32, Appl | 519 | 48 | 100.0 | 10 | 5 | US-10-501-071-12 | Sequence 12, Appl |
| 447 | 48 | 100.0 | 9 | 4 | US-10-723-933-66 | Sequence 66, Appl | 520 | 48 | 100.0 | 10 | 5 | US-10-496-905-640 | Sequence 640, App |
| 448 | 48 | 100.0 | 9 | 5 | US-10-729-527-32 | Sequence 32, Appl | 521 | 48 | 100.0 | 10 | 5 | US-10-496-905-641 | Sequence 641, App |
| 449 | 48 | 100.0 | 9 | 5 | US-10-727-898-32 | Sequence 32, Appl | 522 | 48 | 100.0 | 10 | 5 | US-10-496-905-642 | Sequence 642, App |
| 450 | 48 | 100.0 | 9 | 5 | US-10-728-696-32 | Sequence 32, Appl | 523 | 48 | 100.0 | 10 | 5 | US-10-496-905-643 | Sequence 643, App |
| 451 | 48 | 100.0 | 9 | 5 | US-10-850-873-27 | Sequence 27, Appl | 524 | 48 | 100.0 | 10 | 5 | US-10-496-905-644 | Sequence 644, App |
| 452 | 48 | 100.0 | 9 | 5 | US-10-946-786-6 | Sequence 6, Appl1 | 525 | 48 | 100.0 | 10 | 5 | US-10-496-905-645 | Sequence 645, App |
| 453 | 48 | 100.0 | 9 | 5 | US-10-899-771-28 | Sequence 28, Appl | 526 | 48 | 100.0 | 10 | 6 | US-11-099-302-3 | Sequence 3, Appl1 |
| 454 | 48 | 100.0 | 9 | 5 | US-10-687-060-27 | Sequence 27, Appl | 527 | 48 | 100.0 | 11 | 3 | US-09-773-866-2 | Sequence 2, Appl1 |
| 455 | 48 | 100.0 | 9 | 5 | US-10-485-048-27 | Sequence 27, Appl | 528 | 48 | 100.0 | 11 | 3 | US-09-814-569-2 | Sequence 2, Appl1 |
| 456 | 48 | 100.0 | 9 | 5 | US-10-485-048-29 | Sequence 29, Appl | 529 | 48 | 100.0 | 11 | 3 | US-09-887-853-11 | Sequence 11, Appl |
| 457 | 48 | 100.0 | 9 | 5 | US-10-658-752-5 | Sequence 5, Appl1 | 530 | 48 | 100.0 | 11 | 3 | US-09-815-534A-8 | Sequence 8, Appl1 |
| 458 | 48 | 100.0 | 9 | 5 | US-10-944-496-16 | Sequence 16, Appl | 531 | 48 | 100.0 | 11 | 4 | US-10-105-717-4 | Sequence 4, Appl1 |
| 459 | 48 | 100.0 | 9 | 5 | US-10-501-071-1 | Sequence 1, Appl1 | 532 | 48 | 100.0 | 11 | 4 | US-10-271-145-4 | Sequence 4, Appl1 |
| 460 | 48 | 100.0 | 9 | 5 | US-10-501-071-11 | Sequence 11, Appl | 533 | 48 | 100.0 | 11 | 4 | US-10-380-932-1 | Sequence 1, Appl1 |
| 461 | 48 | 100.0 | 9 | 5 | US-10-413-537-25 | Sequence 25, Appl | 534 | 48 | 100.0 | 11 | 4 | US-10-665-227-8 | Sequence 8, Appl1 |
| 462 | 48 | 100.0 | 9 | 6 | US-11-015-730-4 | Sequence 4, Appl1 | 535 | 48 | 100.0 | 11 | 4 | US-10-685-105-26 | Sequence 26, Appl |
| 463 | 48 | 100.0 | 9 | 6 | US-11-144-912-15 | Sequence 15, Appl | 536 | 48 | 100.0 | 11 | 4 | US-10-467-048A-9 | Sequence 9, Appl1 |
| 464 | 48 | 100.0 | 9 | 6 | US-11-001-241-32 | Sequence 32, Appl | 537 | 48 | 100.0 | 11 | 4 | US-10-723-933-59 | Sequence 59, Appl |
| 465 | 48 | 100.0 | 10 | 2 | US-08-981-490B-5 | Sequence 5, Appl1 | 538 | 48 | 100.0 | 11 | 4 | US-10-723-933-64 | Sequence 64, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|----|---|-------------------|--------------------|-----|----|-------|----|---|----------------------|--------------------|
| 539 | 48 | 100.0 | 11 | 4 | US-10-723-933-71 | Sequence 71, Appl | 612 | 48 | 100.0 | 14 | 2 | US-08-464-363-76 | Sequence 76, Appl |
| 540 | 48 | 100.0 | 11 | 4 | US-10-723-933-72 | Sequence 72, Appl | 613 | 48 | 100.0 | 14 | 3 | US-09-374-671-58 | Sequence 58, Appl |
| 541 | 48 | 100.0 | 11 | 4 | US-10-748-055-25 | Sequence 25, Appl | 614 | 48 | 100.0 | 14 | 3 | US-09-823-266-1 | Sequence 1, Appl |
| 542 | 48 | 100.0 | 11 | 5 | US-10-859-700-8 | Sequence 8, Appl | 615 | 48 | 100.0 | 14 | 3 | US-09-900-530A-19 | Sequence 19, Appl |
| 543 | 48 | 100.0 | 11 | 5 | US-10-946-786-8 | Sequence 8, Appl | 616 | 48 | 100.0 | 14 | 3 | US-09-784-199-9 | Sequence 9, Appl |
| 544 | 48 | 100.0 | 11 | 5 | US-10-683-547-11 | Sequence 11, Appl | 617 | 48 | 100.0 | 14 | 4 | US-10-004-81-32 | Sequence 32, Appl |
| 545 | 48 | 100.0 | 11 | 5 | US-10-612-358-8 | Sequence 8, Appl | 618 | 48 | 100.0 | 14 | 4 | US-10-196-107A-58 | Sequence 58, Appl |
| 546 | 48 | 100.0 | 11 | 5 | US-10-491-677-1 | Sequence 1, Appl | 619 | 48 | 100.0 | 14 | 4 | US-10-155-419-1 | Sequence 1, Appl |
| 547 | 48 | 100.0 | 11 | 5 | US-10-508-791-1 | Sequence 1, Appl | 620 | 48 | 100.0 | 14 | 4 | US-10-357-822-30 | Sequence 30, Appl |
| 548 | 48 | 100.0 | 11 | 5 | US-10-681-207-3 | Sequence 3, Appl | 621 | 48 | 100.0 | 14 | 4 | US-10-463-113-76 | Sequence 76, Appl |
| 549 | 48 | 100.0 | 11 | 5 | US-10-681-207-7 | Sequence 7, Appl | 622 | 48 | 100.0 | 14 | 4 | US-10-456-129-16 | Sequence 16, Appl |
| 550 | 48 | 100.0 | 11 | 5 | US-10-508-894-1 | Sequence 1, Appl | 623 | 48 | 100.0 | 14 | 4 | US-10-247-539-100 | Sequence 100, Appl |
| 551 | 48 | 100.0 | 11 | 5 | US-10-470-958-5 | Sequence 5, Appl | 624 | 48 | 100.0 | 14 | 4 | US-10-257-884A-11 | Sequence 11, Appl |
| 552 | 48 | 100.0 | 11 | 5 | US-10-508-822-1 | Sequence 1, Appl | 625 | 48 | 100.0 | 14 | 4 | US-10-478-442-15 | Sequence 15, Appl |
| 553 | 48 | 100.0 | 11 | 5 | US-10-511-055-10 | Sequence 10, Appl | 626 | 48 | 100.0 | 14 | 4 | US-10-608-540-49 | Sequence 49, Appl |
| 554 | 48 | 100.0 | 11 | 6 | US-11-014-187-49 | Sequence 49, Appl | 627 | 48 | 100.0 | 14 | 5 | US-10-653-350-2 | Sequence 2, Appl |
| 555 | 48 | 100.0 | 12 | 3 | US-09-921-992-83 | Sequence 83, Appl | 628 | 48 | 100.0 | 14 | 5 | US-10-851-918B-7 | Sequence 7, Appl |
| 556 | 48 | 100.0 | 12 | 3 | US-09-946-893-3 | Sequence 3, Appl | 629 | 48 | 100.0 | 14 | 5 | US-10-975-582-32 | Sequence 32, Appl |
| 557 | 48 | 100.0 | 12 | 3 | US-09-927-436-1 | Sequence 1, Appl | 630 | 48 | 100.0 | 15 | 3 | US-09-374-671-53 | Sequence 53, Appl |
| 558 | 48 | 100.0 | 12 | 4 | US-10-171-417-4 | Sequence 4, Appl | 631 | 48 | 100.0 | 15 | 3 | US-09-821-883-16 | Sequence 16, Appl |
| 559 | 48 | 100.0 | 12 | 4 | US-10-008-960-4 | Sequence 4, Appl | 632 | 48 | 100.0 | 15 | 3 | US-09-921-992-85 | Sequence 85, Appl |
| 560 | 48 | 100.0 | 12 | 4 | US-10-465-789A-47 | Sequence 47, Appl | 633 | 48 | 100.0 | 15 | 3 | US-09-728-653-2 | Sequence 2, Appl |
| 561 | 48 | 100.0 | 12 | 4 | US-10-081-736-10 | Sequence 10, Appl | 634 | 48 | 100.0 | 15 | 4 | US-10-010-184A-4 | Sequence 4, Appl |
| 562 | 48 | 100.0 | 12 | 4 | US-10-381-870-13 | Sequence 13, Appl | 635 | 48 | 100.0 | 15 | 4 | US-10-196-407A-53 | Sequence 53, Appl |
| 563 | 48 | 100.0 | 12 | 4 | US-10-665-227-9 | Sequence 9, Appl | 636 | 48 | 100.0 | 15 | 4 | US-10-015-328-2 | Sequence 2, Appl |
| 564 | 48 | 100.0 | 12 | 4 | US-10-723-933-61 | Sequence 61, Appl | 637 | 48 | 100.0 | 15 | 4 | US-10-221-655-5 | Sequence 5, Appl |
| 565 | 48 | 100.0 | 12 | 5 | US-10-659-549-63 | Sequence 43, Appl | 638 | 48 | 100.0 | 15 | 4 | US-10-313-638-2 | Sequence 2, Appl |
| 566 | 48 | 100.0 | 12 | 5 | US-10-946-786-9 | Sequence 9, Appl | 639 | 48 | 100.0 | 15 | 5 | US-10-683-451-38 | Sequence 38, Appl |
| 567 | 48 | 100.0 | 12 | 5 | US-10-842-989-9 | Sequence 9, Appl | 640 | 48 | 100.0 | 15 | 5 | US-10-457-091-254 | Sequence 254, Appl |
| 568 | 48 | 100.0 | 12 | 5 | US-10-854-735-31 | Sequence 31, Appl | 641 | 48 | 100.0 | 15 | 5 | US-10-959-653-37 | Sequence 37, Appl |
| 569 | 48 | 100.0 | 12 | 5 | US-10-486-578-10 | Sequence 10, Appl | 642 | 48 | 100.0 | 15 | 5 | US-10-871-369-8 | Sequence 8, Appl |
| 570 | 48 | 100.0 | 12 | 5 | US-10-473-571-9 | Sequence 9, Appl | 643 | 48 | 100.0 | 15 | 5 | US-10-872-770-8 | Sequence 8, Appl |
| 571 | 48 | 100.0 | 12 | 5 | US-10-835-533-31 | Sequence 31, Appl | 644 | 48 | 100.0 | 15 | 5 | US-10-903-476-8 | Sequence 8, Appl |
| 572 | 48 | 100.0 | 12 | 5 | US-10-868-247-10 | Sequence 10, Appl | 645 | 48 | 100.0 | 15 | 5 | US-10-958-216-2 | Sequence 2, Appl |
| 573 | 48 | 100.0 | 12 | 5 | US-10-473-524-9 | Sequence 9, Appl | 646 | 48 | 100.0 | 15 | 5 | US-10-953-901-2 | Sequence 2, Appl |
| 574 | 48 | 100.0 | 12 | 5 | US-10-954-924-8 | Sequence 8, Appl | 647 | 48 | 100.0 | 15 | 5 | US-10-922-802-8 | Sequence 8, Appl |
| 575 | 48 | 100.0 | 12 | 5 | US-10-974-559-83 | Sequence 83, Appl | 648 | 48 | 100.0 | 15 | 5 | US-10-806-062-2 | Sequence 2, Appl |
| 576 | 48 | 100.0 | 12 | 6 | US-11-102-757-3 | Sequence 3, Appl | 649 | 48 | 100.0 | 15 | 5 | US-10-961-826-8 | Sequence 8, Appl |
| 577 | 48 | 100.0 | 12 | 6 | US-11-033-489-47 | Sequence 47, Appl | 650 | 48 | 100.0 | 15 | 5 | US-10-965-066-8 | Sequence 8, Appl |
| 578 | 48 | 100.0 | 12 | 6 | US-11-043-611-13 | Sequence 13, Appl | 651 | 48 | 100.0 | 15 | 5 | US-10-974-559-85 | Sequence 85, Appl |
| 579 | 48 | 100.0 | 13 | 3 | US-09-821-883-17 | Sequence 17, Appl | 652 | 48 | 100.0 | 15 | 6 | US-11-044-312-16 | Sequence 16, Appl |
| 580 | 48 | 100.0 | 13 | 3 | US-09-823-266-2 | Sequence 2, Appl | 653 | 48 | 100.0 | 15 | 6 | US-11-047-365-8 | Sequence 8, Appl |
| 581 | 48 | 100.0 | 13 | 3 | US-09-823-266-3 | Sequence 3, Appl | 654 | 48 | 100.0 | 16 | 3 | US-09-822-765A-1 | Sequence 1, Appl |
| 582 | 48 | 100.0 | 13 | 3 | US-09-823-266-4 | Sequence 4, Appl | 655 | 48 | 100.0 | 16 | 3 | US-09-809-517A-4 | Sequence 4, Appl |
| 583 | 48 | 100.0 | 13 | 3 | US-09-823-266-5 | Sequence 5, Appl | 656 | 48 | 100.0 | 16 | 3 | US-09-809-517A-29 | Sequence 29, Appl |
| 584 | 48 | 100.0 | 13 | 4 | US-10-188-602-1 | Sequence 1, Appl | 657 | 48 | 100.0 | 16 | 3 | US-09-367-309A-3 | Sequence 3, Appl |
| 585 | 48 | 100.0 | 13 | 4 | US-10-108-195-13 | Sequence 13, Appl | 658 | 48 | 100.0 | 16 | 3 | US-09-948-018-25 | Sequence 25, Appl |
| 586 | 48 | 100.0 | 13 | 4 | US-10-140-045-32 | Sequence 32, Appl | 659 | 48 | 100.0 | 16 | 3 | US-09-911-569-103 | Sequence 103, Appl |
| 587 | 48 | 100.0 | 13 | 4 | US-10-222-952A-11 | Sequence 11, Appl | 660 | 48 | 100.0 | 16 | 3 | US-09-911-569-105 | Sequence 105, Appl |
| 588 | 48 | 100.0 | 13 | 4 | US-10-155-419-2 | Sequence 2, Appl | 661 | 48 | 100.0 | 16 | 3 | US-09-405-032-168 | Sequence 168, Appl |
| 589 | 48 | 100.0 | 13 | 4 | US-10-155-419-3 | Sequence 3, Appl | 662 | 48 | 100.0 | 16 | 4 | US-10-104-610-19 | Sequence 19, Appl |
| 590 | 48 | 100.0 | 13 | 4 | US-10-155-419-4 | Sequence 4, Appl | 663 | 48 | 100.0 | 16 | 4 | US-10-200-879-103 | Sequence 103, Appl |
| 591 | 48 | 100.0 | 13 | 4 | US-10-155-419-5 | Sequence 5, Appl | 664 | 48 | 100.0 | 16 | 4 | US-10-200-879-105 | Sequence 105, Appl |
| 592 | 48 | 100.0 | 13 | 4 | US-10-009-792A-1 | Sequence 1, Appl | 665 | 48 | 100.0 | 16 | 4 | US-10-282-122A-43329 | Sequence 43329, A |
| 593 | 48 | 100.0 | 13 | 4 | US-10-356-088-64 | Sequence 64, Appl | 666 | 48 | 100.0 | 16 | 5 | US-10-681-181B-48 | Sequence 48, Appl |
| 594 | 48 | 100.0 | 13 | 4 | US-10-414-760-20 | Sequence 20, Appl | 667 | 48 | 100.0 | 16 | 5 | US-10-738-423-23 | Sequence 23, Appl |
| 595 | 48 | 100.0 | 13 | 4 | US-10-385-415-87 | Sequence 87, Appl | 668 | 48 | 100.0 | 16 | 5 | US-10-658-352-4 | Sequence 4, Appl |
| 596 | 48 | 100.0 | 13 | 4 | US-10-676-299-11 | Sequence 11, Appl | 669 | 48 | 100.0 | 16 | 5 | US-10-658-752-29 | Sequence 29, Appl |
| 597 | 48 | 100.0 | 13 | 4 | US-10-676-296-11 | Sequence 11, Appl | 670 | 48 | 100.0 | 16 | 5 | US-10-762-159-168 | Sequence 168, Appl |
| 598 | 48 | 100.0 | 13 | 4 | US-10-706-116-21 | Sequence 21, Appl | 671 | 48 | 100.0 | 17 | 6 | US-11-058-073-168 | Sequence 168, Appl |
| 599 | 48 | 100.0 | 13 | 4 | US-10-799-326-64 | Sequence 64, Appl | 672 | 48 | 100.0 | 17 | 3 | US-09-809-517A-32 | Sequence 32, Appl |
| 600 | 48 | 100.0 | 13 | 5 | US-10-715-810-3 | Sequence 3, Appl | 673 | 48 | 100.0 | 17 | 3 | US-09-051-013-6 | Sequence 6, Appl |
| 601 | 48 | 100.0 | 13 | 5 | US-10-921-676-3 | Sequence 3, Appl | 674 | 48 | 100.0 | 17 | 3 | US-09-230-846A-5 | Sequence 5, Appl |
| 602 | 48 | 100.0 | 13 | 5 | US-10-496-905-634 | Sequence 634, Appl | 675 | 48 | 100.0 | 17 | 3 | US-09-925-287-1 | Sequence 1, Appl |
| 603 | 48 | 100.0 | 13 | 5 | US-10-496-905-635 | Sequence 635, Appl | 676 | 48 | 100.0 | 17 | 4 | US-10-083-590-12 | Sequence 12, Appl |
| 604 | 48 | 100.0 | 13 | 5 | US-10-496-905-636 | Sequence 636, Appl | 677 | 48 | 100.0 | 17 | 4 | US-10-047-991-8 | Sequence 8, Appl |
| 605 | 48 | 100.0 | 13 | 5 | US-10-496-905-637 | Sequence 637, Appl | 678 | 48 | 100.0 | 17 | 4 | US-10-404-667-6 | Sequence 6, Appl |
| 606 | 48 | 100.0 | 13 | 5 | US-10-496-905-638 | Sequence 638, Appl | 679 | 48 | 100.0 | 17 | 4 | US-10-441-965-28 | Sequence 28, Appl |
| 607 | 48 | 100.0 | 13 | 5 | US-10-496-905-639 | Sequence 639, Appl | 680 | 48 | 100.0 | 17 | 4 | US-10-441-965-34 | Sequence 34, Appl |
| 608 | 48 | 100.0 | 13 | 5 | US-10-496-905-648 | Sequence 648, Appl | 681 | 48 | 100.0 | 17 | 4 | US-10-429-921-16 | Sequence 16, Appl |
| 609 | 48 | 100.0 | 13 | 6 | US-11-016-126-10 | Sequence 10, Appl | 682 | 48 | 100.0 | 17 | 5 | US-10-658-752-32 | Sequence 32, Appl |
| 610 | 48 | 100.0 | 13 | 6 | US-11-132-241-40 | Sequence 40, Appl | 683 | 48 | 100.0 | 17 | 5 | US-10-787-219A-40 | Sequence 40, Appl |
| 611 | 48 | 100.0 | 13 | 6 | US-11-144-912-17 | Sequence 17, Appl | 684 | 48 | 100.0 | 17 | 5 | US-10-429-921-16 | Sequence 16, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|----|---|---------------------|--------------------|-----|----|-------|----|---|-------------------|-------------------|
| 685 | 48 | 100.0 | 18 | 2 | US-08-954-771-47 | Sequence 47, Appl | 758 | 48 | 100.0 | 21 | 3 | US-09-841-894-41 | Sequence 41, Appl |
| 686 | 48 | 100.0 | 18 | 2 | US-08-462-386D-47 | Sequence 47, Appl | 759 | 48 | 100.0 | 21 | 3 | US-09-991-681-33 | Sequence 29, Appl |
| 687 | 48 | 100.0 | 18 | 3 | US-09-809-517A-1 | Sequence 1, Appl | 760 | 48 | 100.0 | 21 | 3 | US-09-193-881-23 | Sequence 33, Appl |
| 688 | 48 | 100.0 | 18 | 3 | US-09-864-761-34373 | Sequence 34373, A | 761 | 48 | 100.0 | 21 | 3 | US-09-736-084-98 | Sequence 98, Appl |
| 689 | 48 | 100.0 | 18 | 3 | US-09-849-243-17 | Sequence 17, Appl | 762 | 48 | 100.0 | 21 | 3 | US-09-049-695A-22 | Sequence 22, Appl |
| 690 | 48 | 100.0 | 18 | 3 | US-09-876-804A-92 | Sequence 92, Appl | 763 | 48 | 100.0 | 21 | 3 | US-09-092-297-22 | Sequence 22, Appl |
| 691 | 48 | 100.0 | 18 | 3 | US-09-795-872-1 | Sequence 1, Appl | 764 | 48 | 100.0 | 21 | 3 | US-09-092-296-20 | Sequence 20, Appl |
| 692 | 48 | 100.0 | 18 | 3 | US-09-736-476-47 | Sequence 47, Appl | 765 | 48 | 100.0 | 21 | 3 | US-09-104-408-37 | Sequence 37, Appl |
| 693 | 48 | 100.0 | 18 | 4 | US-10-105-717-3 | Sequence 3, Appl | 766 | 48 | 100.0 | 21 | 3 | US-09-939-126-8 | Sequence 8, Appl |
| 694 | 48 | 100.0 | 18 | 4 | US-10-371-145-3 | Sequence 3, Appl | 767 | 48 | 100.0 | 21 | 3 | US-09-939-126-9 | Sequence 9, Appl |
| 695 | 48 | 100.0 | 18 | 4 | US-10-383-675-45 | Sequence 45, Appl | 768 | 48 | 100.0 | 21 | 3 | US-09-939-126-10 | Sequence 10, Appl |
| 696 | 48 | 100.0 | 18 | 4 | US-10-100-699-3 | Sequence 3, Appl | 769 | 48 | 100.0 | 21 | 3 | US-09-939-126-11 | Sequence 11, Appl |
| 697 | 48 | 100.0 | 18 | 4 | US-10-662-824-1 | Sequence 1, Appl | 770 | 48 | 100.0 | 21 | 3 | US-09-939-126-12 | Sequence 12, Appl |
| 698 | 48 | 100.0 | 18 | 4 | US-10-815-402-22 | Sequence 22, Appl | 771 | 48 | 100.0 | 21 | 3 | US-09-832-464-21 | Sequence 21, Appl |
| 699 | 48 | 100.0 | 18 | 5 | US-10-647-654-42 | Sequence 42, Appl | 772 | 48 | 100.0 | 21 | 3 | US-09-104-750-53 | Sequence 53, Appl |
| 700 | 48 | 100.0 | 18 | 5 | US-10-835-517-47 | Sequence 47, Appl | 773 | 48 | 100.0 | 21 | 3 | US-09-080-140-31 | Sequence 31, Appl |
| 701 | 48 | 100.0 | 18 | 5 | US-10-914-165-45 | Sequence 45, Appl | 774 | 48 | 100.0 | 21 | 3 | US-09-789-210-76 | Sequence 76, Appl |
| 702 | 48 | 100.0 | 18 | 5 | US-10-658-752-1 | Sequence 1, Appl | 775 | 48 | 100.0 | 21 | 4 | US-10-000-628-11 | Sequence 11, Appl |
| 703 | 48 | 100.0 | 18 | 5 | US-10-957-433-92 | Sequence 92, Appl | 776 | 48 | 100.0 | 21 | 4 | US-10-025-167-51 | Sequence 51, Appl |
| 704 | 48 | 100.0 | 18 | 5 | US-10-716-095A-7 | Sequence 7, Appl | 777 | 48 | 100.0 | 21 | 4 | US-10-082-659-16 | Sequence 16, Appl |
| 705 | 48 | 100.0 | 18 | 5 | US-10-500-307-3 | Sequence 3, Appl | 778 | 48 | 100.0 | 21 | 4 | US-10-216-408-27 | Sequence 27, Appl |
| 706 | 48 | 100.0 | 19 | 3 | US-09-849-243-12 | Sequence 12, Appl | 779 | 48 | 100.0 | 21 | 4 | US-10-060-275-5 | Sequence 5, Appl |
| 707 | 48 | 100.0 | 19 | 3 | US-09-933-899A-31 | Sequence 31, Appl | 780 | 48 | 100.0 | 21 | 4 | US-10-278-547-49 | Sequence 49, Appl |
| 708 | 48 | 100.0 | 19 | 3 | US-09-996-069-13 | Sequence 13, Appl | 781 | 48 | 100.0 | 21 | 4 | US-10-010-160-68 | Sequence 68, Appl |
| 709 | 48 | 100.0 | 19 | 3 | US-09-876-904A-627 | Sequence 627, Appl | 782 | 48 | 100.0 | 21 | 4 | US-10-338-395-29 | Sequence 29, Appl |
| 710 | 48 | 100.0 | 19 | 4 | US-10-342-103-17 | Sequence 17, Appl | 783 | 48 | 100.0 | 21 | 4 | US-10-185-567-25 | Sequence 25, Appl |
| 711 | 48 | 100.0 | 19 | 4 | US-10-219-700-32 | Sequence 32, Appl | 784 | 48 | 100.0 | 21 | 4 | US-10-191-252-13 | Sequence 13, Appl |
| 712 | 48 | 100.0 | 19 | 4 | US-10-293-580-72 | Sequence 72, Appl | 785 | 48 | 100.0 | 21 | 4 | US-10-192-254-33 | Sequence 33, Appl |
| 713 | 48 | 100.0 | 19 | 4 | US-10-279-733-18 | Sequence 18, Appl | 786 | 48 | 100.0 | 21 | 4 | US-10-449-462-104 | Sequence 104, App |
| 714 | 48 | 100.0 | 19 | 5 | US-10-968-317-31 | Sequence 31, Appl | 787 | 48 | 100.0 | 21 | 4 | US-10-417-997-16 | Sequence 16, Appl |
| 715 | 48 | 100.0 | 20 | 3 | US-09-096-749A-114 | Sequence 114, App | 788 | 48 | 100.0 | 21 | 4 | US-10-441-965-27 | Sequence 27, Appl |
| 716 | 48 | 100.0 | 20 | 3 | US-09-051-013-3 | Sequence 3, Appl | 789 | 48 | 100.0 | 21 | 4 | US-10-441-965-33 | Sequence 33, Appl |
| 717 | 48 | 100.0 | 20 | 3 | US-09-320-907B-5 | Sequence 5, Appl | 790 | 48 | 100.0 | 21 | 4 | US-10-646-873-49 | Sequence 49, Appl |
| 718 | 48 | 100.0 | 20 | 3 | US-09-903-412-114 | Sequence 114, App | 791 | 48 | 100.0 | 21 | 4 | US-10-448-525-37 | Sequence 37, Appl |
| 719 | 48 | 100.0 | 20 | 3 | US-09-300-425B-26 | Sequence 26, Appl | 792 | 48 | 100.0 | 21 | 4 | US-10-763-992-33 | Sequence 35, Appl |
| 720 | 48 | 100.0 | 20 | 4 | US-10-174-17A-114 | Sequence 114, App | 793 | 48 | 100.0 | 21 | 4 | US-10-296-085A-36 | Sequence 36, Appl |
| 721 | 48 | 100.0 | 20 | 4 | US-10-165-155-114 | Sequence 114, App | 794 | 48 | 100.0 | 21 | 4 | US-10-377-268-8 | Sequence 8, Appl |
| 722 | 48 | 100.0 | 20 | 4 | US-10-190-162-114 | Sequence 114, App | 795 | 48 | 100.0 | 21 | 4 | US-10-730-488-98 | Sequence 98, Appl |
| 723 | 48 | 100.0 | 20 | 4 | US-10-408-930-32 | Sequence 32, Appl | 796 | 48 | 100.0 | 21 | 5 | US-10-626-370-8 | Sequence 8, Appl |
| 724 | 48 | 100.0 | 20 | 4 | US-10-192-832-52 | Sequence 52, Appl | 797 | 48 | 100.0 | 21 | 5 | US-10-626-370-9 | Sequence 9, Appl |
| 725 | 48 | 100.0 | 20 | 4 | US-10-192-832-53 | Sequence 53, Appl | 798 | 48 | 100.0 | 21 | 5 | US-10-626-370-10 | Sequence 10, Appl |
| 726 | 48 | 100.0 | 20 | 4 | US-10-321-558-6 | Sequence 6, Appl | 799 | 48 | 100.0 | 21 | 5 | US-10-626-370-11 | Sequence 11, Appl |
| 727 | 48 | 100.0 | 20 | 4 | US-10-447-292-5 | Sequence 5, Appl | 800 | 48 | 100.0 | 21 | 5 | US-10-626-370-12 | Sequence 12, Appl |
| 728 | 48 | 100.0 | 20 | 4 | US-10-420-564-6 | Sequence 6, Appl | 801 | 48 | 100.0 | 21 | 5 | US-10-926-217-22 | Sequence 22, Appl |
| 729 | 48 | 100.0 | 20 | 4 | US-10-456-129-14 | Sequence 14, Appl | 802 | 48 | 100.0 | 21 | 5 | US-10-925-448-20 | Sequence 20, Appl |
| 730 | 48 | 100.0 | 20 | 4 | US-10-250-959-7 | Sequence 7, Appl | 803 | 48 | 100.0 | 21 | 5 | US-10-924-029-5 | Sequence 5, Appl |
| 731 | 48 | 100.0 | 20 | 5 | US-10-742-887-48 | Sequence 48, Appl | 804 | 48 | 100.0 | 21 | 5 | US-10-769-088-16 | Sequence 16, Appl |
| 732 | 48 | 100.0 | 20 | 5 | US-10-820-467-274 | Sequence 274, App | 805 | 48 | 100.0 | 21 | 5 | US-10-499-298-6 | Sequence 6, Appl |
| 733 | 48 | 100.0 | 20 | 5 | US-10-808-248A-7 | Sequence 7, Appl | 806 | 48 | 100.0 | 21 | 5 | US-10-771-833-6 | Sequence 6, Appl |
| 734 | 48 | 100.0 | 20 | 5 | US-10-870-399-6 | Sequence 6, Appl | 807 | 48 | 100.0 | 21 | 5 | US-10-738-780-23 | Sequence 23, Appl |
| 735 | 48 | 100.0 | 20 | 5 | US-10-984-958A-19 | Sequence 19, Appl | 808 | 48 | 100.0 | 21 | 5 | US-10-901-897-21 | Sequence 21, Appl |
| 736 | 48 | 100.0 | 20 | 5 | US-10-871-369-7 | Sequence 7, Appl | 809 | 48 | 100.0 | 21 | 5 | US-10-489-739-37 | Sequence 37, Appl |
| 737 | 48 | 100.0 | 20 | 5 | US-10-872-770-7 | Sequence 7, Appl | 810 | 48 | 100.0 | 21 | 5 | US-10-886-449-6 | Sequence 6, Appl |
| 738 | 48 | 100.0 | 20 | 5 | US-10-903-476-7 | Sequence 7, Appl | 811 | 48 | 100.0 | 21 | 5 | US-10-988-091-33 | Sequence 33, Appl |
| 739 | 48 | 100.0 | 20 | 5 | US-10-958-216-1 | Sequence 1, Appl | 812 | 48 | 100.0 | 21 | 5 | US-10-449-648-114 | Sequence 104, App |
| 740 | 48 | 100.0 | 20 | 5 | US-10-953-901-1 | Sequence 1, Appl | 813 | 48 | 100.0 | 21 | 5 | US-10-750-887-14 | Sequence 14, Appl |
| 741 | 48 | 100.0 | 20 | 5 | US-10-922-802-7 | Sequence 7, Appl | 814 | 48 | 100.0 | 21 | 5 | US-10-719-144-23 | Sequence 23, Appl |
| 742 | 48 | 100.0 | 20 | 5 | US-10-806-062-1 | Sequence 1, Appl | 815 | 48 | 100.0 | 21 | 5 | US-10-719-144-23 | Sequence 23, Appl |
| 743 | 48 | 100.0 | 20 | 5 | US-10-961-826-7 | Sequence 7, Appl | 816 | 48 | 100.0 | 21 | 6 | US-11-007-835-33 | Sequence 33, Appl |
| 744 | 48 | 100.0 | 20 | 5 | US-10-965-006-7 | Sequence 7, Appl | 817 | 48 | 100.0 | 21 | 6 | US-11-049-850-22 | Sequence 22, Appl |
| 745 | 48 | 100.0 | 20 | 6 | US-11-047-365-7 | Sequence 7, Appl | 818 | 48 | 100.0 | 21 | 6 | US-11-049-923-33 | Sequence 33, Appl |
| 746 | 48 | 100.0 | 21 | 2 | US-08-926-626-13 | Sequence 13, Appl | 819 | 48 | 100.0 | 21 | 6 | US-11-043-675-31 | Sequence 31, Appl |
| 747 | 48 | 100.0 | 21 | 3 | US-09-050-516-49 | Sequence 49, Appl | 820 | 48 | 100.0 | 21 | 6 | US-11-115-678-22 | Sequence 22, Appl |
| 748 | 48 | 100.0 | 21 | 3 | US-09-276-600-11 | Sequence 11, Appl | 821 | 48 | 100.0 | 21 | 6 | US-11-122-741-37 | Sequence 37, Appl |
| 749 | 48 | 100.0 | 21 | 3 | US-09-065-383-33 | Sequence 33, Appl | 822 | 48 | 100.0 | 21 | 6 | US-11-126-456-22 | Sequence 22, Appl |
| 750 | 48 | 100.0 | 21 | 3 | US-09-099-823-27 | Sequence 27, Appl | 823 | 48 | 100.0 | 21 | 6 | US-11-021-823-68 | Sequence 68, Appl |
| 751 | 48 | 100.0 | 21 | 3 | US-09-234-717-25 | Sequence 25, Appl | 824 | 48 | 100.0 | 21 | 6 | US-11-155-678-11 | Sequence 11, Appl |
| 752 | 48 | 100.0 | 21 | 3 | US-09-850-178-19 | Sequence 19, Appl | 825 | 48 | 100.0 | 22 | 3 | US-09-331-631A-16 | Sequence 16, Appl |
| 753 | 48 | 100.0 | 21 | 3 | US-09-193-538-23 | Sequence 23, Appl | 826 | 48 | 100.0 | 22 | 4 | US-09-911-569-102 | Sequence 102, App |
| 754 | 48 | 100.0 | 21 | 3 | US-09-250-883-23 | Sequence 23, Appl | 827 | 48 | 100.0 | 22 | 4 | US-10-200-879-102 | Sequence 102, App |
| 755 | 48 | 100.0 | 21 | 3 | US-09-096-359-33 | Sequence 33, Appl | 828 | 48 | 100.0 | 22 | 4 | US-10-147-095-16 | Sequence 16, Appl |
| 756 | 48 | 100.0 | 21 | 3 | US-09-215-652-48 | Sequence 48, Appl | 829 | 48 | 100.0 | 23 | 3 | US-09-939-126-7 | Sequence 7, Appl |
| 757 | 48 | 100.0 | 21 | 3 | US-09-347-064-18 | Sequence 18, Appl | 830 | 48 | 100.0 | 23 | 3 | US-09-897-776A-31 | Sequence 31, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|----|---|---------------------|-------------------|-----|----|-------|----|---|---------------------|-------------------|
| 831 | 48 | 100.0 | 23 | 3 | US-09-969-748C-26 | Sequence 26, Appl | 904 | 48 | 100.0 | 26 | 5 | US-10-766-102-25 | Sequence 25, Appl |
| 832 | 48 | 100.0 | 23 | 3 | US-09-949-039-6 | Sequence 6, Appl1 | 905 | 48 | 100.0 | 26 | 5 | US-10-877-952-25 | Sequence 25, Appl |
| 833 | 48 | 100.0 | 23 | 4 | US-10-105-717-5 | Sequence 5, Appl1 | 906 | 48 | 100.0 | 27 | 3 | US-09-846-729A-22 | Sequence 22, Appl |
| 834 | 48 | 100.0 | 23 | 4 | US-10-171-417-5 | Sequence 5, Appl1 | 907 | 48 | 100.0 | 27 | 3 | US-09-846-729A-26 | Sequence 26, Appl |
| 835 | 48 | 100.0 | 23 | 4 | US-10-171-417-6 | Sequence 6, Appl1 | 908 | 48 | 100.0 | 27 | 3 | US-09-898-461-9 | Sequence 9, Appl1 |
| 836 | 48 | 100.0 | 23 | 4 | US-10-771-145-5 | Sequence 5, Appl1 | 909 | 48 | 100.0 | 27 | 4 | US-10-342-103-4 | Sequence 4, Appl1 |
| 837 | 48 | 100.0 | 23 | 4 | US-10-354-774-24 | Sequence 24, Appl | 910 | 48 | 100.0 | 27 | 4 | US-10-441-667-22 | Sequence 22, Appl |
| 838 | 48 | 100.0 | 23 | 4 | US-10-271-012-24 | Sequence 24, Appl | 911 | 48 | 100.0 | 27 | 4 | US-10-441-667-26 | Sequence 26, Appl |
| 839 | 48 | 100.0 | 23 | 4 | US-10-465-789A-48 | Sequence 48, Appl | 912 | 48 | 100.0 | 27 | 4 | US-10-029-386-30005 | Sequence 30005, A |
| 840 | 48 | 100.0 | 23 | 4 | US-10-729-122-24 | Sequence 24, Appl | 913 | 48 | 100.0 | 27 | 4 | US-10-275-589-21 | Sequence 21, Appl |
| 841 | 48 | 100.0 | 23 | 4 | US-10-729-039-24 | Sequence 24, Appl | 914 | 48 | 100.0 | 27 | 5 | US-10-675-982-9 | Sequence 9, Appl1 |
| 842 | 48 | 100.0 | 23 | 4 | US-10-350-555-56 | Sequence 56, Appl | 915 | 48 | 100.0 | 28 | 3 | US-09-897-776A-10 | Sequence 10, Appl |
| 843 | 48 | 100.0 | 23 | 4 | US-10-344-607-2 | Sequence 2, Appl1 | 916 | 48 | 100.0 | 28 | 3 | US-09-774-954-14 | Sequence 14, Appl |
| 844 | 48 | 100.0 | 23 | 4 | US-10-625-047-56 | Sequence 56, Appl | 917 | 48 | 100.0 | 28 | 5 | US-10-766-102-20 | Sequence 20, Appl |
| 845 | 48 | 100.0 | 23 | 5 | US-10-622-088-92 | Sequence 92, Appl | 918 | 48 | 100.0 | 28 | 5 | US-10-877-952-20 | Sequence 20, Appl |
| 846 | 48 | 100.0 | 23 | 5 | US-10-622-088-97 | Sequence 97, Appl | 919 | 48 | 100.0 | 29 | 3 | US-09-880-901-2 | Sequence 2, Appl1 |
| 847 | 48 | 100.0 | 23 | 5 | US-10-470-987-15 | Sequence 15, Appl | 920 | 48 | 100.0 | 29 | 3 | US-09-962-756-2202 | Sequence 2202, Ap |
| 848 | 48 | 100.0 | 23 | 5 | US-10-729-527-24 | Sequence 24, Appl | 921 | 48 | 100.0 | 29 | 4 | US-10-282-121-12 | Sequence 12, Appl |
| 849 | 48 | 100.0 | 23 | 5 | US-10-727-898-24 | Sequence 24, Appl | 922 | 48 | 100.0 | 29 | 4 | US-10-149-085-14 | Sequence 14, Appl |
| 850 | 48 | 100.0 | 23 | 5 | US-10-728-696-24 | Sequence 24, Appl | 923 | 48 | 100.0 | 29 | 4 | US-10-029-386-30014 | Sequence 30014, A |
| 851 | 48 | 100.0 | 23 | 5 | US-10-626-370-7 | Sequence 7, Appl1 | 924 | 48 | 100.0 | 29 | 4 | US-10-253-471-2202 | Sequence 2202, Ap |
| 852 | 48 | 100.0 | 23 | 5 | US-10-631-258-56 | Sequence 56, Appl | 925 | 48 | 100.0 | 29 | 4 | US-10-253-493-2202 | Sequence 2202, Ap |
| 853 | 48 | 100.0 | 23 | 5 | US-10-495-715-70 | Sequence 70, Appl | 926 | 48 | 100.0 | 29 | 4 | US-10-297-585-2 | Sequence 2, Appl1 |
| 854 | 48 | 100.0 | 23 | 5 | US-10-766-102-31 | Sequence 31, Appl | 927 | 48 | 100.0 | 29 | 4 | US-10-692-151-41 | Sequence 41, Appl |
| 855 | 48 | 100.0 | 23 | 5 | US-10-966-097A-6 | Sequence 6, Appl1 | 928 | 48 | 100.0 | 29 | 4 | US-10-692-151-42 | Sequence 42, Appl |
| 856 | 48 | 100.0 | 23 | 5 | US-10-496-905-652 | Sequence 652, App | 929 | 48 | 100.0 | 29 | 4 | US-10-692-151-43 | Sequence 43, Appl |
| 857 | 48 | 100.0 | 23 | 6 | US-11-034-275-42 | Sequence 42, Appl | 930 | 48 | 100.0 | 29 | 4 | US-10-692-151-44 | Sequence 44, Appl |
| 858 | 48 | 100.0 | 23 | 6 | US-11-033-489-48 | Sequence 48, Appl | 931 | 48 | 100.0 | 29 | 4 | US-10-692-151-45 | Sequence 45, Appl |
| 859 | 48 | 100.0 | 23 | 6 | US-11-001-241-24 | Sequence 24, Appl | 932 | 48 | 100.0 | 29 | 4 | US-10-692-151-46 | Sequence 46, Appl |
| 860 | 48 | 100.0 | 24 | 3 | US-09-841-132-221 | Sequence 221, App | 933 | 48 | 100.0 | 29 | 4 | US-10-692-151-47 | Sequence 47, Appl |
| 861 | 48 | 100.0 | 24 | 3 | US-09-934-465-8 | Sequence 8, Appl | 934 | 48 | 100.0 | 29 | 4 | US-10-692-151-48 | Sequence 48, Appl |
| 862 | 48 | 100.0 | 24 | 4 | US-10-884-733-9 | Sequence 9, Appl1 | 935 | 48 | 100.0 | 29 | 5 | US-10-489-386-39 | Sequence 39, Appl |
| 863 | 48 | 100.0 | 24 | 4 | US-10-080-455-5 | Sequence 5, Appl1 | 936 | 48 | 100.0 | 29 | 5 | US-10-877-952-117 | Sequence 117, App |
| 864 | 48 | 100.0 | 24 | 4 | US-10-112-193-9 | Sequence 9, Appl1 | 937 | 48 | 100.0 | 29 | 5 | US-10-757-720-2 | Sequence 2, Appl1 |
| 865 | 48 | 100.0 | 24 | 4 | US-10-189-916A-2 | Sequence 2, Appl1 | 938 | 48 | 100.0 | 30 | 3 | US-09-664-761-36251 | Sequence 36251, A |
| 866 | 48 | 100.0 | 24 | 5 | US-10-713-391-5 | Sequence 5, Appl1 | 939 | 48 | 100.0 | 30 | 3 | US-09-754-826-3 | Sequence 3, Appl1 |
| 867 | 48 | 100.0 | 24 | 5 | US-10-872-155-221 | Sequence 221, App | 940 | 48 | 100.0 | 30 | 3 | US-09-911-569-98 | Sequence 98, Appl |
| 868 | 48 | 100.0 | 24 | 5 | US-10-861-685-8 | Sequence 8, Appl1 | 941 | 48 | 100.0 | 30 | 3 | US-09-911-569-100 | Sequence 100, App |
| 869 | 48 | 100.0 | 24 | 5 | US-10-652-879-8 | Sequence 8, Appl1 | 942 | 48 | 100.0 | 30 | 4 | US-09-911-569-104 | Sequence 104, App |
| 870 | 48 | 100.0 | 24 | 5 | US-10-750-887-10 | Sequence 10, Appl | 943 | 48 | 100.0 | 30 | 4 | US-10-200-879-98 | Sequence 98, Appl |
| 871 | 48 | 100.0 | 24 | 5 | US-10-496-905-647 | Sequence 647, App | 944 | 48 | 100.0 | 30 | 4 | US-10-200-879-100 | Sequence 100, App |
| 872 | 48 | 100.0 | 24 | 6 | US-11-033-489-121 | Sequence 121, App | 945 | 48 | 100.0 | 30 | 4 | US-10-200-879-104 | Sequence 104, App |
| 873 | 48 | 100.0 | 24 | 6 | US-11-032-294-22 | Sequence 22, Appl | 946 | 48 | 100.0 | 30 | 4 | US-10-192-832-66 | Sequence 66, Appl |
| 874 | 48 | 100.0 | 25 | 3 | US-09-864-761-45218 | Sequence 45218, A | 947 | 48 | 100.0 | 30 | 4 | US-10-192-832-67 | Sequence 67, Appl |
| 875 | 48 | 100.0 | 25 | 3 | US-09-911-569-96 | Sequence 96, Appl | 948 | 48 | 100.0 | 30 | 4 | US-10-192-832-76 | Sequence 76, Appl |
| 876 | 48 | 100.0 | 25 | 3 | US-09-897-776A-22 | Sequence 22, Appl | 949 | 48 | 100.0 | 30 | 4 | US-10-385-432-76 | Sequence 149, App |
| 877 | 48 | 100.0 | 25 | 4 | US-10-200-879-96 | Sequence 96, Appl | 950 | 48 | 100.0 | 30 | 4 | US-10-227-012-5 | Sequence 5, Appl1 |
| 878 | 48 | 100.0 | 25 | 4 | US-10-381-846-5 | Sequence 5, Appl1 | 951 | 48 | 100.0 | 30 | 5 | US-10-650-280-11 | Sequence 11, Appl |
| 879 | 48 | 100.0 | 25 | 4 | US-10-321-843-5 | Sequence 5, Appl1 | 952 | 48 | 100.0 | 31 | 3 | US-09-925-442-37 | Sequence 37, Appl |
| 880 | 48 | 100.0 | 25 | 4 | US-10-432-905-5 | Sequence 5, Appl1 | 953 | 48 | 100.0 | 31 | 3 | US-09-259-658-58 | Sequence 58, Appl |
| 881 | 48 | 100.0 | 25 | 4 | US-10-451-926-5 | Sequence 5, Appl1 | 954 | 48 | 100.0 | 31 | 3 | US-09-996-069-4 | Sequence 4, Appl1 |
| 882 | 48 | 100.0 | 25 | 4 | US-10-469-140-5 | Sequence 5, Appl1 | 955 | 48 | 100.0 | 31 | 3 | US-09-996-069-12 | Sequence 12, Appl |
| 883 | 48 | 100.0 | 25 | 4 | US-10-468-454-5 | Sequence 5, Appl1 | 956 | 48 | 100.0 | 31 | 3 | US-09-897-776A-35 | Sequence 35, Appl |
| 884 | 48 | 100.0 | 25 | 4 | US-10-467-823-5 | Sequence 5, Appl1 | 957 | 48 | 100.0 | 31 | 3 | US-09-962-756-2203 | Sequence 2203, Ap |
| 885 | 48 | 100.0 | 25 | 4 | US-10-759-138-5 | Sequence 5, Appl1 | 958 | 48 | 100.0 | 31 | 4 | US-10-003-681-1 | Sequence 1, Appl1 |
| 886 | 48 | 100.0 | 25 | 4 | US-10-344-607-14 | Sequence 14, Appl | 959 | 48 | 100.0 | 31 | 4 | US-10-253-471-2203 | Sequence 2203, Ap |
| 887 | 48 | 100.0 | 25 | 4 | US-10-344-607-18 | Sequence 18, Appl | 960 | 48 | 100.0 | 31 | 4 | US-10-253-493-2203 | Sequence 2203, Ap |
| 888 | 48 | 100.0 | 25 | 5 | US-10-482-793-29 | Sequence 29, Appl | 961 | 48 | 100.0 | 31 | 5 | US-10-766-102-35 | Sequence 35, Appl |
| 889 | 48 | 100.0 | 25 | 5 | US-10-766-102-22 | Sequence 22, Appl | 962 | 48 | 100.0 | 31 | 6 | US-11-040-686-29 | Sequence 29, Appl |
| 890 | 48 | 100.0 | 25 | 5 | US-10-481-013A-5 | Sequence 5, Appl1 | 963 | 48 | 100.0 | 32 | 3 | US-09-906-179A-214 | Sequence 214, App |
| 891 | 48 | 100.0 | 25 | 5 | US-10-978-413-5 | Sequence 5, Appl1 | 964 | 48 | 100.0 | 32 | 4 | US-10-450-295-4 | Sequence 4, Appl1 |
| 892 | 48 | 100.0 | 25 | 5 | US-10-916-548-5 | Sequence 5, Appl1 | 965 | 48 | 100.0 | 32 | 5 | US-10-997-651-27 | Sequence 27, Appl |
| 893 | 48 | 100.0 | 25 | 5 | US-10-959-509-5 | Sequence 5, Appl1 | 966 | 48 | 100.0 | 33 | 3 | US-09-839-577A-6 | Sequence 6, Appl1 |
| 894 | 48 | 100.0 | 25 | 5 | US-10-959-505-5 | Sequence 5, Appl1 | 967 | 48 | 100.0 | 33 | 3 | US-09-839-577A-7 | Sequence 7, Appl1 |
| 895 | 48 | 100.0 | 25 | 5 | US-10-978-331-5 | Sequence 5, Appl1 | 968 | 48 | 100.0 | 33 | 3 | US-09-259-658-49 | Sequence 49, Appl |
| 896 | 48 | 100.0 | 25 | 5 | US-10-507-611-5 | Sequence 5, Appl1 | 969 | 48 | 100.0 | 33 | 3 | US-09-866-538-21 | Sequence 21, Appl |
| 897 | 48 | 100.0 | 25 | 5 | US-10-979-154-5 | Sequence 5, Appl1 | 970 | 48 | 100.0 | 33 | 3 | US-09-897-776A-28 | Sequence 28, Appl |
| 898 | 48 | 100.0 | 26 | 3 | US-09-773-385-18 | Sequence 18, Appl | 971 | 48 | 100.0 | 33 | 3 | US-09-794-308-21 | Sequence 21, Appl |
| 899 | 48 | 100.0 | 26 | 3 | US-09-864-761-47310 | Sequence 47310, A | 972 | 48 | 100.0 | 33 | 3 | US-10-121-258-22 | Sequence 22, Appl |
| 900 | 48 | 100.0 | 26 | 3 | US-09-897-776A-25 | Sequence 25, Appl | 973 | 48 | 100.0 | 33 | 4 | US-10-455-713-6 | Sequence 6, Appl1 |
| 901 | 48 | 100.0 | 26 | 4 | US-10-209-041-12 | Sequence 12, Appl | 974 | 48 | 100.0 | 33 | 4 | US-10-455-713-7 | Sequence 7, Appl1 |
| 902 | 48 | 100.0 | 26 | 4 | US-10-385-415-147 | Sequence 147, App | 975 | 48 | 100.0 | 33 | 4 | US-10-455-713-7 | Sequence 7, Appl1 |
| 903 | 48 | 100.0 | 26 | 4 | US-10-433-452A-46 | Sequence 46, Appl | 976 | 48 | 100.0 | 33 | 4 | US-10-346-658-2 | Sequence 2, Appl1 |

```
977 48 100.0 33 4 US-10-723-947-144 Sequence 144, App
978 48 100.0 33 3 US-10-723-947-145 Sequence 145, App
979 48 100.0 33 5 US-10-759-762-2 Sequence 2, Appl
980 48 100.0 33 5 US-10-885-988-21 Sequence 21, Appl
981 48 100.0 33 5 US-10-766-102-28 Sequence 28, Appl
982 48 100.0 33 5 US-10-931-304-22 Sequence 22, Appl
983 48 100.0 34 4 US-10-417-923-21 Sequence 21, Appl
984 48 100.0 34 5 US-10-450-763-41501 Sequence 41501, A
985 48 100.0 34 5 US-10-997-651-26 Sequence 26, Appl
986 48 100.0 34 5 US-10-997-651-28 Sequence 28, Appl
987 48 100.0 35 3 US-09-862-756-2204 Sequence 2204, Ap
988 48 100.0 35 4 US-10-083-815-68 Sequence 68, Appl
989 48 100.0 35 4 US-10-253-471-2204 Sequence 2204, Ap
990 48 100.0 35 4 US-10-253-493-2204 Sequence 2204, Ap
991 48 100.0 35 4 US-10-425-115-194568 Sequence 194568,
992 48 100.0 35 5 US-10-997-651-24 Sequence 24, Appl
993 48 100.0 35 5 US-10-997-651-25 Sequence 25, Appl
994 48 100.0 35 5 US-10-997-651-29 Sequence 29, Appl
995 48 100.0 36 3 US-09-276-455-8 Sequence 8, Appl
996 48 100.0 36 4 US-10-216-289-12 Sequence 12, Appl
997 48 100.0 36 5 US-10-474-298-33 Sequence 33, Appl
998 48 100.0 37 3 US-09-575-847-5 Sequence 5, Appl
999 48 100.0 37 3 US-09-911-569-97 Sequence 97, Appl
1000 48 100.0 37 4 US-10-200-879-97 Sequence 97, Appl
```

ALIGNMENTS

RESULT 1

US-09-280-030-61

```
; Sequence 61, Application US/09280030A
; Patent No. US20010021515A1
```

GENERAL INFORMATION:

```
; APPLICANT: Sato, Seiji
; APPLICANT: Higaahikuni, Naohiko
; APPLICANT: Kudo, Toshiyuki
; APPLICANT: Kondo, Masaaki
; TITLE OF INVENTION: DNAS ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
; TITLE OF INVENTION: PREPARING USEFUL POLYPEPTIDES THROUGH EXPRESSION OF THE
; TITLE OF INVENTION: DNAS
; FILE REFERENCE: 382.1026
; CURRENT APPLICATION NUMBER: US/09/280.030A
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: JP10-87339/1998
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designated is
; OTHER INFORMATION: a tag for separation/purification of a fusion
; OTHER INFORMATION: protein
US-09-280-030-61
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6
```

RESULT 2

US-09-771-956-11

```
; Sequence 11, Application US/09771956
; Patent No. US20010031474A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michele
```

```
; APPLICANT: Brodbeck, Robbin
; APPLICANT: Krause, James
; TITLE OF INVENTION: Chimeric Neuropeptide Y Receptors
; FILE REFERENCE: N2000.001
; CURRENT APPLICATION NUMBER: US/09/771.956
; CURRENT FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HEXAHISTADINE
; OTHER INFORMATION: TAG
US-09-771-956-11
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6
```

RESULT 3

US-09-822-485-30

```
; Sequence 30, Application US/09822485
; Patent No. US20020001825A1
```

GENERAL INFORMATION:

```
; APPLICANT: Itoh, No. US20020001825A1yuki
; TITLE OF INVENTION: No. US20020001825A1el Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 08035.0001-01000
; CURRENT APPLICATION NUMBER: US/09/822.485
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: protein tag
US-09-822-485-30
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6
```

RESULT 4

US-09-760-008A-9

```
; Sequence 9, Application US/09760008A
; Patent No. US20020004483A1
```

GENERAL INFORMATION:

```
; APPLICANT: NISSEN, TORBEN LAUESGAARD
; APPLICANT: ANDERSEN, KIM VILBOUR
; APPLICANT: HANSEN, CHRISTIAN KARSTEN
; APPLICANT: MIKELSEN, JAN MOLLER
; TITLE OF INVENTION: G-CSF CONJUGATES
; FILE REFERENCE: 31-000700US
; CURRENT APPLICATION NUMBER: US/09/760.008A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/176.376
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/189.506
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/215.644
```

```
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 00024
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: DK PA 2000 00341
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: DK PA 2000 00943
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-09-760-008A-9
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 5
; US-09-728-911-12
; Sequence 12, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenteng
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His Tag amino acid sequence
; US-09-728-911-12
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 6
; US-09-313-942-1
; Sequence 1, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: 019957-012910US
; CURRENT APPLICATION NUMBER: US/09/211,691
```

```
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tag sequence
; US-09-313-942-1
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 7
; US-09-809-517A-11
; Sequence 11, Application US/09809517A
; Patent No. US20020034733A1
; GENERAL INFORMATION:
; APPLICANT: Lobnitz, Corinna
; TITLE OF INVENTION: No. US20020034733A1 methods for displaying (poly)peptides/pro
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
; US-09-809-517A-11
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 8
; US-09-211-691-14
; Sequence 14, Application US/09211691
; Patent No. US20020034805A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Young, N. Martin
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Fusion Proteins for Use in Enzymatic Synthesis of
; FILE REFERENCE: 019957-012910US
; CURRENT APPLICATION NUMBER: US/09/211,691
```

```
/ CURRENT FILING DATE: 1998-12-14
/ PRIOR APPLICATION NUMBER: US 60/069,443
/ PRIOR FILING DATE: 1997-12-15
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:6-His tail for
US-09-211-691-14
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 9
US-09-808-037-33
/ Sequence 33, Application US/09808037
/ Patent No. US20020052311A1
/ GENERAL INFORMATION:
/ APPLICANT: SOLOMON, Bekka
/ APPLICANT: HANAN, Elia
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
/ FILE REFERENCE: NEUROLOGICAL DISEASES AND DISORDERS
/ CURRENT APPLICATION NUMBER: US/09/808,037
/ CURRENT FILING DATE: 2001-03-15
/ PRIOR APPLICATION NUMBER: 09/629,971
/ PRIOR FILING DATE: 2000-07-31
/ PRIOR APPLICATION NUMBER: US 09/473,653
/ PRIOR FILING DATE: 1999-12-29
/ PRIOR APPLICATION NUMBER: US 60/152,417
/ PRIOR FILING DATE: 1999-09-03
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patentln version 3.0
/ SEQ ID NO 33
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: synthetic construct
US-09-808-037-33
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 10
US-09-888-615-149
/ Sequence 149, Application US/09888615
/ Patent No. US20020064856A1
/ GENERAL INFORMATION:
/ APPLICANT: PLOMMAN, GREGORY
/ APPLICANT: WHYTE, DAVID
/ APPLICANT: CAENEPEEL, SEAN
/ APPLICANT: CHARYDCZAK, GLEN
/ APPLICANT: MANNING, GERARD
/ APPLICANT: SUDARSANAM, SUCHA
/ TITLE OF INVENTION: NOVEL PROTEASES
/ FILE REFERENCE: 038602/1214
/ CURRENT APPLICATION NUMBER: US/09/888,615
/ CURRENT FILING DATE: 2001-06-26
```

```
/ PRIOR APPLICATION NUMBER: 60/214,047
/ PRIOR FILING DATE: 2000-06-26
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 149
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: His tag
US-09-888-615-149
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 11
US-09-875-519A-26
/ Sequence 26, Application US/09875519A
/ Patent No. US20020068059A1
/ GENERAL INFORMATION:
/ APPLICANT: Farries, Timothy C.
/ APPLICANT: Harrison, Richard A.
/ TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
/ FILE REFERENCE: 4-30443/A/IMU/PCT
/ CURRENT APPLICATION NUMBER: US/09/875,519A
/ CURRENT FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: PCT/GB97/00603
/ PRIOR FILING DATE: 1997-03-04
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: amino acid
US-09-875-519A-26
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 12
US-09-367-309A-4
/ Sequence 4, Application US/09367309A
/ Publication No. US20020081329A1
/ GENERAL INFORMATION:
/ APPLICANT: MACFARLAN, RODERICK I.
/ APPLICANT: MALIAROS, JIM
/ TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
/ FILE REFERENCE: 017227/0149
/ CURRENT APPLICATION NUMBER: US/09/367,309A
/ CURRENT FILING DATE: 1999-08-11
/ PRIOR APPLICATION NUMBER: PCT/AU98/00080
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: AU PO 5178
/ PRIOR FILING DATE: 1997-02-19
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 6
```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-367-309A-4

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 13

US-09-837-992-44
Sequence 44, Application US/09837992
Patent No. US20020081687A1
GENERAL INFORMATION:
APPLICANT: Tian, Hui
APPLICANT: Schultz, Joshua
APPLICANT: Shan, Bei
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Siderostolemia Susceptibility Gene (SSG) : Compositions
TITLE OF INVENTION: and Methods of Use
FILE REFERENCE: 018781-006020US
CURRENT APPLICATION NUMBER: US/09/837,992
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 60/198,465
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 60/204,234
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6-His epitope
US-09-837-992-44

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 14

US-09-871-856-18
Sequence 18, Application US/09871856
Patent No. US20020081720A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA: 1856
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: US/08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-871-856-18

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 15

US-09-801-968-22
Sequence 22, Application US/09801968
Patent No. US20020082205A1
GENERAL INFORMATION:
APPLICANT: Itoh, No. US20020082205A1uyuki
APPLICANT: Kavanaugh, W. Michael
TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
PRODUCTS
FILE REFERENCE: PP-17150.001/201130.40901
CURRENT APPLICATION NUMBER: US/09/801,968
CURRENT FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H1e6 tag
US-09-801-968-22

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
DB 1 HHHHHH 6

RESULT 16
US-09-865-363-18
Sequence 18, Application US/09865363

Publication No. US20020086826A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskevsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,363
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-865-363-18
Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHHHH 6
Db 1 HHHHH 6
RESULT 17
US-09-871-291-18
Sequence 18, Application US/09871291
Publication No. US20020086827A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskevsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,291
FILING DATE: 30-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-871-291-18
Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHHHH 6
Db 1 HHHHH 6
RESULT 18
US-09-875-338-93
Sequence 93, Application US/09875338
Patent No. US20020095024A1
GENERAL INFORMATION:
APPLICANT: MIKESELL, GLEN E.
APPLICANT: CHANG, HAN
APPLICANT: PINGER, JOSHUA N.
APPLICANT: YANG, GUOCHEN
APPLICANT: ZHOU, XIA-DI
APPLICANT: LU, PIN
APPLICANT: PEACH, ROBERT
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR
TITLE OF INVENTION: IMMUNOMODULATION
FILE REFERENCE: 3053-4071US2
CURRENT APPLICATION NUMBER: US/09/875,338
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/272,107
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/209,811
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 93
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Epitope tag
US-09-875-338-93
Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 19
US-09-988-899-5

; Sequence 5, Application US/09988899
; Patent No. US20020102613A1
; GENERAL INFORMATION:
; APPLICANT: HOGENDOORN, HENDRICUS R.J.M.
; TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
; FILE REFERENCE: DX/003 CON
; CURRENT APPLICATION NUMBER: US/09/988,899
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/US00/13682
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 99201558.6
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6X-His tag
US-09-988-899-5

Query Match

Best Local Similarity 100.0%; Score 48; DB 3; Length 6;
Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 20

US-09-798-584-16
; Sequence 16, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB: A NO. US20020102676A1 Potassium Channel Protein
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; CURRENT FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6-His epitope
US-09-798-584-16

Query Match

Best Local Similarity 100.0%; Score 48; DB 3; Length 6;
Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 21

US-09-817-764-9
; Sequence 9, Application US/09817764
; Patent No. US20020102678A1
; GENERAL INFORMATION:
; APPLICANT: HAROCH, JULIEN
; APPLICANT: ALLIGNET, JEANINE
; APPLICANT: EL SOLH, NEYNE
; TITLE OF INVENTION: STAPHYLOCOCCAL GENE, VGAC, CONFERRING RESISTANCE TO
; TITLE OF INVENTION: STREPTOGRAMIN A AND RELATED COMPOUNDS
; FILE REFERENCE: 03495.0201
; CURRENT APPLICATION NUMBER: US/09/817,764
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/197,372
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic His
US-09-817-764-9

Query Match

Best Local Similarity 100.0%; Score 48; DB 3; Length 6;
Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 22

US-09-943-382-1
; Sequence 1, Application US/09943382
; Publication No. US20020103230A1
; GENERAL INFORMATION:
; APPLICANT: RENHOME, PAUL A.
; APPLICANT: MACHAJEWSKI, TIMOTHY D.
; APPLICANT: SHAVER, CYNTHIA M.
; APPLICANT: WERNETTE-HAMMOND, MARY-ELLEN
; APPLICANT: PECCHI, SABINA
; TITLE OF INVENTION: HETEROCYCLIC COMPOUNDS
; FILE REFERENCE: 072121-0139
; CURRENT APPLICATION NUMBER: US/09/943,382
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/231,829
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6X-His tag
US-09-943-382-1

Query Match

Best Local Similarity 100.0%; Score 48; DB 3; Length 6;
Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6

Db 1 HHHHHH 6

RESULT 23

US-09-951-265-2

```
/ Sequence 2, Application US/09951265
/ Publication No. US20020107392A1
/ GENERAL INFORMATION:
/ APPLICANT: RENHORE, PAUL A.
/ APPLICANT: PECCHI, SABINA
/ APPLICANT: MACHAJEWSKI, TIMOTHY D.
/ APPLICANT: SCHAFER, CYNTHIA M.
/ APPLICANT: TAYLOR, CLARKE
/ APPLICANT: MCCREA, WILLIAM R. JR
/ APPLICANT: MCBRIDE, CHRISTOPHER
/ APPLICANT: JAZAN, ELISA
/ TITLE OF INVENTION: QUINOLINONE DERIVATIVES
/ FILE REFERENCE: 072121/0141
/ CURRENT APPLICATION NUMBER: US/09/951,265
/ PRIOR FILING DATE: 2002-12-13
/ PRIOR APPLICATION NUMBER: 60/232,159
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6X
US-09-951-265-2
```

```
Query Match      100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
DB      1 HHHHHH 6
```

```
RESULT 24
US-09-801-676A-2
/ Sequence 2, Application US/09801676A
/ Patent No. US20020114734A1
/ GENERAL INFORMATION:
/ APPLICANT: Pantoliano, Michael W.
/ APPLICANT: Bone, Roger F.
/ APPLICANT: Rhind, Alexander W.
/ APPLICANT: Saleme, Francis R.
/ TITLE OF INVENTION: Computer Program for Thermal Shift Assay
/ TITLE OF INVENTION: Apparatus for Ligand Development and
/ FILE REFERENCE: 1503.011000E
/ CURRENT APPLICATION NUMBER: US/09/801,676A
/ CURRENT FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 09/459,996
/ PRIOR FILING DATE: 1999-12-14
/ PRIOR APPLICATION NUMBER: 60/017,860
/ PRIOR FILING DATE: 1996-05-09
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 3.1
/ SEQ ID NO 2
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Six histidine epitope tag of His6D(II)-FGFR1
US-09-801-676A-2
```

```
Query Match      100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
DB      1 HHHHHH 6
```

```
RESULT 25
US-09-916-940-99
/ Sequence 99, Application US/09916940
/ Patent No. US20020127564A1
/ GENERAL INFORMATION:
/ APPLICANT: No. US20020127564A1an, Gary P
/ TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
/ FILE REFERENCE: A-64260-6/RMS/AMS
/ CURRENT APPLICATION NUMBER: US/09/916,940
/ CURRENT FILING DATE: 2001-07-27
/ PRIOR APPLICATION NUMBER: US 09/727,715
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 08/963,368
/ PRIOR FILING DATE: 1997-11-03
/ PRIOR APPLICATION NUMBER: US 08/589,109
/ PRIOR FILING DATE: 1996-01-23
/ PRIOR APPLICATION NUMBER: US 08/589,911
/ PRIOR FILING DATE: 1996-01-23
/ PRIOR APPLICATION NUMBER: US 08/789,333
/ PRIOR FILING DATE: 1997-01-23
/ PRIOR APPLICATION NUMBER: US 08/787,738
/ PRIOR FILING DATE: 1997-01-23
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 99
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: histidine tag
US-09-916-940-99
```

```
Query Match      100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
DB      1 HHHHHH 6
```

```
RESULT 26
US-09-780-933-14
/ Sequence 14, Application US/09780933
/ Patent No. US20020127652A1
/ GENERAL INFORMATION:
/ APPLICANT: SCHAMAYE, HANS T.
/ APPLICANT: ANDERSEN, KIM V.
/ APPLICANT: VAN DEN HAZEL, BART
/ APPLICANT: CHRISTIANSEN, JESPER
/ APPLICANT: UEPSEST, CLAUD B.
/ TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
/ FILE REFERENCE: 31-001000US
/ CURRENT APPLICATION NUMBER: US/09/780,933
/ CURRENT FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: PA 2000 00220
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: 60/184,035
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: PA 2000 01092
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 60/225,558
/ PRIOR FILING DATE: 2000-08-16
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
```

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-780-933-14

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 27
US-09-900-530A-15
Sequence 15, Application US/09900530A
Patent No. US20020128438A1
GENERAL INFORMATION:
APPLICANT: Seol, Dae-Mu
APPLICANT: Billiar, Timothy R.
TITLE OF INVENTION: DNA Cassette for the Production of
TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline
TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector, Their
FILE REFERENCE: 5006-1-002
CURRENT APPLICATION NUMBER: US/09/900,530A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: KR 2000-38441
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: His-tag
US-09-900-530A-15

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 28
US-09-973-145-4
Sequence 4, Application US/09973145
Patent No. US20020132248A1
GENERAL INFORMATION:
APPLICANT: Rothschild, Kenneth J.
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins
FILE REFERENCE: AMBER-06819
CURRENT APPLICATION NUMBER: US/09/973,145
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/382,950
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
NAME/KEY: misc_feature

OTHER INFORMATION: Synthetic
US-09-973-145-4

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 29
US-09-731-558-11
Sequence 11, Application US/09731558
Patent No. US20020146691A1
GENERAL INFORMATION:
APPLICANT: Case, Casey Christopher
APPLICANT: Liu, Qiang
APPLICANT: Rebar, Edward J.
TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger
TITLE OF INVENTION: Proteins for the Identification of Gene Function
FILE REFERENCE: 019496-003210US
CURRENT APPLICATION NUMBER: US/09/731,558
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: US 09/456,100
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6xHis tag
US-09-731-558-11

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 30
US-09-822-698A-22
Sequence 22, Application US/09822698A
Patent No. US20020146750A1
GENERAL INFORMATION:
APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Hendelrix, Maria P.G.
TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
FILE REFERENCE: DYX-015.1 US
CURRENT APPLICATION NUMBER: US/09/822,698A
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 09/538,913
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Microsoft Word
SEQ ID NO 22
LENGTH: 6
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: hexahistidine peptide
US-09-822-698A-22

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 31
US-09-144-886-5
Sequence 5, Application US/091444886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: His6
US-09-144-886-5

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 32
US-09-935-868-1
Sequence 1, Application US/09935868
Patent No. US20020164690A1
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Tag sequence
US-09-935-868-1

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 33
US-09-877-650-18
Sequence 18, Application US/09877650
Patent No. US20020169117A1

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: US98/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-877-650-18

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 34
US-09-814-604-9
Sequence 9, Application US/09814604
Publication No. US20030003517A1
GENERAL INFORMATION:
APPLICANT: Klein, Elliott S.
APPLICANT: Chandrasekhar Roshantha A.
TITLE OF INVENTION: Methods of Detecting Dissociated Nuclear
TITLE OF INVENTION: Hormone Receptor Ligands
FILE REFERENCE: P-AR 4528
CURRENT APPLICATION NUMBER: US/09/814,604
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: synthetic peptide
US-09-814-604-9

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
| | | | |
Db 1 HHHHHH 6

RESULT 35

US-09-939-769-94
Sequence 94, Application US/09939769
Publication No. US20030017149A1

GENERAL INFORMATION:
APPLICANT: HOFFLER, JAMES P.

APPLICANT: RUSSELL, MARIJANE

TITLE OF INVENTION: SINGLE CHAIN ANTIBODY FUSION REAGENTS THAT REGULATE
TITLE OF INVENTION: TRANSCRIPTION IN VIVO

FILE REFERENCE: 039322/0226

CURRENT APPLICATION NUMBER: US/09/939,769

CURRENT FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: 08/728,890

PRIOR FILING DATE: 1996-10-10

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 94

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: 6-His tag

US-09-939-769-94

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
| | | | |
Db 1 HHHHHH 6

RESULT 36

US-09-935-430-698

Sequence 698, Application US/09935430
Publication No. US20030017466A1

GENERAL INFORMATION:
APPLICANT: PARIS, MARY

APPLICANT: HUBERT, RENE

APPLICANT: RAITANO, ARTHUR

APPLICANT: AFAR, DANIEL

APPLICANT: LEVIN, ELANA

APPLICANT: CHALITA-ETD, PIA

APPLICANT: JAKOBOVITZ, AVA

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

FILE REFERENCE: 51158-20050.00

CURRENT APPLICATION NUMBER: US/09/935,430

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/227,098

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: 60/282,739

PRIOR FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 700

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 698

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6-His tag
US-09-935-430-698

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
| | | | |
Db 1 HHHHHH 6

RESULT 37

US-09-821-726-19
Sequence 19, Application US/09821726
Publication No. US20030017548A1

GENERAL INFORMATION:
APPLICANT: MARTIN, TERENCE E.

APPLICANT: TOBACK, F. GARY

APPLICANT: POWELL, C. THOMAS

APPLICANT: AGARWAL, KAN

TITLE OF INVENTION: GASTROKINES AND DERIVED PEPTIDES INCLUDING INHIBITORS
FILE REFERENCE: 21459/90913

CURRENT APPLICATION NUMBER: US/09/821,726

CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic His

US-09-821-726-19

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
| | | | |
Db 1 HHHHHH 6

RESULT 38

US-09-945-248B-3

Sequence 3, Application US/09945248B
Publication No. US20030017971A1

GENERAL INFORMATION:
APPLICANT: REED, ROBIN

APPLICANT: LUO, MING-JUAN

APPLICANT: ZHOU, ZHAOLAN

TITLE OF INVENTION: METHOD FOR INCREASING LEVELS OF EXPORT OF MENA FROM THE
TITLE OF INVENTION: NUCLEUS TO THE CYTOPLASM BY PROVIDING IN THE NUCLEUS

FILE REFERENCE: 55047 (70207)

CURRENT APPLICATION NUMBER: US/09/945,248B

CURRENT FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 60/229,765

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: 6-His tag

US-09-945-248B-3

Query Match 100.0%; Score 48; DB 3; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 39

US-09-997-623-41
; Sequence 41, Application US/09997623
; Publication No. US20030018175A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u8410 - protein C
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US/09/997,623
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide tag
US-09-997-623-41

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 40

US-09-978-917A-41
; Sequence 41, Application US/0978917A
; Publication No. US20030027299A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps; Maxygen Holdings
; TITLE OF INVENTION: Protein C or activated protein C-like molecules
; FILE REFERENCE: 0219u8310 - protein C
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US/09/978,917A
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide tag
US-09-978-917A-41

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 41
US-09-948-391A-43
; Sequence 43, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: six histidine
; OTHER INFORMATION: residue tag at amino terminus
US-09-948-391A-43

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 42

US-09-989-981A-11
; Sequence 11, Application US/0989981A
; Publication No. US20030049730A1
; GENERAL INFORMATION:
; APPLICANT: Hobbs, Helen H.
; APPLICANT: Shan, Bei
; APPLICANT: Barnes, Robert
; APPLICANT: Tian, Hui
; APPLICANT: Tularek Inc.
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use
; FILE REFERENCE: 018781-007320US
; CURRENT APPLICATION NUMBER: US/09/989,981A
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/252,235
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/253,645
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6-His epitope
; OTHER INFORMATION: tag
US-09-989-981A-11

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 43
US-09-904-1968-9
Sequence 9, Application US/099041968
Publication No. US20030064922A1
GENERAL INFORMATION:
APPLICANT: NISSEN, TORBEN LAUGSGAARD
APPLICANT: ANDERSEN, KIM VILBOUR
APPLICANT: HANSEN, CHRISTIAN KARSTEN
APPLICANT: MIKKELSEN, JEN MOLLER
TITLE OF INVENTION: G-CSF CONJUGATES
FILE REFERENCE: 31-000700US
CURRENT APPLICATION NUMBER: US/09/904,1968
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/760,008
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/176,376
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/189,506
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/215,644
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DK PA 2000 00024
PRIOR FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: DK PA 2000 00341
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: DK PA 2000 00943
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 9
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-904-1968-9

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 44
US-09-911-569-106
Sequence 106, Application US/09911569
Publication No. US20030069173A1
GENERAL INFORMATION:
APPLICANT: HAWLEY-NELSON, PAMELA
LAN, JIANQING
SHIH, POJEN
JESSE, JOEL A.
SCHIEFERLI, KEVIN P.
GEBREYERU, GULIAT
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREENLEE, WINNER & SULLIVAN
STREET: 5170 MANHATTAN CIRCLE, SUITE 201
CITY: BOULDER
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,569
FILING DATE: 23-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/039,780
FILING DATE: 16-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 32-95D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-911-569-106

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 45
US-09-922-226-43
Sequence 43, Application US/09922226
Publication No. US20030077664A1
GENERAL INFORMATION:
APPLICANT: Zhao, Yi
APPLICANT: Thacher, Scott M.
APPLICANT: Kusari, Jyotirmoy
APPLICANT: Xiaojia, Jia-Hao
APPLICANT: Chandraratna, Roshantha A.
TITLE OF INVENTION: Methods of Screening For Compounds That
Modulate Hormone Receptor Activity
FILE REFERENCE: P-AR 4681
CURRENT APPLICATION NUMBER: US/09/922,226
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: US 60/284,797
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-922-226-43

Query Match 100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 46
US-09-906-311C-15

```
/ Sequence 15, Application US/09906311C
/ Publication No. US20030087827A1
/ GENERAL INFORMATION:
/ APPLICANT: Lindberg, Iris
/ APPLICANT: Cameron, Angus
/ APPLICANT: Appel, Jon
/ APPLICANT: Houghten, Richard
/ TITLE OF INVENTION: Inhibiting Furin With Polypeptide Peptides
/ FILE REFERENCE: 01m36 Lindberg
/ CURRENT APPLICATION NUMBER: US/09/906,311C
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: PatentIn version 3.0, WordPerfect version 8
/ SEQ ID NO 15
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: De novo designed peptide
US-09-906-311C-15
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 47
US-09-782-587B-12
/ Sequence 12, Application US/09782587B
/ Publication No. US20030096338A1
/ GENERAL INFORMATION:
/ APPLICANT: PEDERSEN, ANDERS H.
/ APPLICANT: ANDERSON, KIM V.
/ APPLICANT: BORNAES, CLAUS
/ TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
/ FILE REFERENCE: 31-001100US
/ CURRENT APPLICATION NUMBER: US/09/782,587B
/ CURRENT FILING DATE: 2002-03-26
/ PRIOR APPLICATION NUMBER: PA 2000 00218
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: 60/184,036
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: 60/241,916
/ PRIOR FILING DATE: 2000-10-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide tag
US-09-782-587B-12
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 48
US-09-802-154-22
/ Sequence 22, Application US/09802154
/ Publication No. US20030105302A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Itoh, No. US20030105302A1Iuyuki
/ APPLICANT: Kavanagh, W. Michael
/ TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
/ TITLE OF INVENTION: PRODUCTS
/ FILE REFERENCE: PP-17149.001/201130.409
/ CURRENT APPLICATION NUMBER: US/09/802,154
/ CURRENT FILING DATE: 2001-03-07
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 22
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: His6 tag
US-09-802-154-22
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 49
US-09-961-400-43
/ Sequence 43, Application US/09961400
/ Publication No. US2003012411A1
/ GENERAL INFORMATION:
/ APPLICANT: RYBAK, SUSANNA M.
/ APPLICANT: GOLDENBERG, DAVID M.
/ APPLICANT: NEWTON, DIANNE L.
/ TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
/ TITLE OF INVENTION: CELLS
/ FILE REFERENCE: 018733/1059
/ CURRENT APPLICATION NUMBER: US/09/961,400
/ CURRENT FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 60/079,751
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 43
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-961-400-43
```

```
Query Match          100.0%; Score 48; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HHHHHH 6
    |||||
Db 1 HHHHHH 6
```

```
RESULT 50
US-09-932-165-1480
/ Sequence 1480, Application US/09932165
/ Publication No. US20030134784A1
/ GENERAL INFORMATION:
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: CHALLITA-ETID, PIA M.
/ APPLICANT: PARIS, MARY
```

APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: APAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AVA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 832H3 AND CatP2E1 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1480
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6-His tag
US-09-932-165-1480

Query Match 100.0%; Score 48; DB 3; Length 6;
Best local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHHHHH 6
Db 1 HHHHHH 6

Search completed: March 21, 2006, 11:12:34
Job time : 178 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 11:09:51 ; Search time 23 Seconds
(without alignments)
7.467 Million cell updates/sec

Title: US-10-719-523-5

Perfect score: 48

Sequence: 1 HHHHHH 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New: *
1: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubppaa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/prodata/1/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1 | 48 | 100.0 | 6 | US-10-512-184-46 | Sequence 46, App1 |
| 2 | 48 | 100.0 | 6 | US-10-967-671-18 | Sequence 18, App1 |
| 3 | 48 | 100.0 | 6 | US-10-966-648-29 | Sequence 29, App1 |
| 4 | 48 | 100.0 | 6 | US-10-497-767-5 | Sequence 5, App1 |
| 5 | 48 | 100.0 | 6 | US-10-983-174-1 | Sequence 1, App1 |
| 6 | 48 | 100.0 | 6 | US-10-475-204-28 | Sequence 28, App1 |
| 7 | 48 | 100.0 | 6 | US-10-957-351-357 | Sequence 357, App |
| 8 | 48 | 100.0 | 6 | US-10-895-064-27 | Sequence 27, App1 |
| 9 | 48 | 100.0 | 6 | US-10-950-747-12 | Sequence 12, App1 |
| 10 | 48 | 100.0 | 6 | US-10-989-767A-698 | Sequence 698, App |
| 11 | 48 | 100.0 | 6 | US-10-903-612B-120 | Sequence 120, App |
| 12 | 48 | 100.0 | 6 | US-10-857-435A-622 | Sequence 622, App |
| 13 | 48 | 100.0 | 6 | US-10-861-105-2 | Sequence 2, App1 |
| 14 | 48 | 100.0 | 6 | US-10-968-629-13 | Sequence 13, App1 |
| 15 | 48 | 100.0 | 6 | US-10-498-665-72 | Sequence 72, App1 |
| 16 | 48 | 100.0 | 6 | US-11-085-864-6 | Sequence 6, App1 |
| 17 | 48 | 100.0 | 6 | US-11-158-848-35 | Sequence 35, App1 |
| 18 | 48 | 100.0 | 6 | US-11-040-159-21 | Sequence 21, App1 |
| 19 | 48 | 100.0 | 6 | US-11-040-114-9 | Sequence 9, App1 |
| 20 | 48 | 100.0 | 6 | US-11-073-605-16 | Sequence 16, App1 |
| 21 | 48 | 100.0 | 6 | US-11-102-428-8 | Sequence 8, App1 |
| 22 | 48 | 100.0 | 6 | US-11-127-004-4 | Sequence 4, App1 |
| 23 | 48 | 100.0 | 6 | US-11-000-365-46 | Sequence 46, App1 |
| 24 | 48 | 100.0 | 6 | US-11-032-794-46 | Sequence 46, App1 |
| 25 | 48 | 100.0 | 6 | US-11-097-749-40 | Sequence 40, App1 |

| | | | | | |
|----|----|-------|----|--------------------|-------------------|
| 26 | 48 | 100.0 | 6 | US-11-006-031-20 | Sequence 20, App1 |
| 27 | 48 | 100.0 | 6 | US-11-073-927-6 | Sequence 6, App1 |
| 28 | 48 | 100.0 | 6 | US-11-114-922-91 | Sequence 91, App1 |
| 29 | 48 | 100.0 | 6 | US-11-037-243-148 | Sequence 149, App |
| 30 | 48 | 100.0 | 6 | US-11-033-039-357 | Sequence 357, App |
| 31 | 48 | 100.0 | 6 | US-11-047-383-32 | Sequence 32, App1 |
| 32 | 48 | 100.0 | 6 | US-11-124-635-14 | Sequence 14, App1 |
| 33 | 48 | 100.0 | 6 | US-11-155-446-3 | Sequence 3, App1 |
| 34 | 48 | 100.0 | 6 | US-11-202-516-22 | Sequence 22, App1 |
| 35 | 48 | 100.0 | 6 | US-11-008-570-129 | Sequence 129, App |
| 36 | 48 | 100.0 | 6 | US-11-056-182-19 | Sequence 19, App1 |
| 37 | 48 | 100.0 | 6 | US-11-153-086-5 | Sequence 5, App1 |
| 38 | 48 | 100.0 | 6 | US-11-121-612-400 | Sequence 400, App |
| 39 | 48 | 100.0 | 6 | US-11-131-744-9 | Sequence 9, App1 |
| 40 | 48 | 100.0 | 6 | US-11-194-110-20 | Sequence 20, App1 |
| 41 | 48 | 100.0 | 6 | US-11-051-178A-21 | Sequence 21, App1 |
| 42 | 48 | 100.0 | 6 | US-11-129-741-27 | Sequence 27, App1 |
| 43 | 48 | 100.0 | 6 | US-11-151-762-1 | Sequence 1, App1 |
| 44 | 48 | 100.0 | 6 | US-11-108-088-71 | Sequence 71, App1 |
| 45 | 48 | 100.0 | 6 | US-11-123-893-18 | Sequence 18, App1 |
| 46 | 48 | 100.0 | 6 | US-11-179-363-29 | Sequence 29, App1 |
| 47 | 48 | 100.0 | 7 | US-11-108-001-13 | Sequence 13, App1 |
| 48 | 48 | 100.0 | 7 | US-11-222-451-21 | Sequence 21, App1 |
| 49 | 48 | 100.0 | 8 | US-10-950-747-13 | Sequence 13, App1 |
| 50 | 48 | 100.0 | 8 | US-10-498-665-73 | Sequence 73, App1 |
| 51 | 48 | 100.0 | 8 | US-11-158-848-36 | Sequence 36, App1 |
| 52 | 48 | 100.0 | 8 | US-11-032-773-936 | Sequence 936, App |
| 53 | 48 | 100.0 | 8 | US-11-192-341-20 | Sequence 20, App1 |
| 54 | 48 | 100.0 | 9 | US-10-956-755A-100 | Sequence 100, App |
| 55 | 48 | 100.0 | 9 | US-11-119-212-27 | Sequence 27, App1 |
| 56 | 48 | 100.0 | 9 | US-11-119-212-29 | Sequence 29, App1 |
| 57 | 48 | 100.0 | 10 | US-11-157-360-9 | Sequence 9, App1 |
| 58 | 48 | 100.0 | 10 | US-11-150-533-51 | Sequence 51, App1 |
| 59 | 48 | 100.0 | 10 | US-11-187-622-31 | Sequence 31, App1 |
| 60 | 48 | 100.0 | 11 | US-10-508-893-1 | Sequence 1, App1 |
| 61 | 48 | 100.0 | 11 | US-11-154-852-1 | Sequence 1, App1 |
| 62 | 48 | 100.0 | 12 | US-11-179-363-30 | Sequence 30, App1 |
| 63 | 48 | 100.0 | 14 | US-11-192-341-10 | Sequence 10, App1 |
| 64 | 48 | 100.0 | 15 | US-10-967-671-8 | Sequence 8, App1 |
| 65 | 48 | 100.0 | 15 | US-10-903-612B-97 | Sequence 97, App1 |
| 66 | 48 | 100.0 | 15 | US-11-047-383-8 | Sequence 8, App1 |
| 67 | 48 | 100.0 | 15 | US-11-237-597-22 | Sequence 22, App1 |
| 68 | 48 | 100.0 | 15 | US-11-073-942-9 | Sequence 9, App1 |
| 69 | 48 | 100.0 | 16 | US-10-903-612B-104 | Sequence 104, App |
| 70 | 48 | 100.0 | 16 | US-11-082-544-23 | Sequence 23, App1 |
| 71 | 48 | 100.0 | 16 | US-11-195-739-13 | Sequence 13, App1 |
| 72 | 48 | 100.0 | 17 | US-11-065-943-40 | Sequence 40, App1 |
| 73 | 48 | 100.0 | 18 | US-10-914-165-45 | Sequence 45, App1 |
| 74 | 48 | 100.0 | 18 | US-10-903-612B-98 | Sequence 98, App1 |
| 75 | 48 | 100.0 | 18 | US-10-903-612B-99 | Sequence 99, App1 |
| 76 | 48 | 100.0 | 18 | US-10-903-612B-101 | Sequence 101, App |
| 77 | 48 | 100.0 | 18 | US-10-903-612B-102 | Sequence 102, App |
| 78 | 48 | 100.0 | 18 | US-10-903-612B-103 | Sequence 103, App |
| 79 | 48 | 100.0 | 18 | US-11-137-671-17 | Sequence 17, App1 |
| 80 | 48 | 100.0 | 18 | US-11-197-721-55 | Sequence 55, App1 |
| 81 | 48 | 100.0 | 18 | US-11-155-446-4 | Sequence 4, App1 |
| 82 | 48 | 100.0 | 19 | US-10-903-612B-105 | Sequence 105, App |
| 83 | 48 | 100.0 | 19 | US-10-903-612B-106 | Sequence 106, App |
| 84 | 48 | 100.0 | 19 | US-10-903-612B-107 | Sequence 107, App |
| 85 | 48 | 100.0 | 19 | US-10-903-612B-108 | Sequence 108, App |
| 86 | 48 | 100.0 | 19 | US-10-903-612B-109 | Sequence 109, App |
| 87 | 48 | 100.0 | 19 | US-11-137-671-12 | Sequence 12, App1 |
| 88 | 48 | 100.0 | 20 | US-10-967-671-7 | Sequence 7, App1 |
| 89 | 48 | 100.0 | 20 | US-10-850-207-5 | Sequence 5, App1 |
| 90 | 48 | 100.0 | 20 | US-10-503-939-14 | Sequence 14, App1 |
| 91 | 48 | 100.0 | 20 | US-11-053-187-19 | Sequence 19, App1 |
| 92 | 48 | 100.0 | 20 | US-11-047-383-7 | Sequence 7, App1 |
| 93 | 48 | 100.0 | 21 | US-11-185-111-41 | Sequence 41, App1 |
| 94 | 48 | 100.0 | 21 | US-11-148-108-51 | Sequence 51, App1 |
| 95 | 48 | 100.0 | 21 | US-11-094-071-31 | Sequence 31, App1 |
| 96 | 48 | 100.0 | 21 | US-11-201-347-25 | Sequence 25, App1 |
| 97 | 48 | 100.0 | 22 | US-11-019-027-37 | Sequence 37, App1 |
| 98 | 48 | 100.0 | 23 | US-11-225-709-37 | Sequence 37, App1 |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|--------------------|-------------------|-----|----|-------|-----|---|----------------------|-------------------|
| 99 | 48 | 100.0 | 24 | 6 | US-10-985-321A-15 | Sequence 15, Appl | 172 | 48 | 100.0 | 129 | 7 | US-11-064-774A-111 | Sequence 111, App |
| 100 | 48 | 100.0 | 24 | 7 | US-11-224-268-2 | Sequence 2, Appl1 | 173 | 48 | 100.0 | 129 | 7 | US-11-064-774A-113 | Sequence 113, App |
| 101 | 48 | 100.0 | 24 | 7 | US-11-225-709-39 | Sequence 39, Appl | 174 | 48 | 100.0 | 129 | 7 | US-11-096-568A-956 | Sequence 956, App |
| 102 | 48 | 100.0 | 24 | 7 | US-11-174-467-1 | Sequence 9, Appl1 | 175 | 48 | 100.0 | 133 | 7 | US-11-088-008-1 | Sequence 1, Appl1 |
| 103 | 48 | 100.0 | 25 | 7 | US-11-096-051-38 | Sequence 38, Appl | 176 | 48 | 100.0 | 133 | 7 | US-11-174-784-1 | Sequence 4, Appl1 |
| 104 | 48 | 100.0 | 25 | 7 | US-11-189-832-5 | Sequence 5, Appl1 | 177 | 48 | 100.0 | 139 | 7 | US-11-085-792-4 | Sequence 4, Appl1 |
| 105 | 48 | 100.0 | 25 | 7 | US-11-191-024-5 | Sequence 5, Appl1 | 178 | 48 | 100.0 | 139 | 7 | US-11-096-568A-7287 | Sequence 7287, Ap |
| 106 | 48 | 100.0 | 25 | 7 | US-11-247-356-5 | Sequence 5, Appl1 | 179 | 48 | 100.0 | 140 | 7 | US-11-082-544-60 | Sequence 60, Appl |
| 107 | 48 | 100.0 | 26 | 6 | US-10-850-207-6 | Sequence 6, Appl1 | 180 | 48 | 100.0 | 143 | 7 | US-11-116-144-166 | Sequence 166, App |
| 108 | 48 | 100.0 | 27 | 6 | US-11-086-482-2 | Sequence 2, Appl1 | 181 | 48 | 100.0 | 143 | 7 | US-11-102-883-12 | Sequence 12, Appl |
| 109 | 48 | 100.0 | 29 | 6 | US-10-850-207-7 | Sequence 7, Appl1 | 182 | 48 | 100.0 | 144 | 7 | US-11-143-947A-3 | Sequence 3, Appl1 |
| 110 | 48 | 100.0 | 29 | 6 | US-11-157-360-17 | Sequence 17, Appl | 183 | 48 | 100.0 | 144 | 7 | US-11-143-947A-3 | Sequence 3, Appl1 |
| 111 | 48 | 100.0 | 33 | 6 | US-10-209-208-22 | Sequence 22, Appl | 184 | 48 | 100.0 | 149 | 7 | US-11-156-909-19 | Sequence 19, Appl |
| 112 | 48 | 100.0 | 33 | 7 | US-11-122-795-6 | Sequence 6, Appl1 | 185 | 48 | 100.0 | 149 | 7 | US-11-156-909-23 | Sequence 23, Appl |
| 113 | 48 | 100.0 | 33 | 7 | US-11-122-795-7 | Sequence 7, Appl1 | 186 | 48 | 100.0 | 149 | 7 | US-11-156-909-27 | Sequence 27, Appl |
| 114 | 48 | 100.0 | 33 | 7 | US-11-218-880-22 | Sequence 22, Appl | 187 | 48 | 100.0 | 149 | 7 | US-11-156-909-31 | Sequence 31, Appl |
| 115 | 48 | 100.0 | 37 | 7 | US-11-219-282-15 | Sequence 15, Appl | 188 | 48 | 100.0 | 149 | 7 | US-11-156-909-35 | Sequence 35, Appl |
| 116 | 48 | 100.0 | 38 | 7 | US-11-122-795-12 | Sequence 12, Appl | 189 | 48 | 100.0 | 149 | 7 | US-11-156-909-39 | Sequence 39, Appl |
| 117 | 48 | 100.0 | 41 | 7 | US-11-131-744-5 | Sequence 5, Appl1 | 190 | 48 | 100.0 | 150 | 7 | US-11-267-310-67 | Sequence 67, Appl |
| 118 | 48 | 100.0 | 41 | 7 | US-11-121-612-296 | Sequence 296, App | 191 | 48 | 100.0 | 150 | 7 | US-11-267-310-9 | Sequence 9, Appl |
| 119 | 48 | 100.0 | 44 | 6 | US-10-816-768-91 | Sequence 91, Appl | 192 | 48 | 100.0 | 152 | 7 | US-11-075-047A-107 | Sequence 107, App |
| 120 | 48 | 100.0 | 46 | 6 | US-11-151-598-5 | Sequence 5, Appl1 | 193 | 48 | 100.0 | 152 | 7 | US-11-267-310-7 | Sequence 7, Appl |
| 121 | 48 | 100.0 | 49 | 6 | US-10-968-629-26 | Sequence 26, Appl | 194 | 48 | 100.0 | 153 | 7 | US-11-267-310-5 | Sequence 5, Appl1 |
| 122 | 48 | 100.0 | 57 | 6 | US-10-968-629-23 | Sequence 23, Appl | 195 | 48 | 100.0 | 153 | 7 | US-11-267-310-11 | Sequence 11, Appl |
| 123 | 48 | 100.0 | 57 | 6 | US-10-968-629-23 | Sequence 23, Appl | 196 | 48 | 100.0 | 155 | 6 | US-10-952-535A-17 | Sequence 17, Appl |
| 124 | 48 | 100.0 | 64 | 6 | US-10-816-768-108 | Sequence 108, App | 197 | 48 | 100.0 | 160 | 7 | US-11-143-943A-1 | Sequence 1, Appl1 |
| 125 | 48 | 100.0 | 68 | 6 | US-10-968-629-25 | Sequence 25, Appl | 198 | 48 | 100.0 | 160 | 7 | US-11-143-947A-1 | Sequence 1, Appl1 |
| 126 | 48 | 100.0 | 73 | 6 | US-10-968-629-30 | Sequence 30, Appl | 199 | 48 | 100.0 | 161 | 6 | US-10-623-155-423 | Sequence 423, App |
| 127 | 48 | 100.0 | 80 | 7 | US-10-623-155-361 | Sequence 361, App | 200 | 48 | 100.0 | 164 | 7 | US-11-108-001-2 | Sequence 2, Appl1 |
| 128 | 48 | 100.0 | 80 | 7 | US-11-030-313-1 | Sequence 1, Appl1 | 201 | 48 | 100.0 | 168 | 7 | US-11-075-047A-109 | Sequence 109, App |
| 129 | 48 | 100.0 | 82 | 6 | US-10-968-629-27 | Sequence 27, Appl | 202 | 48 | 100.0 | 170 | 6 | US-10-990-627-6 | Sequence 6, Appl1 |
| 130 | 48 | 100.0 | 89 | 6 | US-10-816-768-98 | Sequence 98, Appl | 203 | 48 | 100.0 | 172 | 7 | US-11-102-883-18 | Sequence 18, Appl |
| 131 | 48 | 100.0 | 91 | 7 | US-11-131-744-1 | Sequence 1, Appl1 | 204 | 48 | 100.0 | 173 | 7 | US-11-156-909-17 | Sequence 17, Appl |
| 132 | 48 | 100.0 | 92 | 6 | US-10-968-629-31 | Sequence 31, Appl | 205 | 48 | 100.0 | 173 | 7 | US-11-156-909-21 | Sequence 21, Appl |
| 133 | 48 | 100.0 | 95 | 7 | US-11-119-212-11 | Sequence 11, Appl | 206 | 48 | 100.0 | 173 | 7 | US-11-156-909-29 | Sequence 29, Appl |
| 134 | 48 | 100.0 | 95 | 7 | US-11-119-212-23 | Sequence 23, Appl | 207 | 48 | 100.0 | 173 | 7 | US-11-156-909-33 | Sequence 33, Appl |
| 135 | 48 | 100.0 | 96 | 6 | US-10-925-366A-222 | Sequence 222, App | 208 | 48 | 100.0 | 173 | 7 | US-11-156-909-37 | Sequence 37, Appl |
| 136 | 48 | 100.0 | 98 | 6 | US-10-952-535A-15 | Sequence 15, Appl | 209 | 48 | 100.0 | 173 | 7 | US-11-143-943A-8 | Sequence 8, Appl1 |
| 137 | 48 | 100.0 | 109 | 6 | US-10-968-629-28 | Sequence 28, Appl | 210 | 48 | 100.0 | 173 | 7 | US-11-143-947A-8 | Sequence 8, Appl1 |
| 138 | 48 | 100.0 | 111 | 6 | US-10-816-768-96 | Sequence 96, Appl | 211 | 48 | 100.0 | 174 | 7 | US-11-156-909-25 | Sequence 25, Appl |
| 139 | 48 | 100.0 | 113 | 6 | US-10-968-629-32 | Sequence 32, Appl | 212 | 48 | 100.0 | 177 | 7 | US-11-131-744-3 | Sequence 3, Appl1 |
| 140 | 48 | 100.0 | 113 | 6 | US-10-952-535A-16 | Sequence 16, Appl | 213 | 48 | 100.0 | 180 | 7 | US-11-096-568A-21170 | Sequence 21170, A |
| 141 | 48 | 100.0 | 126 | 7 | US-11-064-774A-43 | Sequence 43, Appl | 214 | 48 | 100.0 | 180 | 7 | US-11-143-943A-2 | Sequence 2, Appl1 |
| 142 | 48 | 100.0 | 126 | 7 | US-11-064-774A-53 | Sequence 53, Appl | 215 | 48 | 100.0 | 180 | 7 | US-11-143-947A-2 | Sequence 2, Appl1 |
| 143 | 48 | 100.0 | 126 | 7 | US-11-064-774A-55 | Sequence 55, Appl | 216 | 48 | 100.0 | 181 | 7 | US-11-143-943A-4 | Sequence 4, Appl1 |
| 144 | 48 | 100.0 | 126 | 7 | US-11-064-774A-57 | Sequence 57, Appl | 217 | 48 | 100.0 | 181 | 7 | US-11-143-947A-4 | Sequence 4, Appl1 |
| 145 | 48 | 100.0 | 126 | 7 | US-11-064-774A-61 | Sequence 61, Appl | 218 | 48 | 100.0 | 185 | 7 | US-11-096-568A-22116 | Sequence 22116, A |
| 146 | 48 | 100.0 | 126 | 7 | US-11-064-774A-63 | Sequence 63, Appl | 219 | 48 | 100.0 | 192 | 7 | US-11-096-568A-7286 | Sequence 7286, Ap |
| 147 | 48 | 100.0 | 126 | 7 | US-11-064-774A-65 | Sequence 65, Appl | 220 | 48 | 100.0 | 194 | 7 | US-11-096-568A-22115 | Sequence 22115, A |
| 148 | 48 | 100.0 | 127 | 7 | US-11-064-774A-47 | Sequence 47, Appl | 221 | 48 | 100.0 | 203 | 6 | US-10-816-768-100 | Sequence 100, App |
| 149 | 48 | 100.0 | 127 | 7 | US-11-064-774A-83 | Sequence 83, Appl | 222 | 48 | 100.0 | 204 | 7 | US-11-087-099-12123 | Sequence 12123, A |
| 150 | 48 | 100.0 | 127 | 7 | US-11-064-774A-85 | Sequence 85, Appl | 223 | 48 | 100.0 | 209 | 6 | US-10-518-701-6 | Sequence 6, Appl1 |
| 151 | 48 | 100.0 | 127 | 7 | US-11-064-774A-87 | Sequence 87, Appl | 224 | 48 | 100.0 | 212 | 7 | US-11-096-568A-16894 | Sequence 16894, A |
| 152 | 48 | 100.0 | 127 | 7 | US-11-064-774A-89 | Sequence 89, Appl | 225 | 48 | 100.0 | 215 | 7 | US-11-119-212-9 | Sequence 9, Appl1 |
| 153 | 48 | 100.0 | 127 | 7 | US-11-064-774A-91 | Sequence 91, Appl | 226 | 48 | 100.0 | 220 | 7 | US-11-222-451-10 | Sequence 10, Appl |
| 154 | 48 | 100.0 | 127 | 7 | US-11-064-774A-93 | Sequence 93, Appl | 227 | 48 | 100.0 | 221 | 7 | US-11-194-246-339 | Sequence 339, App |
| 155 | 48 | 100.0 | 127 | 7 | US-11-064-774A-95 | Sequence 95, Appl | 228 | 48 | 100.0 | 224 | 7 | US-11-096-568A-16893 | Sequence 16893, A |
| 156 | 48 | 100.0 | 127 | 7 | US-11-064-774A-97 | Sequence 97, Appl | 229 | 48 | 100.0 | 225 | 7 | US-11-151-598-7 | Sequence 7, Appl1 |
| 157 | 48 | 100.0 | 127 | 7 | US-11-176-525-2 | Sequence 2, Appl1 | 230 | 48 | 100.0 | 225 | 7 | US-11-151-598-8 | Sequence 8, Appl1 |
| 158 | 48 | 100.0 | 128 | 7 | US-11-064-774A-45 | Sequence 45, Appl | 231 | 48 | 100.0 | 227 | 7 | US-11-151-598-8 | Sequence 8, Appl1 |
| 159 | 48 | 100.0 | 128 | 7 | US-11-064-774A-67 | Sequence 67, Appl | 232 | 48 | 100.0 | 227 | 7 | US-11-096-568A-21272 | Sequence 21272, A |
| 160 | 48 | 100.0 | 128 | 7 | US-11-064-774A-69 | Sequence 69, Appl | 233 | 48 | 100.0 | 230 | 7 | US-11-222-451-6 | Sequence 6, Appl1 |
| 161 | 48 | 100.0 | 128 | 7 | US-11-064-774A-71 | Sequence 71, Appl | 234 | 48 | 100.0 | 231 | 7 | US-11-201-519-28 | Sequence 28, Appl |
| 162 | 48 | 100.0 | 128 | 7 | US-11-064-774A-73 | Sequence 73, Appl | 235 | 48 | 100.0 | 232 | 7 | US-11-143-943A-5 | Sequence 5, Appl1 |
| 163 | 48 | 100.0 | 128 | 7 | US-11-064-774A-75 | Sequence 75, Appl | 236 | 48 | 100.0 | 232 | 7 | US-11-143-947A-5 | Sequence 5, Appl1 |
| 164 | 48 | 100.0 | 128 | 7 | US-11-064-774A-79 | Sequence 79, Appl | 237 | 48 | 100.0 | 233 | 6 | US-10-949-720-388 | Sequence 388, App |
| 165 | 48 | 100.0 | 129 | 7 | US-11-064-774A-49 | Sequence 49, Appl | 238 | 48 | 100.0 | 239 | 7 | US-11-096-568A-7444 | Sequence 7444, Ap |
| 166 | 48 | 100.0 | 129 | 7 | US-11-064-774A-99 | Sequence 99, Appl | 239 | 48 | 100.0 | 239 | 7 | US-11-096-568A-16892 | Sequence 16892, A |
| 167 | 48 | 100.0 | 129 | 7 | US-11-064-774A-101 | Sequence 101, App | 240 | 48 | 100.0 | 243 | 7 | US-11-108-172-1122 | Sequence 1122, Ap |
| 168 | 48 | 100.0 | 129 | 7 | US-11-064-774A-103 | Sequence 103, App | 241 | 48 | 100.0 | 247 | 7 | US-11-199-915-3 | Sequence 3, Appl1 |
| 169 | 48 | 100.0 | 129 | 7 | US-11-064-774A-105 | Sequence 105, App | 242 | 48 | 100.0 | 249 | 6 | US-10-909-957-2 | Sequence 2, Appl1 |
| 170 | 48 | 100.0 | 129 | 7 | US-11-064-774A-107 | Sequence 107, App | 243 | 48 | 100.0 | 249 | 7 | US-11-201-825-7 | Sequence 7, Appl1 |
| 171 | 48 | 100.0 | 129 | 7 | US-11-064-774A-109 | Sequence 109, App | 244 | 48 | 100.0 | 249 | 7 | US-11-201-825-24 | Sequence 24, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|----------------------|---------------------|-----|----|-------|-----|---|----------------------|--------------------|
| 245 | 48 | 100.0 | 249 | 7 | US-11-096-568A-21271 | Sequence 21271, A | 318 | 48 | 100.0 | 315 | 7 | US-11-198-794-91 | Sequence 91, Appl |
| 246 | 48 | 100.0 | 252 | 7 | US-11-096-568A-12561 | Sequence 12561, A | 319 | 48 | 100.0 | 315 | 7 | US-11-198-657-91 | Sequence 2, Appl |
| 247 | 48 | 100.0 | 254 | 6 | US-10-714-887-126 | Sequence 126, App | 320 | 48 | 100.0 | 317 | 6 | US-10-000-997-2 | Sequence 2, Appl |
| 248 | 48 | 100.0 | 255 | 7 | US-11-197-488-37 | Sequence 37, Appl | 321 | 48 | 100.0 | 317 | 6 | US-10-000-997-4 | Sequence 4, Appl |
| 249 | 48 | 100.0 | 256 | 7 | US-11-124-635-7 | Sequence 7, Appl | 322 | 48 | 100.0 | 317 | 6 | US-10-000-997-6 | Sequence 8, Appl |
| 250 | 48 | 100.0 | 258 | 7 | US-11-201-825-8 | Sequence 8, Appl | 323 | 48 | 100.0 | 317 | 6 | US-10-000-997-8 | Sequence 8, Appl |
| 251 | 48 | 100.0 | 258 | 7 | US-11-201-825-25 | Sequence 25, Appl | 324 | 48 | 100.0 | 319 | 7 | US-11-032-773-955 | Sequence 955, App |
| 252 | 48 | 100.0 | 260 | 7 | US-11-197-488-23 | Sequence 23, Appl | 325 | 48 | 100.0 | 319 | 7 | US-11-096-568A-19888 | Sequence 19888, A |
| 253 | 48 | 100.0 | 260 | 7 | US-11-197-488-39 | Sequence 39, Appl | 326 | 48 | 100.0 | 320 | 7 | US-11-096-568A-6440 | Sequence 6440, App |
| 254 | 48 | 100.0 | 260 | 7 | US-11-096-568A-12560 | Sequence 12560, App | 327 | 48 | 100.0 | 322 | 6 | US-10-330-773-977 | Sequence 977, App |
| 255 | 48 | 100.0 | 261 | 7 | US-11-087-099-11099 | Sequence 11099, A | 328 | 48 | 100.0 | 324 | 7 | US-11-119-212-15 | Sequence 15, Appl |
| 256 | 48 | 100.0 | 262 | 7 | US-11-201-825-9 | Sequence 9, Appl | 329 | 48 | 100.0 | 324 | 7 | US-11-196-618-16 | Sequence 16, Appl |
| 257 | 48 | 100.0 | 262 | 7 | US-11-199-820-4 | Sequence 4, Appl | 330 | 48 | 100.0 | 324 | 7 | US-11-196-618-18 | Sequence 18, Appl |
| 258 | 48 | 100.0 | 264 | 7 | US-11-176-525-1 | Sequence 1, Appl | 331 | 48 | 100.0 | 326 | 7 | US-11-119-212-19 | Sequence 19, Appl |
| 259 | 48 | 100.0 | 267 | 6 | US-10-623-155-352 | Sequence 352, App | 332 | 48 | 100.0 | 326 | 6 | US-11-096-568A-11596 | Sequence 11596, A |
| 260 | 48 | 100.0 | 267 | 6 | US-10-503-939-15 | Sequence 15, Appl | 333 | 48 | 100.0 | 327 | 6 | US-10-055-877-183 | Sequence 183, App |
| 261 | 48 | 100.0 | 267 | 6 | US-10-503-939-16 | Sequence 16, Appl | 334 | 48 | 100.0 | 328 | 6 | US-10-714-887-350 | Sequence 350, App |
| 262 | 48 | 100.0 | 267 | 6 | US-10-503-939-17 | Sequence 17, Appl | 335 | 48 | 100.0 | 328 | 6 | US-11-096-568A-5465 | Sequence 5465, App |
| 263 | 48 | 100.0 | 267 | 6 | US-10-503-939-18 | Sequence 18, Appl | 336 | 48 | 100.0 | 329 | 7 | US-11-087-099-2753 | Sequence 2753, App |
| 264 | 48 | 100.0 | 267 | 6 | US-10-503-939-19 | Sequence 19, Appl | 337 | 48 | 100.0 | 331 | 7 | US-11-201-519-4 | Sequence 4, Appl |
| 265 | 48 | 100.0 | 267 | 6 | US-10-503-939-20 | Sequence 20, Appl | 338 | 48 | 100.0 | 331 | 7 | US-11-087-099-6481 | Sequence 6481, App |
| 266 | 48 | 100.0 | 267 | 6 | US-10-503-939-21 | Sequence 21, Appl | 339 | 48 | 100.0 | 331 | 7 | US-11-096-568A-11595 | Sequence 11595, A |
| 267 | 48 | 100.0 | 267 | 6 | US-10-503-939-22 | Sequence 22, Appl | 340 | 48 | 100.0 | 332 | 6 | US-10-949-720-405 | Sequence 405, App |
| 268 | 48 | 100.0 | 267 | 6 | US-10-503-939-23 | Sequence 23, Appl | 341 | 48 | 100.0 | 333 | 7 | US-11-096-568A-6439 | Sequence 6439, App |
| 269 | 48 | 100.0 | 267 | 6 | US-11-151-598-2 | Sequence 2, Appl | 342 | 48 | 100.0 | 334 | 6 | US-10-514-057-6 | Sequence 46, Appl |
| 270 | 48 | 100.0 | 267 | 7 | US-11-179-363-3 | Sequence 3, Appl | 343 | 48 | 100.0 | 334 | 6 | US-10-714-887-46 | Sequence 46, Appl |
| 271 | 48 | 100.0 | 272 | 7 | US-11-119-212-31 | Sequence 31, Appl | 344 | 48 | 100.0 | 337 | 7 | US-11-096-568A-5464 | Sequence 5464, App |
| 272 | 48 | 100.0 | 273 | 7 | US-11-131-744-6 | Sequence 6, Appl | 345 | 48 | 100.0 | 339 | 7 | US-11-096-568A-28931 | Sequence 28931, A |
| 273 | 48 | 100.0 | 274 | 7 | US-11-102-883-34 | Sequence 34, Appl | 346 | 48 | 100.0 | 341 | 7 | US-11-096-568A-11981 | Sequence 11981, A |
| 274 | 48 | 100.0 | 276 | 7 | US-11-038-901-19 | Sequence 19, Appl | 347 | 48 | 100.0 | 341 | 7 | US-11-087-099-11420 | Sequence 11420, A |
| 275 | 48 | 100.0 | 277 | 6 | US-10-996-0078-13 | Sequence 13, Appl | 348 | 48 | 100.0 | 346 | 7 | US-11-108-172-1085 | Sequence 1085, App |
| 276 | 48 | 100.0 | 277 | 6 | US-10-996-0078-14 | Sequence 14, Appl | 349 | 48 | 100.0 | 346 | 7 | US-11-087-099-9486 | Sequence 9486, App |
| 277 | 48 | 100.0 | 277 | 6 | US-10-996-0078-15 | Sequence 15, Appl | 350 | 48 | 100.0 | 347 | 7 | US-11-102-883-4 | Sequence 4, Appl |
| 278 | 48 | 100.0 | 279 | 7 | US-11-096-568A-21270 | Sequence 21270, A | 351 | 48 | 100.0 | 348 | 7 | US-11-096-568A-11980 | Sequence 11980, A |
| 279 | 48 | 100.0 | 285 | 6 | US-10-714-887-304 | Sequence 304, App | 352 | 48 | 100.0 | 348 | 6 | US-10-055-877-169 | Sequence 169, App |
| 280 | 48 | 100.0 | 289 | 7 | US-11-102-883-2 | Sequence 2, Appl | 353 | 48 | 100.0 | 349 | 6 | US-10-055-877-170 | Sequence 170, App |
| 281 | 48 | 100.0 | 290 | 7 | US-11-032-773-957 | Sequence 957, App | 354 | 48 | 100.0 | 349 | 6 | US-10-055-877-171 | Sequence 171, App |
| 282 | 48 | 100.0 | 292 | 7 | US-11-102-883-24 | Sequence 24, Appl | 355 | 48 | 100.0 | 350 | 7 | US-11-096-568A-32434 | Sequence 32434, A |
| 283 | 48 | 100.0 | 293 | 6 | US-10-841-956A-9 | Sequence 9, Appl | 356 | 48 | 100.0 | 351 | 7 | US-11-099-558-2 | Sequence 2, Appl |
| 284 | 48 | 100.0 | 294 | 7 | US-11-102-883-30 | Sequence 30, Appl | 357 | 48 | 100.0 | 353 | 6 | US-10-055-877-30 | Sequence 30, Appl |
| 285 | 48 | 100.0 | 295 | 7 | US-11-096-568A-7443 | Sequence 7443, App | 358 | 48 | 100.0 | 355 | 7 | US-11-096-568A-11556 | Sequence 12556, A |
| 286 | 48 | 100.0 | 296 | 7 | US-11-096-051-18 | Sequence 18, Appl | 359 | 48 | 100.0 | 356 | 6 | US-10-055-877-185 | Sequence 184, App |
| 287 | 48 | 100.0 | 298 | 7 | US-11-087-099-10462 | Sequence 10462, A | 360 | 48 | 100.0 | 356 | 6 | US-10-055-877-185 | Sequence 185, App |
| 288 | 48 | 100.0 | 299 | 6 | US-10-623-155-354 | Sequence 354, App | 361 | 48 | 100.0 | 356 | 7 | US-11-217-137-10 | Sequence 10, Appl |
| 289 | 48 | 100.0 | 299 | 7 | US-11-201-519-19 | Sequence 19, Appl | 362 | 48 | 100.0 | 359 | 7 | US-11-096-568A-28234 | Sequence 28234, A |
| 290 | 48 | 100.0 | 299 | 7 | US-11-087-099-2899 | Sequence 2899, App | 363 | 48 | 100.0 | 362 | 7 | US-11-102-883-8 | Sequence 8, Appl |
| 291 | 48 | 100.0 | 300 | 7 | US-11-102-883-6 | Sequence 6, Appl | 364 | 48 | 100.0 | 363 | 7 | US-11-096-568A-5463 | Sequence 5463, App |
| 292 | 48 | 100.0 | 301 | 7 | US-11-116-319-2 | Sequence 2, Appl | 365 | 48 | 100.0 | 364 | 7 | US-11-087-099-9934 | Sequence 9934, App |
| 293 | 48 | 100.0 | 302 | 6 | US-10-857-435A-615 | Sequence 615, App | 366 | 48 | 100.0 | 365 | 7 | US-11-096-568A-11594 | Sequence 11594, A |
| 294 | 48 | 100.0 | 302 | 7 | US-11-119-212-13 | Sequence 13, Appl | 367 | 48 | 100.0 | 366 | 7 | US-11-087-099-11191 | Sequence 11191, A |
| 295 | 48 | 100.0 | 302 | 7 | US-11-119-212-25 | Sequence 25, Appl | 368 | 48 | 100.0 | 368 | 7 | US-11-201-519-24 | Sequence 24, Appl |
| 296 | 48 | 100.0 | 303 | 7 | US-11-087-099-8877 | Sequence 8877, App | 369 | 48 | 100.0 | 368 | 7 | US-11-096-568A-32433 | Sequence 32433, A |
| 297 | 48 | 100.0 | 304 | 7 | US-11-087-099-1559 | Sequence 7559, App | 370 | 48 | 100.0 | 369 | 7 | US-11-087-099-8929 | Sequence 8929, App |
| 298 | 48 | 100.0 | 304 | 7 | US-11-096-568A-32073 | Sequence 32073, A | 371 | 48 | 100.0 | 371 | 6 | US-10-623-155-433 | Sequence 433, App |
| 299 | 48 | 100.0 | 306 | 6 | US-10-000-997-44 | Sequence 44, Appl | 372 | 48 | 100.0 | 371 | 7 | US-11-137-671-16 | Sequence 16, Appl |
| 300 | 48 | 100.0 | 306 | 7 | US-11-096-568A-32672 | Sequence 32672, A | 373 | 48 | 100.0 | 375 | 7 | US-11-096-568A-28233 | Sequence 28233, A |
| 301 | 48 | 100.0 | 308 | 6 | US-10-914-573A-1 | Sequence 1, Appl | 374 | 48 | 100.0 | 376 | 7 | US-11-087-099-6311 | Sequence 6311, App |
| 302 | 48 | 100.0 | 308 | 6 | US-10-914-573A-2 | Sequence 2, Appl | 375 | 48 | 100.0 | 378 | 7 | US-11-201-606-26 | Sequence 26, Appl |
| 303 | 48 | 100.0 | 308 | 6 | US-10-914-769-1 | Sequence 1, Appl | 376 | 48 | 100.0 | 379 | 7 | US-11-096-568A-7314 | Sequence 7314, App |
| 304 | 48 | 100.0 | 308 | 6 | US-10-914-769-2 | Sequence 2, Appl | 377 | 48 | 100.0 | 384 | 7 | US-11-075-551-32 | Sequence 32, Appl |
| 305 | 48 | 100.0 | 308 | 7 | US-11-046-456-6 | Sequence 6, Appl | 378 | 48 | 100.0 | 384 | 7 | US-11-087-099-6623 | Sequence 6623, App |
| 306 | 48 | 100.0 | 308 | 7 | US-11-046-456-6 | Sequence 6, Appl | 379 | 48 | 100.0 | 385 | 7 | US-11-096-568A-28232 | Sequence 28232, A |
| 307 | 48 | 100.0 | 308 | 7 | US-11-046-456-6 | Sequence 6, Appl | 380 | 48 | 100.0 | 385 | 7 | US-10-980-866-7 | Sequence 7, Appl |
| 308 | 48 | 100.0 | 308 | 7 | US-11-096-568A-14791 | Sequence 14791, A | 381 | 48 | 100.0 | 385 | 7 | US-11-080-866-7 | Sequence 7, Appl |
| 309 | 48 | 100.0 | 309 | 7 | US-11-245-053-9 | Sequence 28932, A | 382 | 48 | 100.0 | 381 | 7 | US-11-019-969-7 | Sequence 7, Appl |
| 310 | 48 | 100.0 | 310 | 7 | US-11-245-053-9 | Sequence 9, Appl | 383 | 48 | 100.0 | 382 | 7 | US-11-196-019A-7 | Sequence 7, Appl |
| 311 | 48 | 100.0 | 310 | 7 | US-11-086-482-3 | Sequence 3, Appl | 384 | 48 | 100.0 | 332 | 7 | US-11-143-943A-6 | Sequence 6, Appl |
| 312 | 48 | 100.0 | 310 | 7 | US-11-245-053-11 | Sequence 11, Appl | 385 | 48 | 100.0 | 333 | 7 | US-11-143-943A-6 | Sequence 6, Appl |
| 313 | 48 | 100.0 | 311 | 6 | US-10-055-877-181 | Sequence 181, App | 386 | 48 | 100.0 | 338 | 7 | US-11-123-893-11 | Sequence 11, Appl |
| 314 | 48 | 100.0 | 312 | 6 | US-10-055-877-182 | Sequence 182, App | 387 | 48 | 100.0 | 339 | 6 | US-10-853-533-3 | Sequence 3, Appl |
| 315 | 48 | 100.0 | 312 | 6 | US-10-714-887-14 | Sequence 14, App | 388 | 48 | 100.0 | 401 | 6 | US-10-949-720-419 | Sequence 419, App |
| 316 | 48 | 100.0 | 312 | 7 | US-11-245-053-10 | Sequence 10, Appl | 389 | 48 | 100.0 | 401 | 7 | US-11-053-185-6 | Sequence 6, Appl |
| 317 | 48 | 100.0 | 315 | 7 | US-11-096-568A-32071 | Sequence 32071, A | 390 | 48 | 100.0 | 404 | 7 | US-11-075-551-23 | Sequence 23, Appl |
| | | | | | US-11-198-746-91 | Sequence 91, Appl | | | | 404 | 7 | US-11-075-551-23 | Sequence 25, Appl |

| | | | | | | | | | | | | | |
|-----|----|-------|-----|---|----------------------|--------------------|-----|----|-------|------|---|----------------------|--------------------|
| 391 | 48 | 100.0 | 404 | 7 | US-11-096-568A-19887 | Sequence 19887, A | 464 | 48 | 100.0 | 614 | 7 | US-11-015-546A-20 | Sequence 20, Appl |
| 392 | 48 | 100.0 | 407 | 6 | US-10-996-104A-20 | Sequence 20, Appl | 465 | 48 | 100.0 | 615 | 6 | US-10-512-184-50 | Sequence 50, Appl |
| 393 | 48 | 100.0 | 411 | 7 | US-11-119-212-17 | Sequence 17, Appl | 466 | 48 | 100.0 | 616 | 7 | US-11-087-099-8299 | Sequence 8299, Ap |
| 394 | 48 | 100.0 | 412 | 7 | US-11-168-874-12 | Sequence 12, Appl | 467 | 48 | 100.0 | 618 | 6 | US-10-512-184-48 | Sequence 48, Appl |
| 395 | 48 | 100.0 | 413 | 7 | US-11-119-212-21 | Sequence 21, Appl | 468 | 48 | 100.0 | 619 | 7 | US-11-087-099-12402 | Sequence 12402, A |
| 396 | 48 | 100.0 | 414 | 7 | US-11-096-568A-23357 | Sequence 23357, A | 469 | 48 | 100.0 | 620 | 7 | US-11-087-099-3888 | Sequence 3888, Ap |
| 397 | 48 | 100.0 | 415 | 6 | US-10-980-866-5 | Sequence 5, Appl1 | 470 | 48 | 100.0 | 623 | 7 | US-11-087-099-5188 | Sequence 5188, Ap |
| 398 | 48 | 100.0 | 415 | 6 | US-11-019-969-5 | Sequence 5, Appl1 | 471 | 48 | 100.0 | 625 | 6 | US-10-512-184-47 | Sequence 47, Appl |
| 399 | 48 | 100.0 | 416 | 7 | US-11-196-019A-5 | Sequence 5, Appl1 | 472 | 48 | 100.0 | 626 | 6 | US-10-512-184-49 | Sequence 49, Appl |
| 400 | 48 | 100.0 | 415 | 6 | US-10-996-104A-6 | Sequence 6, Appl1 | 473 | 48 | 100.0 | 633 | 7 | US-11-087-099-554 | Sequence 554, App |
| 401 | 48 | 100.0 | 423 | 7 | US-11-096-568A-32432 | Sequence 32432, A | 474 | 48 | 100.0 | 644 | 7 | US-11-087-099-9298 | Sequence 9298, Ap |
| 402 | 48 | 100.0 | 427 | 6 | US-10-714-887-122 | Sequence 122, App | 475 | 48 | 100.0 | 645 | 7 | US-11-067-260-44 | Sequence 44, Appl |
| 403 | 48 | 100.0 | 430 | 7 | US-11-096-568A-23356 | Sequence 23356, A | 476 | 48 | 100.0 | 648 | 7 | US-11-067-260-28 | Sequence 28, Appl |
| 404 | 48 | 100.0 | 431 | 6 | US-10-949-720-410 | Sequence 410, App | 477 | 48 | 100.0 | 651 | 6 | US-10-994-820A-34 | Sequence 34, Appl |
| 405 | 48 | 100.0 | 431 | 6 | US-10-499-246-11 | Sequence 11, Appl | 478 | 48 | 100.0 | 672 | 7 | US-11-067-260-36 | Sequence 36, Appl |
| 406 | 48 | 100.0 | 433 | 7 | US-11-201-519-14 | Sequence 14, Appl | 479 | 48 | 100.0 | 675 | 7 | US-11-067-260-34 | Sequence 34, Appl |
| 407 | 48 | 100.0 | 437 | 6 | US-10-980-866-3 | Sequence 3, Appl1 | 480 | 48 | 100.0 | 680 | 6 | US-10-467-962B-101 | Sequence 101, App |
| 408 | 48 | 100.0 | 437 | 6 | US-11-019-969-3 | Sequence 3, Appl1 | 481 | 48 | 100.0 | 684 | 7 | US-11-096-568A-23369 | Sequence 23369, A |
| 409 | 48 | 100.0 | 437 | 7 | US-11-196-019A-3 | Sequence 3, Appl1 | 482 | 48 | 100.0 | 685 | 7 | US-11-169-041-194 | Sequence 194, App |
| 410 | 48 | 100.0 | 440 | 6 | US-10-933-115-2 | Sequence 2, Appl1 | 483 | 48 | 100.0 | 710 | 7 | US-11-126-022-34 | Sequence 34, Appl |
| 411 | 48 | 100.0 | 444 | 7 | US-11-131-744-7 | Sequence 7, Appl1 | 484 | 48 | 100.0 | 717 | 7 | US-11-201-519-16 | Sequence 16, Appl |
| 412 | 48 | 100.0 | 444 | 7 | US-11-143-947A-7 | Sequence 7, Appl1 | 485 | 48 | 100.0 | 725 | 6 | US-10-499-290-3 | Sequence 3, Appl1 |
| 413 | 48 | 100.0 | 446 | 7 | US-11-143-947A-7 | Sequence 7, Appl1 | 486 | 48 | 100.0 | 729 | 7 | US-11-201-519-2 | Sequence 2, Appl1 |
| 414 | 48 | 100.0 | 446 | 7 | US-11-108-172-1121 | Sequence 1121, Ap | 487 | 48 | 100.0 | 729 | 7 | US-11-222-451-12 | Sequence 12, Appl1 |
| 415 | 48 | 100.0 | 447 | 7 | US-11-096-568A-30971 | Sequence 30971, A | 488 | 48 | 100.0 | 738 | 6 | US-10-523-038-39 | Sequence 39, Appl |
| 416 | 48 | 100.0 | 449 | 7 | US-11-169-041-138 | Sequence 138, App | 489 | 48 | 100.0 | 751 | 7 | US-11-067-260-40 | Sequence 40, Appl |
| 417 | 48 | 100.0 | 449 | 7 | US-11-234-786-617 | Sequence 617, App | 490 | 48 | 100.0 | 751 | 7 | US-11-067-260-38 | Sequence 38, Appl |
| 418 | 48 | 100.0 | 460 | 6 | US-10-996-104A-22 | Sequence 22, Appl | 491 | 48 | 100.0 | 753 | 7 | US-11-067-260-48 | Sequence 48, Appl |
| 419 | 48 | 100.0 | 465 | 7 | US-11-096-568A-32100 | Sequence 32100, A | 492 | 48 | 100.0 | 763 | 7 | US-11-013-247A-35 | Sequence 35, Appl |
| 420 | 48 | 100.0 | 469 | 7 | US-11-087-099-321 | Sequence 321, App | 493 | 48 | 100.0 | 766 | 6 | US-10-821-234-1661 | Sequence 1691, Ap |
| 421 | 48 | 100.0 | 469 | 7 | US-11-087-099-6164 | Sequence 6164, Ap | 494 | 48 | 100.0 | 766 | 7 | US-11-189-301-21 | Sequence 21, Appl |
| 422 | 48 | 100.0 | 475 | 7 | US-11-096-568A-23355 | Sequence 23355, A | 495 | 48 | 100.0 | 806 | 7 | US-11-217-137-11 | Sequence 11, Appl |
| 423 | 48 | 100.0 | 475 | 7 | US-11-096-568A-32099 | Sequence 32099, A | 496 | 48 | 100.0 | 802 | 7 | US-11-201-519-10 | Sequence 10, Appl |
| 424 | 48 | 100.0 | 483 | 7 | US-11-087-099-4840 | Sequence 4840, Ap | 497 | 48 | 100.0 | 806 | 7 | US-11-067-260-38 | Sequence 38, Appl |
| 425 | 48 | 100.0 | 484 | 6 | US-10-980-866-1 | Sequence 1, Appl1 | 498 | 48 | 100.0 | 806 | 7 | US-11-067-260-42 | Sequence 42, Appl |
| 426 | 48 | 100.0 | 484 | 7 | US-11-019-869-1 | Sequence 1, Appl1 | 499 | 48 | 100.0 | 847 | 7 | US-11-038-284-42 | Sequence 42, Appl |
| 427 | 48 | 100.0 | 484 | 7 | US-11-196-019A-1 | Sequence 1, Appl1 | 500 | 48 | 100.0 | 856 | 7 | US-11-201-519-12 | Sequence 12, Appl |
| 428 | 48 | 100.0 | 487 | 7 | US-11-179-363-1 | Sequence 1, Appl1 | 501 | 48 | 100.0 | 862 | 7 | US-11-096-051-20 | Sequence 20, Appl |
| 429 | 48 | 100.0 | 489 | 6 | US-10-835-475-11 | Sequence 11, Appl | 502 | 48 | 100.0 | 879 | 7 | US-11-077-550-159 | Sequence 159, App |
| 430 | 48 | 100.0 | 490 | 7 | US-11-065-716-16 | Sequence 16, Appl | 503 | 48 | 100.0 | 881 | 6 | US-10-623-155-430 | Sequence 430, Appl |
| 431 | 48 | 100.0 | 490 | 7 | US-11-087-099-9408 | Sequence 9408, Ap | 504 | 48 | 100.0 | 884 | 7 | US-11-201-606-15 | Sequence 15, Appl |
| 432 | 48 | 100.0 | 492 | 7 | US-11-197-488-27 | Sequence 27, Appl | 505 | 48 | 100.0 | 887 | 7 | US-11-077-550-161 | Sequence 161, App |
| 433 | 48 | 100.0 | 494 | 7 | US-11-087-099-3900 | Sequence 3900, Ap | 506 | 48 | 100.0 | 920 | 6 | US-10-623-165-357 | Sequence 357, App |
| 434 | 48 | 100.0 | 494 | 7 | US-11-087-099-4874 | Sequence 4874, Ap | 507 | 48 | 100.0 | 936 | 7 | US-11-201-606-33 | Sequence 30, Appl |
| 435 | 48 | 100.0 | 496 | 7 | US-11-096-568A-29371 | Sequence 29371, A | 508 | 48 | 100.0 | 952 | 7 | US-11-087-099-8167 | Sequence 8167, Ap |
| 436 | 48 | 100.0 | 496 | 7 | US-11-096-568A-28930 | Sequence 28930, A | 509 | 48 | 100.0 | 952 | 7 | US-11-087-099-11814 | Sequence 11814, A |
| 437 | 48 | 100.0 | 510 | 7 | US-11-179-363-2 | Sequence 2, Appl1 | 510 | 48 | 100.0 | 966 | 7 | US-11-108-172-1087 | Sequence 1087, Ap |
| 438 | 48 | 100.0 | 514 | 6 | US-10-835-475-2 | Sequence 2, Appl1 | 511 | 48 | 100.0 | 1002 | 7 | US-11-201-606-34 | Sequence 34, Appl |
| 439 | 48 | 100.0 | 530 | 7 | US-11-207-078-603 | Sequence 603, App | 512 | 48 | 100.0 | 1010 | 6 | US-10-959-611-2 | Sequence 2, Appl1 |
| 440 | 48 | 100.0 | 543 | 6 | US-10-495-664-3 | Sequence 3, Appl1 | 513 | 48 | 100.0 | 1154 | 7 | US-11-207-078-611 | Sequence 611, App |
| 441 | 48 | 100.0 | 545 | 7 | US-11-096-568A-32098 | Sequence 32098, A | 514 | 48 | 100.0 | 1168 | 6 | US-10-509-422-2 | Sequence 2, Appl1 |
| 442 | 48 | 100.0 | 548 | 7 | US-11-096-568A-29370 | Sequence 29370, A | 515 | 48 | 100.0 | 1178 | 7 | US-11-087-099-10105 | Sequence 10105, A |
| 443 | 48 | 100.0 | 570 | 6 | US-10-949-720-386 | Sequence 386, App | 516 | 48 | 100.0 | 1200 | 7 | US-11-207-078-612 | Sequence 612, App |
| 444 | 48 | 100.0 | 578 | 7 | US-11-222-451-8 | Sequence 451, App | 517 | 48 | 100.0 | 1312 | 7 | US-11-067-260-32 | Sequence 32, Appl |
| 445 | 48 | 100.0 | 586 | 6 | US-10-623-155-127 | Sequence 427, App | 518 | 48 | 100.0 | 1312 | 7 | US-11-067-260-30 | Sequence 30, Appl |
| 446 | 48 | 100.0 | 589 | 6 | US-10-623-155-486 | Sequence 466, App | 519 | 48 | 100.0 | 1389 | 7 | US-11-067-260-54 | Sequence 52, Appl |
| 447 | 48 | 100.0 | 590 | 7 | US-11-067-260-50 | Sequence 50, Appl | 520 | 48 | 100.0 | 1392 | 7 | US-11-067-260-22 | Sequence 24, Appl |
| 448 | 48 | 100.0 | 593 | 7 | US-11-067-260-30 | Sequence 30, Appl | 521 | 48 | 100.0 | 1444 | 7 | US-11-067-260-46 | Sequence 46, Appl |
| 449 | 48 | 100.0 | 596 | 7 | US-11-201-519-26 | Sequence 26, Appl | 522 | 48 | 100.0 | 1474 | 7 | US-11-067-260-18 | Sequence 18, Appl |
| 450 | 48 | 100.0 | 599 | 7 | US-11-165-441-33 | Sequence 33, Appl | 523 | 48 | 100.0 | 1620 | 6 | US-10-453-372-868 | Sequence 868, App |
| 451 | 48 | 100.0 | 600 | 7 | US-11-201-519-22 | Sequence 22, Appl | 524 | 48 | 100.0 | 1633 | 6 | US-10-453-372-866 | Sequence 866, App |
| 452 | 48 | 100.0 | 605 | 7 | US-11-087-099-9709 | Sequence 9709, Ap | 525 | 48 | 100.0 | 2236 | 7 | US-11-126-113-33 | Sequence 33, Appl |
| 453 | 48 | 100.0 | 608 | 7 | US-11-085-864-2 | Sequence 2, Appl1 | 527 | 48 | 100.0 | 2505 | 7 | US-11-126-113-33 | Sequence 33, Appl |
| 454 | 48 | 100.0 | 608 | 7 | US-11-127-004-2 | Sequence 2, Appl1 | 528 | 48 | 100.0 | 3353 | 7 | US-11-037-243-64 | Sequence 64, Appl |
| 455 | 48 | 100.0 | 608 | 7 | US-11-130-408-2 | Sequence 2, Appl1 | 529 | 48 | 100.0 | 89 | 9 | US-11-096-568A-2163 | Sequence 2163, Ap |
| 456 | 48 | 100.0 | 611 | 7 | US-11-010-239-129 | Sequence 129, App | 530 | 48 | 87.5 | 236 | 7 | US-11-091-100-15 | Sequence 2162, Ap |
| 457 | 48 | 100.0 | 611 | 7 | US-11-087-099-8358 | Sequence 8358, App | 531 | 48 | 87.5 | 309 | 6 | US-10-714-887-62 | Sequence 62, Appl |
| 458 | 48 | 100.0 | 612 | 7 | US-11-087-099-3012 | Sequence 3012, Ap | 532 | 48 | 87.5 | 434 | 7 | US-11-096-568A-6229 | Sequence 6230, Ap |
| 459 | 48 | 100.0 | 612 | 7 | US-11-087-099-6389 | Sequence 6389, Ap | 533 | 48 | 87.5 | 437 | 7 | US-11-096-568A-6228 | Sequence 6228, Ap |
| 460 | 48 | 100.0 | 612 | 7 | US-11-087-099-6541 | Sequence 6541, Ap | 534 | 48 | 87.5 | 435 | 7 | US-11-096-568A-6228 | Sequence 6228, Ap |
| 461 | 48 | 100.0 | 612 | 7 | US-11-087-099-10495 | Sequence 10495, A | 535 | 48 | 87.5 | | | | |
| 462 | 48 | 100.0 | 612 | 7 | US-11-067-260-56 | Sequence 56, Appl | 536 | 48 | 87.5 | | | | |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|----------------------|-------------------|-----|----|------|-----|---|----------------------|--------------------|
| 537 | 42 | 87.5 | 1480 | 7 | US-11-076-074-10 | Sequence 10, Appl | 610 | 40 | 83.3 | 316 | 7 | US-11-096-568A-911 | Sequence 911, App |
| 538 | 42 | 87.5 | 1482 | 7 | US-11-181-330-2 | Sequence 2, Appl | 611 | 40 | 83.3 | 317 | 7 | US-11-096-568A-5036 | Sequence 5036, App |
| 539 | 42 | 87.5 | 1484 | 6 | US-10-912-971-6 | Sequence 6, Appl | 612 | 40 | 83.3 | 317 | 7 | US-11-096-568A-19449 | Sequence 19449, A |
| 540 | 42 | 87.5 | 1484 | 7 | US-11-181-330-6 | Sequence 6, Appl | 613 | 40 | 83.3 | 318 | 6 | US-10-131-826A-374 | Sequence 374, App |
| 541 | 42 | 87.5 | 1839 | 7 | US-11-087-099-9631 | Sequence 9631, Ap | 614 | 40 | 83.3 | 318 | 6 | US-10-973-115B-374 | Sequence 19448, A |
| 542 | 41 | 85.4 | 139 | 6 | US-10-793-626-2970 | Sequence 2970, Ap | 615 | 40 | 83.3 | 320 | 7 | US-11-096-568A-15448 | Sequence 23622, A |
| 543 | 41 | 85.4 | 167 | 7 | US-11-096-568A-33470 | Sequence 33469, A | 616 | 40 | 83.3 | 322 | 7 | US-11-096-568A-15863 | Sequence 15862, A |
| 544 | 41 | 85.4 | 198 | 7 | US-11-096-568A-33469 | Sequence 33469, A | 617 | 40 | 83.3 | 322 | 7 | US-11-096-568A-23621 | Sequence 23621, A |
| 545 | 41 | 85.4 | 222 | 7 | US-11-087-099-9791 | Sequence 9791, Ap | 618 | 40 | 83.3 | 325 | 7 | US-11-096-568A-15862 | Sequence 15862, A |
| 546 | 41 | 85.4 | 246 | 7 | US-11-096-568A-10949 | Sequence 10949, A | 619 | 40 | 83.3 | 326 | 7 | US-11-096-568A-28259 | Sequence 28259, A |
| 547 | 41 | 85.4 | 263 | 7 | US-11-096-568A-31149 | Sequence 31149, A | 620 | 40 | 83.3 | 328 | 7 | US-11-087-099-5132 | Sequence 5192, Ap |
| 548 | 41 | 85.4 | 271 | 7 | US-11-096-568A-31148 | Sequence 31148, A | 621 | 40 | 83.3 | 328 | 7 | US-11-096-568A-23320 | Sequence 22320, A |
| 549 | 41 | 85.4 | 284 | 6 | US-10-714-887-102 | Sequence 102, App | 622 | 40 | 83.3 | 330 | 6 | US-10-714-887-116 | Sequence 116, App |
| 550 | 41 | 85.4 | 286 | 7 | US-11-087-099-420 | Sequence 420, App | 623 | 40 | 83.3 | 330 | 6 | US-11-096-568A-33374 | Sequence 33374, A |
| 551 | 41 | 85.4 | 286 | 7 | US-11-096-568A-31147 | Sequence 31147, A | 624 | 40 | 83.3 | 331 | 7 | US-11-087-099-2717 | Sequence 2717, Ap |
| 552 | 41 | 85.4 | 314 | 7 | US-11-096-568A-10948 | Sequence 10948, A | 625 | 40 | 83.3 | 331 | 7 | US-11-087-099-7366 | Sequence 7366, Ap |
| 553 | 41 | 85.4 | 331 | 7 | US-11-096-568A-3911 | Sequence 3911, Ap | 626 | 40 | 83.3 | 331 | 7 | US-11-087-099-10734 | Sequence 10734, A |
| 554 | 41 | 85.4 | 338 | 7 | US-11-087-099-346 | Sequence 346, App | 627 | 40 | 83.3 | 331 | 7 | US-11-096-568A-1910 | Sequence 19447, A |
| 555 | 41 | 85.4 | 371 | 6 | US-10-467-962B-41 | Sequence 41, Appl | 628 | 40 | 83.3 | 333 | 7 | US-11-096-568A-910 | Sequence 910, App |
| 556 | 41 | 85.4 | 384 | 7 | US-11-096-568A-33509 | Sequence 33509, A | 629 | 40 | 83.3 | 336 | 7 | US-11-096-568A-15861 | Sequence 15861, A |
| 557 | 41 | 85.4 | 386 | 7 | US-11-087-099-12167 | Sequence 12167, A | 630 | 40 | 83.3 | 336 | 7 | US-11-096-568A-33621 | Sequence 33621, A |
| 558 | 41 | 85.4 | 388 | 7 | US-11-096-568A-33508 | Sequence 33508, A | 631 | 40 | 83.3 | 342 | 7 | US-11-225-709-1 | Sequence 1, Appl |
| 559 | 41 | 85.4 | 396 | 7 | US-11-096-568A-33507 | Sequence 33507, A | 632 | 40 | 83.3 | 343 | 7 | US-11-096-568A-33373 | Sequence 33373, A |
| 560 | 41 | 85.4 | 409 | 7 | US-11-096-568A-10947 | Sequence 10947, A | 633 | 40 | 83.3 | 343 | 7 | US-11-096-568A-20943 | Sequence 20943, A |
| 561 | 41 | 85.4 | 451 | 7 | US-11-096-568A-32057 | Sequence 32057, A | 634 | 40 | 83.3 | 347 | 7 | US-11-096-568A-25772 | Sequence 25772, A |
| 562 | 41 | 85.4 | 577 | 7 | US-11-096-568A-32056 | Sequence 32056, A | 635 | 40 | 83.3 | 347 | 7 | US-11-096-568A-25771 | Sequence 25771, A |
| 563 | 41 | 85.4 | 745 | 7 | US-11-147-109-8 | Sequence 8, Appl | 636 | 40 | 83.3 | 325 | 7 | US-11-096-568A-33620 | Sequence 33620, A |
| 564 | 41 | 85.4 | 1516 | 6 | US-10-501-035-284 | Sequence 284, App | 637 | 40 | 83.3 | 325 | 7 | US-11-087-099-5803 | Sequence 5803, Ap |
| 565 | 40 | 83.3 | 5 | 6 | US-10-989-226-9 | Sequence 9, Appl | 638 | 40 | 83.3 | 360 | 7 | US-11-096-568A-15133 | Sequence 15133, A |
| 566 | 40 | 83.3 | 5 | 7 | US-11-006-031-19 | Sequence 19, Appl | 639 | 40 | 83.3 | 350 | 7 | US-11-096-568A-23620 | Sequence 23620, A |
| 567 | 40 | 83.3 | 5 | 7 | US-11-066-967-36 | Sequence 36, Appl | 640 | 40 | 83.3 | 351 | 7 | US-11-096-568A-4672 | Sequence 4672, Ap |
| 568 | 40 | 83.3 | 5 | 7 | US-11-194-110-19 | Sequence 19, Appl | 641 | 40 | 83.3 | 352 | 7 | US-11-096-568A-15485 | Sequence 15485, A |
| 569 | 40 | 83.3 | 6 | 7 | US-11-189-321-11 | Sequence 11, Appl | 642 | 40 | 83.3 | 377 | 7 | US-11-087-099-11030 | Sequence 11030, A |
| 570 | 40 | 83.3 | 12 | 6 | US-10-507-028-3 | Sequence 3, Appl | 643 | 40 | 83.3 | 377 | 7 | US-11-096-568A-4671 | Sequence 4671, Ap |
| 571 | 40 | 83.3 | 64 | 6 | US-10-952-535A-23 | Sequence 23, Appl | 644 | 40 | 83.3 | 378 | 7 | US-11-185-859-6 | Sequence 6, Appl |
| 572 | 40 | 83.3 | 69 | 6 | US-10-952-535A-9 | Sequence 9, Appl | 645 | 40 | 83.3 | 382 | 7 | US-11-054-281-104 | Sequence 104, App |
| 573 | 40 | 83.3 | 113 | 6 | US-10-952-535A-20 | Sequence 20, Appl | 646 | 40 | 83.3 | 386 | 7 | US-11-096-568A-4670 | Sequence 4670, Ap |
| 574 | 40 | 83.3 | 115 | 7 | US-11-072-512-2510 | Sequence 2510, Ap | 647 | 40 | 83.3 | 387 | 7 | US-11-087-099-8387 | Sequence 8387, Ap |
| 575 | 40 | 83.3 | 120 | 7 | US-11-087-099-4618 | Sequence 4618, Ap | 648 | 40 | 83.3 | 388 | 7 | US-11-087-099-8387 | Sequence 1094, Ap |
| 576 | 40 | 83.3 | 184 | 7 | US-11-087-099-6552 | Sequence 6552, Ap | 649 | 40 | 83.3 | 394 | 7 | US-11-055-822-1094 | Sequence 25770, A |
| 577 | 40 | 83.3 | 189 | 6 | US-10-990-627-12 | Sequence 12, Appl | 650 | 40 | 83.3 | 398 | 7 | US-11-096-568A-33372 | Sequence 33372, A |
| 578 | 40 | 83.3 | 192 | 7 | US-11-096-568A-21315 | Sequence 21315, A | 651 | 40 | 83.3 | 399 | 7 | US-11-096-568A-15132 | Sequence 15132, A |
| 579 | 40 | 83.3 | 195 | 7 | US-11-096-568A-26956 | Sequence 26956, A | 652 | 40 | 83.3 | 411 | 7 | US-11-096-568A-10858 | Sequence 10858, A |
| 580 | 40 | 83.3 | 213 | 6 | US-10-990-627-1 | Sequence 1, Appl | 653 | 40 | 83.3 | 411 | 7 | US-11-096-568A-27631 | Sequence 27631, A |
| 581 | 40 | 83.3 | 218 | 7 | US-11-096-568A-24967 | Sequence 24967, A | 654 | 40 | 83.3 | 414 | 7 | US-11-096-568A-15131 | Sequence 15131, A |
| 582 | 40 | 83.3 | 223 | 7 | US-11-096-568A-15487 | Sequence 15487, A | 655 | 40 | 83.3 | 417 | 6 | US-10-971-560-4 | Sequence 4, Appl |
| 583 | 40 | 83.3 | 224 | 6 | US-10-714-887-340 | Sequence 340, App | 656 | 40 | 83.3 | 424 | 7 | US-11-096-568A-24510 | Sequence 24510, A |
| 584 | 40 | 83.3 | 234 | 7 | US-11-096-568A-20994 | Sequence 20994, A | 657 | 40 | 83.3 | 430 | 7 | US-11-096-568A-27630 | Sequence 27630, A |
| 585 | 40 | 83.3 | 240 | 6 | US-10-467-657-9060 | Sequence 9060, Ap | 658 | 40 | 83.3 | 430 | 7 | US-11-096-568A-29710 | Sequence 29710, A |
| 586 | 40 | 83.3 | 243 | 7 | US-11-096-568A-24644 | Sequence 24644, A | 659 | 40 | 83.3 | 437 | 6 | US-10-453-372-438 | Sequence 438, App |
| 587 | 40 | 83.3 | 247 | 7 | US-11-087-099-9043 | Sequence 9043, Ap | 660 | 40 | 83.3 | 438 | 7 | US-11-096-568A-25770 | Sequence 25770, A |
| 588 | 40 | 83.3 | 254 | 7 | US-11-096-568A-21961 | Sequence 21961, A | 661 | 40 | 83.3 | 441 | 7 | US-11-096-568A-15395 | Sequence 15395, A |
| 589 | 40 | 83.3 | 254 | 7 | US-11-004-399-620 | Sequence 620, App | 662 | 40 | 83.3 | 442 | 7 | US-11-096-568A-23708 | Sequence 23708, A |
| 590 | 40 | 83.3 | 257 | 7 | US-11-096-568A-20993 | Sequence 20993, A | 663 | 40 | 83.3 | 458 | 7 | US-11-096-568A-29709 | Sequence 29709, A |
| 591 | 40 | 83.3 | 257 | 7 | US-11-096-568A-24966 | Sequence 24966, A | 664 | 40 | 83.3 | 470 | 6 | US-10-878-556A-101 | Sequence 101, App |
| 592 | 40 | 83.3 | 264 | 6 | US-10-714-887-108 | Sequence 108, App | 665 | 40 | 83.3 | 472 | 7 | US-11-087-099-12191 | Sequence 12191, A |
| 593 | 40 | 83.3 | 266 | 7 | US-11-096-568A-20944 | Sequence 20944, A | 666 | 40 | 83.3 | 480 | 7 | US-11-132-142-6 | Sequence 6, Appl |
| 594 | 40 | 83.3 | 269 | 7 | US-11-096-568A-9091 | Sequence 9091, Ap | 667 | 40 | 83.3 | 493 | 7 | US-11-010-239-81 | Sequence 81, Appl |
| 595 | 40 | 83.3 | 269 | 7 | US-11-096-568A-9093 | Sequence 9093, Ap | 668 | 40 | 83.3 | 501 | 7 | US-11-076-427A-2 | Sequence 4, Appl |
| 596 | 40 | 83.3 | 271 | 7 | US-11-096-568A-1301 | Sequence 1301, Ap | 669 | 40 | 83.3 | 504 | 6 | US-10-971-560-7 | Sequence 2, Appl |
| 597 | 40 | 83.3 | 275 | 7 | US-11-096-568A-15046 | Sequence 15046, A | 670 | 40 | 83.3 | 504 | 6 | US-10-971-560-2 | Sequence 10, Appl |
| 598 | 40 | 83.3 | 276 | 7 | US-11-091-100-16 | Sequence 16, Appl | 671 | 40 | 83.3 | 501 | 6 | US-10-971-560-10 | Sequence 10, Appl |
| 599 | 40 | 83.3 | 276 | 7 | US-11-096-568A-15486 | Sequence 15486, A | 672 | 40 | 83.3 | 501 | 6 | US-10-500-441-1 | Sequence 1, Appl |
| 600 | 40 | 83.3 | 277 | 6 | US-10-793-626-314 | Sequence 314, App | 673 | 40 | 83.3 | 501 | 7 | US-11-067-121-1 | Sequence 1, Appl |
| 601 | 40 | 83.3 | 277 | 6 | US-10-793-626-3178 | Sequence 2178, Ap | 674 | 40 | 83.3 | 501 | 7 | US-11-076-427A-2 | Sequence 2, Appl |
| 602 | 40 | 83.3 | 279 | 7 | US-11-096-568A-1300 | Sequence 1300, Ap | 675 | 40 | 83.3 | 513 | 6 | US-10-453-372-442 | Sequence 442, App |
| 603 | 40 | 83.3 | 285 | 7 | US-11-096-568A-1299 | Sequence 1299, Ap | 676 | 40 | 83.3 | 519 | 7 | US-11-096-568A-33698 | Sequence 33698, A |
| 604 | 40 | 83.3 | 287 | 7 | US-11-096-568A-5037 | Sequence 5037, Ap | 677 | 40 | 83.3 | 519 | 7 | US-11-096-568A-24530 | Sequence 24530, A |
| 605 | 40 | 83.3 | 290 | 7 | US-11-096-568A-18388 | Sequence 18388, A | 678 | 40 | 83.3 | 523 | 7 | US-11-096-568A-24529 | Sequence 24529, A |
| 606 | 40 | 83.3 | 291 | 7 | US-11-087-099-2426 | Sequence 2426, Ap | 679 | 40 | 83.3 | 527 | 7 | US-11-087-099-1291 | Sequence 1291, Ap |
| 607 | 40 | 83.3 | 291 | 7 | US-11-087-099-9235 | Sequence 9235, Ap | 680 | 40 | 83.3 | 532 | 7 | US-11-087-099-340 | Sequence 340, App |
| 608 | 40 | 83.3 | 299 | 7 | US-11-096-568A-22321 | Sequence 22321, A | 681 | 40 | 83.3 | 535 | 6 | US-10-453-372-436 | Sequence 436, App |
| 609 | 40 | 83.3 | 300 | 7 | US-11-096-568A-27632 | Sequence 27632, A | 682 | 40 | 83.3 | 541 | 7 | US-11-096-568A-20889 | Sequence 20889, A |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|----------------------|--------------------|-----|------|------|------|---|----------------------|--------------------|
| 683 | 40 | 83.3 | 541 | 7 | US-11-096-568A-33697 | Sequence 33697, A | 756 | 37 | 77.1 | 436 | 7 | US-11-042-814-4 | Sequence 4, Appl1 |
| 684 | 40 | 83.3 | 593 | 7 | US-11-087-099-3921 | Sequence 3921, Ap | 757 | 37 | 77.1 | 498 | 7 | US-11-096-568A-157 | Sequence 157, App |
| 685 | 40 | 83.3 | 593 | 7 | US-11-087-099-5800 | Sequence 5800, Ap | 758 | 37 | 77.1 | 564 | 7 | US-11-087-099-9918 | Sequence 9918, Ap |
| 686 | 40 | 83.3 | 635 | 7 | US-11-096-568A-22628 | Sequence 22628, A | 759 | 37 | 77.1 | 578 | 7 | US-11-096-568A-156 | Sequence 156, App |
| 687 | 40 | 83.3 | 635 | 7 | US-11-096-568A-27797 | Sequence 27797, A | 760 | 37 | 77.1 | 534 | 7 | US-11-096-568A-155 | Sequence 155, App |
| 688 | 40 | 83.3 | 646 | 7 | US-11-004-399-289 | Sequence 289, App | 761 | 37 | 77.1 | 710 | 7 | US-11-096-568A-158 | Sequence 158, App |
| 689 | 40 | 83.3 | 676 | 7 | US-11-004-399-3931 | Sequence 3931, Ap | 762 | 37 | 77.1 | 900 | 6 | US-10-501-033-215 | Sequence 215, App |
| 690 | 40 | 83.3 | 699 | 7 | US-11-138-882-4 | Sequence 4, Appl1 | 763 | 37 | 77.1 | 331 | 7 | US-11-087-099-457 | Sequence 457, App |
| 691 | 40 | 83.3 | 699 | 7 | US-11-138-882-5 | Sequence 5, Appl1 | 764 | 36.5 | 76.0 | 449 | 7 | US-11-096-568A-19441 | Sequence 19441, A |
| 692 | 40 | 83.3 | 699 | 7 | US-11-138-882-5 | Sequence 5, Appl1 | 765 | 36.5 | 76.0 | 455 | 7 | US-11-096-568A-19439 | Sequence 19439, A |
| 693 | 40 | 83.3 | 710 | 7 | US-11-096-568A-22627 | Sequence 22627, A | 766 | 36.5 | 76.0 | 457 | 7 | US-11-096-568A-27590 | Sequence 27590, A |
| 694 | 40 | 83.3 | 737 | 6 | US-10-453-372-434 | Sequence 434, App | 767 | 36.5 | 76.0 | 828 | 7 | US-11-096-568A-27590 | Sequence 27590, A |
| 695 | 40 | 83.3 | 737 | 6 | US-10-453-372-446 | Sequence 446, App | 768 | 36.5 | 76.0 | 846 | 7 | US-11-096-568A-27850 | Sequence 27850, A |
| 696 | 40 | 83.3 | 737 | 6 | US-10-453-372-448 | Sequence 448, App | 769 | 36 | 75.0 | 173 | 7 | US-11-096-568A-29046 | Sequence 29046, A |
| 697 | 40 | 83.3 | 737 | 6 | US-10-453-372-450 | Sequence 450, App | 770 | 36 | 75.0 | 231 | 7 | US-11-096-568A-23503 | Sequence 23503, A |
| 698 | 40 | 83.3 | 737 | 6 | US-10-453-372-452 | Sequence 452, App | 771 | 36 | 75.0 | 237 | 6 | US-10-714-887-104 | Sequence 104, App |
| 699 | 40 | 83.3 | 737 | 6 | US-10-453-372-454 | Sequence 454, App | 772 | 36 | 75.0 | 319 | 6 | US-10-793-626-2368 | Sequence 2368, Ap |
| 700 | 40 | 83.3 | 737 | 6 | US-10-453-372-456 | Sequence 456, App | 773 | 36 | 75.0 | 368 | 7 | US-11-096-568A-22501 | Sequence 22501, A |
| 701 | 40 | 83.3 | 749 | 7 | US-11-054-281-103 | Sequence 103, App | 774 | 36 | 75.0 | 380 | 7 | US-10-793-626-2416 | Sequence 2416, Ap |
| 702 | 40 | 83.3 | 752 | 7 | US-11-080-991-52 | Sequence 52, Appl | 775 | 35.5 | 74.0 | 576 | 7 | US-11-087-099-3700 | Sequence 3700, Ap |
| 703 | 40 | 83.3 | 752 | 7 | US-11-054-281-101 | Sequence 101, App | 776 | 35.5 | 74.0 | 577 | 7 | US-11-087-099-3883 | Sequence 3883, Ap |
| 704 | 40 | 83.3 | 755 | 6 | US-10-453-372-1108 | Sequence 1108, Ap | 777 | 35.5 | 74.0 | 577 | 7 | US-11-087-099-3883 | Sequence 3883, Ap |
| 705 | 40 | 83.3 | 755 | 6 | US-11-054-281-26 | Sequence 26, Appl | 778 | 35 | 72.9 | 268 | 7 | US-10-312-954-2 | Sequence 11276, A |
| 706 | 40 | 83.3 | 755 | 7 | US-11-054-281-102 | Sequence 102, App | 779 | 35 | 72.9 | 914 | 6 | US-10-895-064-1823 | Sequence 2, Appl1 |
| 707 | 40 | 83.3 | 884 | 7 | US-11-087-099-11219 | Sequence 11219, A | 780 | 34 | 70.8 | 9 | 7 | US-11-129-741-1823 | Sequence 1823, Ap |
| 708 | 40 | 83.3 | 1035 | 7 | US-11-087-099-5013 | Sequence 5013, Ap | 781 | 34 | 70.8 | 12 | 7 | US-11-145-035-32 | Sequence 32, Appl |
| 709 | 40 | 83.3 | 1607 | 7 | US-11-098-686-10178 | Sequence 10178, A | 782 | 34 | 70.8 | 70 | 6 | US-10-467-657-8668 | Sequence 8668, Ap |
| 710 | 40 | 83.3 | 2233 | 7 | US-11-096-281-13 | Sequence 13, Appl | 783 | 34 | 70.8 | 84 | 7 | US-11-138-882-9 | Sequence 9, Appl1 |
| 711 | 40 | 83.3 | 2339 | 7 | US-11-096-281-11 | Sequence 11, Appl | 784 | 34 | 70.8 | 84 | 7 | US-11-138-882-9 | Sequence 9, Appl1 |
| 712 | 39 | 81.2 | 227 | 7 | US-11-096-568A-26075 | Sequence 26075, A | 785 | 34 | 70.8 | 84 | 7 | US-11-138-882-9 | Sequence 9, Appl1 |
| 713 | 39 | 81.2 | 310 | 6 | US-10-714-887-52 | Sequence 52, Appl | 786 | 34 | 70.8 | 84 | 7 | US-11-138-882-9 | Sequence 9, Appl1 |
| 714 | 39 | 81.2 | 312 | 6 | US-10-714-887-54 | Sequence 54, Appl | 787 | 34 | 70.8 | 151 | 6 | US-10-467-657-132 | Sequence 132, Appl |
| 715 | 39 | 81.2 | 329 | 6 | US-10-467-657-2240 | Sequence 2240, App | 788 | 34 | 70.8 | 151 | 6 | US-10-467-657-5856 | Sequence 5856, Ap |
| 716 | 39 | 81.2 | 344 | 7 | US-11-087-099-3795 | Sequence 3795, Ap | 789 | 34 | 70.8 | 181 | 7 | US-11-098-686-10422 | Sequence 10422, A |
| 717 | 39 | 81.2 | 350 | 7 | US-11-087-099-955 | Sequence 955, App | 790 | 34 | 70.8 | 193 | 7 | US-11-087-099-9209 | Sequence 9209, Ap |
| 718 | 39 | 81.2 | 457 | 7 | US-11-169-041-212 | Sequence 212, App | 791 | 34 | 70.8 | 222 | 7 | US-11-096-568A-8937 | Sequence 8937, Ap |
| 719 | 39 | 81.2 | 730 | 6 | US-10-453-372-444 | Sequence 444, App | 792 | 34 | 70.8 | 235 | 7 | US-11-096-568A-33343 | Sequence 33343, A |
| 720 | 38 | 79.2 | 12 | 6 | US-10-507-028-8 | Sequence 7, Appl1 | 793 | 34 | 70.8 | 242 | 6 | US-10-524-647-6 | Sequence 6, Appl1 |
| 721 | 38 | 79.2 | 95 | 7 | US-11-096-568A-4472 | Sequence 4472, App | 794 | 34 | 70.8 | 242 | 6 | US-10-524-647-8 | Sequence 8, Appl1 |
| 722 | 38 | 79.2 | 97 | 7 | US-11-096-568A-4471 | Sequence 4471, Ap | 795 | 34 | 70.8 | 242 | 6 | US-10-524-647-10 | Sequence 10, Appl |
| 723 | 38 | 79.2 | 218 | 7 | US-11-096-568A-7822 | Sequence 7822, Ap | 796 | 34 | 70.8 | 242 | 6 | US-10-524-647-100 | Sequence 100, App |
| 724 | 38 | 79.2 | 275 | 7 | US-11-096-568A-22436 | Sequence 22436, A | 797 | 34 | 70.8 | 242 | 6 | US-10-524-972-6 | Sequence 6, Appl1 |
| 725 | 38 | 79.2 | 304 | 7 | US-11-096-568A-7821 | Sequence 7821, Ap | 798 | 34 | 70.8 | 242 | 6 | US-10-524-972-8 | Sequence 8, Appl1 |
| 726 | 38 | 79.2 | 311 | 7 | US-11-108-172-1061 | Sequence 1061, Ap | 799 | 34 | 70.8 | 242 | 6 | US-10-524-972-10 | Sequence 10, Appl |
| 727 | 38 | 79.2 | 339 | 7 | US-11-096-568A-1738 | Sequence 1738, App | 800 | 34 | 70.8 | 242 | 6 | US-11-129-143-181 | Sequence 181, App |
| 728 | 38 | 79.2 | 347 | 7 | US-11-096-568A-1737 | Sequence 1737, Ap | 801 | 34 | 70.8 | 242 | 7 | US-11-070-080-33 | Sequence 33, Appl |
| 729 | 38 | 79.2 | 353 | 7 | US-11-096-568A-24793 | Sequence 24793, A | 802 | 34 | 70.8 | 242 | 7 | US-11-087-099-328 | Sequence 328, App |
| 730 | 38 | 79.2 | 364 | 7 | US-11-096-568A-7820 | Sequence 7820, Ap | 803 | 34 | 70.8 | 257 | 7 | US-10-714-887-248 | Sequence 248, App |
| 731 | 38 | 79.2 | 368 | 7 | US-11-096-568A-22435 | Sequence 22435, A | 804 | 34 | 70.8 | 265 | 6 | US-10-714-887-106 | Sequence 106, App |
| 732 | 38 | 79.2 | 376 | 7 | US-11-087-099-6961 | Sequence 6961, Ap | 805 | 34 | 70.8 | 315 | 6 | US-10-714-887-282 | Sequence 282, App |
| 733 | 38 | 79.2 | 376 | 7 | US-11-087-099-12395 | Sequence 12395, A | 806 | 34 | 70.8 | 320 | 7 | US-11-132-864-31 | Sequence 31, Appl |
| 734 | 38 | 79.2 | 380 | 7 | US-11-087-099-1772 | Sequence 1772, Ap | 807 | 34 | 70.8 | 325 | 7 | US-11-096-568A-23538 | Sequence 23538, A |
| 735 | 38 | 79.2 | 380 | 7 | US-11-087-099-9164 | Sequence 9164, Ap | 808 | 34 | 70.8 | 325 | 7 | US-11-096-568A-23537 | Sequence 23537, A |
| 736 | 38 | 79.2 | 380 | 7 | US-11-087-099-9819 | Sequence 9819, Ap | 809 | 34 | 70.8 | 331 | 7 | US-11-096-568A-23537 | Sequence 23537, A |
| 737 | 38 | 79.2 | 381 | 7 | US-11-146-428-73 | Sequence 73, Appl | 810 | 34 | 70.8 | 387 | 7 | US-11-096-568A-33342 | Sequence 33342, A |
| 738 | 38 | 79.2 | 381 | 7 | US-11-096-568A-22434 | Sequence 22434, A | 811 | 34 | 70.8 | 402 | 7 | US-11-183-664-94 | Sequence 94, Appl |
| 739 | 38 | 79.2 | 393 | 7 | US-11-096-568A-23670 | Sequence 23670, A | 812 | 34 | 70.8 | 449 | 7 | US-11-096-568A-33241 | Sequence 3241, A |
| 740 | 38 | 79.2 | 419 | 7 | US-11-096-568A-1102 | Sequence 1102, Ap | 813 | 34 | 70.8 | 449 | 7 | US-11-018-868-49 | Sequence 49, Appl |
| 741 | 38 | 79.2 | 435 | 7 | US-11-096-568A-1101 | Sequence 1101, Ap | 814 | 34 | 70.8 | 453 | 7 | US-11-096-568A-27953 | Sequence 27953, A |
| 742 | 38 | 79.2 | 446 | 7 | US-11-096-568A-1100 | Sequence 1100, Ap | 815 | 34 | 70.8 | 472 | 7 | US-11-087-099-10553 | Sequence 10553, A |
| 743 | 38 | 79.2 | 470 | 7 | US-11-096-568A-23669 | Sequence 23669, A | 816 | 34 | 70.8 | 531 | 7 | US-11-010-239-32 | Sequence 32, Appl |
| 744 | 38 | 79.2 | 504 | 7 | US-11-096-568A-23668 | Sequence 23668, A | 817 | 34 | 70.8 | 688 | 7 | US-11-087-099-8952 | Sequence 8952, Ap |
| 745 | 38 | 79.2 | 643 | 7 | US-11-120-5448-2 | Sequence 2, Appl1 | 818 | 34 | 70.8 | 688 | 7 | US-11-087-099-9341 | Sequence 9341, Ap |
| 746 | 38 | 79.2 | 1138 | 6 | US-10-509-422-4 | Sequence 4, Appl1 | 819 | 34 | 70.8 | 783 | 7 | US-11-186-284-59 | Sequence 59, Appl |
| 747 | 37.5 | 78.1 | 570 | 7 | US-11-087-099-304 | Sequence 304, App | 820 | 34 | 70.8 | 2151 | 7 | US-11-126-313-31 | Sequence 31, Appl |
| 748 | 37.5 | 78.1 | 570 | 7 | US-11-072-512-7718 | Sequence 7718, App | 821 | 34 | 70.8 | 2151 | 6 | US-10-467-657-2322 | Sequence 2322, App |
| 749 | 37.5 | 78.1 | 823 | 7 | US-11-166-892-4 | Sequence 4, Appl1 | 822 | 33 | 68.8 | 165 | 6 | US-10-467-657-2806 | Sequence 2806, Ap |
| 750 | 37.5 | 77.1 | 12 | 6 | US-10-507-028-6 | Sequence 6, Appl1 | 823 | 33 | 68.8 | 229 | 7 | US-11-096-568A-28780 | Sequence 28780, A |
| 751 | 37 | 77.1 | 180 | 7 | US-11-096-568A-10886 | Sequence 10886, A | 824 | 33 | 68.8 | 229 | 7 | US-11-096-568A-33107 | Sequence 32107, A |
| 752 | 37 | 77.1 | 185 | 7 | US-11-096-568A-10885 | Sequence 10885, A | 825 | 33 | 68.8 | 229 | 7 | US-11-096-568A-33106 | Sequence 32106, A |
| 753 | 37 | 77.1 | 249 | 7 | US-11-096-568A-10884 | Sequence 10884, A | 826 | 33 | 68.8 | 228 | 7 | US-11-087-099-7368 | Sequence 7368, Ap |
| 754 | 37 | 77.1 | 260 | 7 | US-11-096-568A-11763 | Sequence 11763, A | 827 | 33 | 68.8 | 235 | 7 | US-11-096-568A-32032 | Sequence 32032, A |
| 755 | 37 | 77.1 | 422 | 7 | US-11-096-568A-7023 | Sequence 7023, Ap | 828 | 33 | 68.8 | 258 | 7 | US-11-096-568A-32031 | Sequence 32031, A |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|----------------------|-------------------|-----|----|------|-----|---|----------------------|--------------------|
| 829 | 33 | 68.8 | 266 | 7 | US-11-072-512-3891 | Sequence 3891, Ap | 902 | 32 | 66.7 | 203 | 7 | US-11-087-099-8087 | Sequence 8087, Ap |
| 830 | 33 | 68.8 | 267 | 7 | US-11-096-568A-26429 | Sequence 26429, A | 903 | 32 | 66.7 | 203 | 7 | US-11-096-568A-9313 | Sequence 9313, Ap |
| 831 | 33 | 68.8 | 268 | 7 | US-11-096-568A-5163 | Sequence 5163, Ap | 904 | 32 | 66.7 | 203 | 7 | US-11-096-568A-9315 | Sequence 9315, Ap |
| 832 | 33 | 68.8 | 269 | 7 | US-11-096-568A-1487 | Sequence 1487, Ap | 905 | 32 | 66.7 | 212 | 7 | US-11-096-568A-12896 | Sequence 12896, A |
| 833 | 33 | 68.8 | 281 | 6 | US-10-714-887-240 | Sequence 240, App | 906 | 32 | 66.7 | 212 | 7 | US-11-096-568A-782 | Sequence 782, App |
| 834 | 33 | 68.8 | 286 | 7 | US-11-096-568A-26428 | Sequence 26428, A | 907 | 32 | 66.7 | 217 | 7 | US-11-096-568A-26474 | Sequence 26474, A |
| 835 | 33 | 68.8 | 296 | 7 | US-11-096-568A-25614 | Sequence 25814, A | 908 | 32 | 66.7 | 217 | 7 | US-11-096-568A-14586 | Sequence 14586, A |
| 836 | 33 | 68.8 | 300 | 6 | US-10-667-295-117 | Sequence 117, App | 909 | 32 | 66.7 | 234 | 7 | US-11-096-568A-9312 | Sequence 9312, Ap |
| 837 | 33 | 68.8 | 302 | 6 | US-10-667-295-116 | Sequence 116, App | 910 | 32 | 66.7 | 235 | 7 | US-11-096-568A-21210 | Sequence 21210, A |
| 838 | 33 | 68.8 | 307 | 7 | US-11-096-568A-5162 | Sequence 5162, Ap | 911 | 32 | 66.7 | 237 | 7 | US-11-096-568A-112 | Sequence 112, App |
| 839 | 33 | 68.8 | 316 | 6 | US-10-667-295-115 | Sequence 115, App | 912 | 32 | 66.7 | 240 | 7 | US-11-096-568A-4645 | Sequence 4645, Ap |
| 840 | 33 | 68.8 | 318 | 7 | US-11-096-568A-5161 | Sequence 5161, Ap | 913 | 32 | 66.7 | 243 | 7 | US-11-096-568A-12443 | Sequence 12443, A |
| 841 | 33 | 68.8 | 325 | 7 | US-11-096-568A-32030 | Sequence 32030, A | 914 | 32 | 66.7 | 244 | 6 | US-10-524-647-102 | Sequence 102, A |
| 842 | 33 | 68.8 | 335 | 7 | US-11-096-568A-18414 | Sequence 18414, A | 915 | 32 | 66.7 | 244 | 6 | US-10-524-972-86 | Sequence 86, App1 |
| 843 | 33 | 68.8 | 336 | 7 | US-11-096-568A-15920 | Sequence 15920, A | 916 | 32 | 66.7 | 250 | 7 | US-11-096-568A-19825 | Sequence 19825, A |
| 844 | 33 | 68.8 | 337 | 7 | US-11-096-568A-18413 | Sequence 18413, A | 917 | 32 | 66.7 | 255 | 7 | US-11-087-099-1551 | Sequence 1551, Ap |
| 845 | 33 | 68.8 | 356 | 7 | US-11-096-568A-29211 | Sequence 29211, A | 918 | 32 | 66.7 | 258 | 6 | US-10-524-647-14 | Sequence 14, App1 |
| 846 | 33 | 68.8 | 360 | 7 | US-11-096-568A-29210 | Sequence 29210, A | 919 | 32 | 66.7 | 258 | 6 | US-10-524-972-114 | Sequence 114, App1 |
| 847 | 33 | 68.8 | 369 | 7 | US-11-096-568A-29209 | Sequence 29209, A | 920 | 32 | 66.7 | 264 | 7 | US-11-096-568A-11433 | Sequence 11433, A |
| 848 | 33 | 68.8 | 378 | 7 | US-11-096-568A-18412 | Sequence 18412, A | 921 | 32 | 66.7 | 267 | 7 | US-11-096-568A-20465 | Sequence 20465, A |
| 849 | 33 | 68.8 | 383 | 6 | US-10-537-897-42 | Sequence 42, App1 | 922 | 32 | 66.7 | 271 | 6 | US-10-714-887-48 | Sequence 48, App1 |
| 850 | 33 | 68.8 | 385 | 7 | US-11-096-568A-4426 | Sequence 4426, Ap | 923 | 32 | 66.7 | 271 | 7 | US-11-096-568A-30118 | Sequence 30118, A |
| 851 | 33 | 68.8 | 397 | 7 | US-11-096-568A-4425 | Sequence 4425, Ap | 924 | 32 | 66.7 | 273 | 7 | US-11-087-099-11050 | Sequence 11050, A |
| 852 | 33 | 68.8 | 398 | 6 | US-10-991-285-894 | Sequence 894, App | 925 | 32 | 66.7 | 273 | 7 | US-11-087-099-12279 | Sequence 12279, A |
| 853 | 33 | 68.8 | 398 | 7 | US-11-087-099-5162 | Sequence 5162, Ap | 926 | 32 | 66.7 | 273 | 7 | US-11-096-568A-27047 | Sequence 27047, A |
| 854 | 33 | 68.8 | 448 | 6 | US-10-312-954-4 | Sequence 4, App1 | 927 | 32 | 66.7 | 280 | 7 | US-11-096-568A-6891 | Sequence 6891, Ap |
| 855 | 33 | 68.8 | 449 | 6 | US-11-096-568A-15309 | Sequence 15309, A | 928 | 32 | 66.7 | 280 | 7 | US-11-096-568A-15872 | Sequence 15872, A |
| 856 | 33 | 68.8 | 451 | 6 | US-10-714-887-182 | Sequence 182, App | 929 | 32 | 66.7 | 282 | 7 | US-11-096-568A-21209 | Sequence 21209, A |
| 857 | 33 | 68.8 | 459 | 6 | US-10-467-657-8726 | Sequence 8726, Ap | 930 | 32 | 66.7 | 288 | 7 | US-11-096-568A-10047 | Sequence 10047, A |
| 858 | 33 | 68.8 | 471 | 7 | US-11-087-099-5840 | Sequence 5840, Ap | 931 | 32 | 66.7 | 288 | 7 | US-11-096-568A-12950 | Sequence 12950, A |
| 859 | 33 | 68.8 | 533 | 6 | US-10-467-657-9063 | Sequence 9063, Ap | 932 | 32 | 66.7 | 288 | 7 | US-11-096-568A-22903 | Sequence 22903, A |
| 860 | 33 | 68.8 | 611 | 7 | US-11-087-099-6674 | Sequence 6674, Ap | 933 | 32 | 66.7 | 291 | 7 | US-11-096-568A-6690 | Sequence 6690, Ap |
| 861 | 33 | 68.8 | 684 | 7 | US-11-096-568A-9418 | Sequence 9418, Ap | 934 | 32 | 66.7 | 292 | 7 | US-11-096-568A-26427 | Sequence 26427, A |
| 862 | 33 | 68.8 | 711 | 7 | US-11-096-568A-9417 | Sequence 9417, Ap | 935 | 32 | 66.7 | 297 | 7 | US-11-096-568A-17628 | Sequence 17628, A |
| 863 | 33 | 68.8 | 2145 | 7 | US-11-087-099-10331 | Sequence 10331, A | 936 | 32 | 66.7 | 294 | 7 | US-11-096-568A-21208 | Sequence 21208, A |
| 864 | 32.5 | 67.7 | 283 | 7 | US-11-096-568A-13650 | Sequence 13650, A | 937 | 32 | 66.7 | 296 | 6 | US-10-714-887-226 | Sequence 226, App |
| 865 | 32.5 | 67.7 | 337 | 7 | US-11-096-568A-13649 | Sequence 13649, A | 938 | 32 | 66.7 | 297 | 7 | US-11-096-568A-21195 | Sequence 21195, A |
| 866 | 32.5 | 67.7 | 791 | 7 | US-11-096-568A-17894 | Sequence 17894, A | 939 | 32 | 66.7 | 297 | 7 | US-11-096-568A-24051 | Sequence 24051, A |
| 867 | 32.5 | 67.7 | 877 | 7 | US-11-087-099-9802 | Sequence 9802, Ap | 940 | 32 | 66.7 | 299 | 7 | US-11-087-099-9568 | Sequence 9568, Ap |
| 868 | 32.5 | 67.7 | 877 | 7 | US-11-087-099-12075 | Sequence 12075, A | 941 | 32 | 66.7 | 300 | 7 | US-11-096-568A-24050 | Sequence 24050, A |
| 869 | 32 | 66.7 | 8 | 7 | US-11-145-035-34 | Sequence 34, App1 | 942 | 32 | 66.7 | 308 | 7 | US-11-052-5544-251 | Sequence 251, App |
| 870 | 32 | 66.7 | 10 | 6 | US-10-498-665-74 | Sequence 74, App1 | 943 | 32 | 66.7 | 308 | 7 | US-11-096-568A-22902 | Sequence 22902, A |
| 871 | 32 | 66.7 | 10 | 6 | US-11-158-848-37 | Sequence 37, App1 | 944 | 32 | 66.7 | 309 | 7 | US-11-087-099-2169 | Sequence 2169, Ap |
| 872 | 32 | 66.7 | 10 | 7 | US-11-051-720-1771 | Sequence 1771, Ap | 945 | 32 | 66.7 | 310 | 7 | US-11-087-099-7821 | Sequence 7821, Ap |
| 873 | 32 | 66.7 | 13 | 7 | US-11-004-399-3100 | Sequence 3100, Ap | 946 | 32 | 66.7 | 310 | 7 | US-11-072-512-3795 | Sequence 3795, Ap |
| 874 | 32 | 66.7 | 14 | 7 | US-11-051-720-1771 | Sequence 1771, Ap | 947 | 32 | 66.7 | 310 | 7 | US-11-087-099-11476 | Sequence 11476, A |
| 875 | 32 | 66.7 | 14 | 7 | US-11-043-806-542 | Sequence 542, App | 948 | 32 | 66.7 | 311 | 6 | US-10-714-887-298 | Sequence 298, App |
| 876 | 32 | 66.7 | 17 | 6 | US-10-895-064-2213 | Sequence 2213, Ap | 949 | 32 | 66.7 | 311 | 7 | US-11-096-568A-1962 | Sequence 1962, Ap |
| 877 | 32 | 66.7 | 17 | 7 | US-11-129-741-2213 | Sequence 2213, Ap | 950 | 32 | 66.7 | 311 | 7 | US-11-096-568A-6889 | Sequence 6889, Ap |
| 878 | 32 | 66.7 | 17 | 7 | US-11-152-974A-151 | Sequence 151, App | 951 | 32 | 66.7 | 313 | 7 | US-11-096-568A-24049 | Sequence 24049, A |
| 879 | 32 | 66.7 | 17 | 7 | US-11-153-143A-151 | Sequence 151, App | 952 | 32 | 66.7 | 313 | 7 | US-11-096-568A-9927 | Sequence 9927, Ap |
| 880 | 32 | 66.7 | 29 | 7 | US-11-108-185-51 | Sequence 51, App1 | 953 | 32 | 66.7 | 316 | 7 | US-11-096-568A-17627 | Sequence 17627, A |
| 881 | 32 | 66.7 | 80 | 7 | US-11-051-720-1312 | Sequence 1312, Ap | 954 | 32 | 66.7 | 319 | 7 | US-11-087-099-455 | Sequence 455, App |
| 882 | 32 | 66.7 | 80 | 7 | US-11-043-806-337 | Sequence 337, App | 955 | 32 | 66.7 | 319 | 7 | US-11-087-099-4262 | Sequence 4262, Ap |
| 883 | 32 | 66.7 | 84 | 7 | US-11-096-568A-6467 | Sequence 6467, Ap | 956 | 32 | 66.7 | 325 | 7 | US-11-096-568A-11432 | Sequence 11432, A |
| 884 | 32 | 66.7 | 97 | 7 | US-11-096-568A-4955 | Sequence 4955, Ap | 957 | 32 | 66.7 | 325 | 7 | US-11-096-568A-21193 | Sequence 21193, A |
| 885 | 32 | 66.7 | 132 | 7 | US-11-096-568A-11864 | Sequence 11864, A | 958 | 32 | 66.7 | 337 | 7 | US-11-096-568A-22901 | Sequence 22901, A |
| 886 | 32 | 66.7 | 132 | 7 | US-11-096-568A-11863 | Sequence 11863, A | 959 | 32 | 66.7 | 337 | 7 | US-11-096-568A-25427 | Sequence 25427, A |
| 887 | 32 | 66.7 | 137 | 6 | US-10-821-234-1242 | Sequence 1242, Ap | 960 | 32 | 66.7 | 339 | 7 | US-11-096-568A-11851 | Sequence 11851, A |
| 888 | 32 | 66.7 | 143 | 7 | US-11-096-568A-11862 | Sequence 11862, A | 961 | 32 | 66.7 | 344 | 7 | US-11-096-568A-31491 | Sequence 31491, A |
| 889 | 32 | 66.7 | 155 | 7 | US-11-096-568A-12951 | Sequence 12951, A | 962 | 32 | 66.7 | 345 | 7 | US-11-087-099-11205 | Sequence 11205, A |
| 890 | 32 | 66.7 | 161 | 7 | US-11-096-568A-90932 | Sequence 9092, Ap | 963 | 32 | 66.7 | 345 | 7 | US-11-096-568A-31856 | Sequence 31856, A |
| 891 | 32 | 66.7 | 164 | 7 | US-11-096-568A-16620 | Sequence 16620, A | 964 | 32 | 66.7 | 347 | 7 | US-11-087-099-1768 | Sequence 1768, Ap |
| 892 | 32 | 66.7 | 167 | 7 | US-11-096-568A-10793 | Sequence 10793, A | 965 | 32 | 66.7 | 348 | 7 | US-11-096-568A-31490 | Sequence 31490, A |
| 893 | 32 | 66.7 | 170 | 7 | US-11-096-568A-19659 | Sequence 19659, A | 966 | 32 | 66.7 | 350 | 7 | US-11-087-099-3229 | Sequence 3229, Ap |
| 894 | 32 | 66.7 | 176 | 6 | US-10-467-657-5812 | Sequence 5812, Ap | 967 | 32 | 66.7 | 350 | 7 | US-11-087-099-8373 | Sequence 8373, Ap |
| 895 | 32 | 66.7 | 182 | 7 | US-11-087-099-7260 | Sequence 7260, Ap | 968 | 32 | 66.7 | 351 | 7 | US-11-096-568A-33855 | Sequence 33855, A |
| 896 | 32 | 66.7 | 187 | 7 | US-11-087-099-9919 | Sequence 9919, Ap | 969 | 32 | 66.7 | 353 | 7 | US-11-096-568A-15722 | Sequence 15722, A |
| 897 | 32 | 66.7 | 187 | 7 | US-11-096-568A-19658 | Sequence 19658, A | 970 | 32 | 66.7 | 354 | 7 | US-11-072-512-3151 | Sequence 3151, Ap |
| 898 | 32 | 66.7 | 189 | 7 | US-11-096-568A-9314 | Sequence 9314, Ap | 971 | 32 | 66.7 | 356 | 7 | US-11-096-568A-31461 | Sequence 31461, Ap |
| 899 | 32 | 66.7 | 195 | 7 | US-11-096-568A-4197 | Sequence 4197, Ap | 972 | 32 | 66.7 | 356 | 7 | US-11-096-568A-31489 | Sequence 31489, A |
| 900 | 32 | 66.7 | 200 | 7 | US-11-096-568A-784 | Sequence 784, App | 973 | 32 | 66.7 | 357 | 7 | US-11-096-568A-11850 | Sequence 11850, A |
| 901 | 32 | 66.7 | 201 | 7 | US-11-096-568A-783 | Sequence 783, App | 974 | 32 | 66.7 | 358 | 7 | US-11-146-428-112 | Sequence 112, App |

```
975 32 66.7 361 7 US-11-096-568A-23570 Sequence 23570, A
976 32 66.7 364 7 US-11-096-568A-22226 Sequence 22226, A
977 32 66.7 367 7 US-11-096-568A-19569 Sequence 19569, A
978 32 66.7 368 7 US-11-096-568A-11631 Sequence 11631, A
979 32 66.7 374 7 US-11-096-568A-19568 Sequence 19568, A
980 32 66.7 376 7 US-11-096-568A-18596 Sequence 18596, A
981 32 66.7 376 7 US-11-096-568A-33854 Sequence 33854, A
982 32 66.7 378 7 US-11-087-099-12233 Sequence 12233, A
983 32 66.7 378 7 US-11-096-568A-12553 Sequence 12553, A
984 32 66.7 383 7 US-11-096-568A-16959 Sequence 16959, A
985 32 66.7 387 6 US-10-714-887-176 Sequence 176, App
986 32 66.7 392 7 US-11-087-099-11744 Sequence 11744, A
987 32 66.7 399 7 US-11-096-568A-11431 Sequence 11431, A
988 32 66.7 403 7 US-11-146-428-90 Sequence 90, Appl
989 32 66.7 406 7 US-11-096-568A-11630 Sequence 11630, A
990 32 66.7 409 7 US-11-087-099-6807 Sequence 6807, Ap
991 32 66.7 411 7 US-11-087-099-6317 Sequence 6317, Ap
992 32 66.7 411 7 US-11-087-099-7760 Sequence 7760, Ap
993 32 66.7 413 7 US-11-096-568A-22225 Sequence 22225, A
994 32 66.7 414 7 US-11-115-868-2 Sequence 2, Appl
995 32 66.7 417 7 US-11-165-305-2 Sequence 2, Appl
996 32 66.7 417 7 US-11-096-568A-19567 Sequence 19567, A
997 32 66.7 419 7 US-11-096-568A-10209 Sequence 10209, A
998 32 66.7 420 7 US-11-096-568A-23920 Sequence 23920, A
999 32 66.7 421 7 US-11-096-568A-11629 Sequence 11629, A
1000 32 66.7 424 7 US-11-096-568A-23919 Sequence 23919, A
```

ALIGNMENTS

```
RESULT 1
US-10-512-184-46
; Sequence 46, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibody fragments, recombinant antibodies, recombinant
; TITLE OF INVENTION: Antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: His6 tag
US-10-512-184-46

Query Match      100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
       1 HHHHHH 6
Db      1 HHHHHH 6

RESULT 2
US-10-967-671-18
; Sequence 18, Application US/10967671
; Publication No. US20050245728A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: KIMBER, MATTHEW
; APPLICANT: VALLER, FRANCOIS
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM PSEUDOMONAS AERUGINOSA
```

```
; FILE REFERENCE: IPT-261.01
; CURRENT APPLICATION NUMBER: US/10/967,671
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: PCT/CA03/00714
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 60/382,443
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-967-671-18

Query Match      100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 3
US-10-966-648-29
; Sequence 29, Application US/10966648
; Publication No. US20050249734A1
; GENERAL INFORMATION:
; APPLICANT: Sutcliffe, J. Gregor
; APPLICANT: de Leca, Luis
; APPLICANT: Henriksen, Steven J.
; APPLICANT: Stiggins, George R.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
; FILE REFERENCE: 14740A-000640US
; CURRENT APPLICATION NUMBER: US/10/966,648
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US 08/648,322
; PRIOR FILING DATE: 1996-05-15
; PRIOR APPLICATION NUMBER: US 08/857,389
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: US 09/766,396
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6xHis tag
US-10-966-648-29

Query Match      100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
       1 HHHHHH 6
Db      1 HHHHHH 6

RESULT 4
US-10-497-767-5
; Sequence 5, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
```

```
/ APPLICANT: SWENSON, LOVORKA
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
/ TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: VPI/01-13 PCT
/ CURRENT APPLICATION NUMBER: US/10/497,767
/ CURRENT FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: 60/337,513
/ PRIOR FILING DATE: 2001-12-05
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: 6x-His tag
US-10-497-767-5

Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHH 6
        |||||
Db      1 HHHHH 6

RESULT 5
US-10-983-174-1
/ Sequence 1, Application US/10983174
/ Publication No. US20050261307A1
/ GENERAL INFORMATION:
/ APPLICANT: CAI, SHAOPEI
/ APPLICANT: CHOU, JOCIE
/ APPLICANT: HARWOOD, ERIC
/ APPLICANT: HEISE, CARLA C.
/ APPLICANT: MACHAJEWSKI, TIMOTHY D.
/ APPLICANT: RYCKMAN, DAVID
/ APPLICANT: SHANG, XIAO
/ APPLICANT: WIESMANN, MARION
/ APPLICANT: ZHU, SHUGUANG
/ TITLE OF INVENTION: INHIBITION OF FGFR3 AND TREATMENT OF MULTIPLE MYELOMA
/ FILE REFERENCE: 072121-0445
/ CURRENT APPLICATION NUMBER: US/10/983,174
/ CURRENT FILING DATE: 2004-11-05
/ PRIOR APPLICATION NUMBER: 60/546,017
/ PRIOR FILING DATE: 2004-02-19
/ PRIOR APPLICATION NUMBER: 60/526,425
/ PRIOR FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: 60/526,426
/ PRIOR FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: 60/517,915
/ PRIOR FILING DATE: 2003-11-07
/ PRIOR APPLICATION NUMBER: 10/644,055
/ PRIOR FILING DATE: 2003-08-19
/ PRIOR APPLICATION NUMBER: 60/405,729
/ PRIOR FILING DATE: 2002-08-23
/ PRIOR APPLICATION NUMBER: 60/428,210
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: 60/484,048
/ PRIOR FILING DATE: 2003-07-01
/ PRIOR APPLICATION NUMBER: 60/426,282
/ PRIOR FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: 60/460,493
/ PRIOR FILING DATE: 2003-04-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 1
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: 6xHis tag
US-10-983-174-1

Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHH 6
        |||||
Db      1 HHHHH 6

RESULT 6
US-10-475-204-28
/ Sequence 28, Application US/10475204
/ Publication No. US20050277116A1
/ GENERAL INFORMATION:
/ APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION OF
/ TITLE OF INVENTION: PROTEIN INTERACTIONS IN VERTEBRATE CELLS
/ FILE REFERENCE: HMY-056.25
/ CURRENT APPLICATION NUMBER: US/10/475,204
/ CURRENT FILING DATE: 2003-10-17
/ PRIOR APPLICATION NUMBER: PCT/US02/13008
/ PRIOR FILING DATE: 2002-09-27
/ PRIOR APPLICATION NUMBER: 60/285,509
/ PRIOR FILING DATE: 2001-04-20
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 28
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6x
US-10-475-204-28

Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHH 6
        |||||
Db      1 HHHHH 6

RESULT 7
US-10-957-351-357
/ Sequence 357, Application US/10957351
/ Publication No. US2006000844A1
/ GENERAL INFORMATION:
/ APPLICANT: Stemmer, Willem P. C.
/ APPLICANT: Perltroth, D. Victor
/ APPLICANT: Satval, Sanjeev
/ APPLICANT: Avidia Research Institute
/ TITLE OF INVENTION: C-Met Kinase Binding Proteins
/ FILE REFERENCE: 022013-001400US
/ CURRENT APPLICATION NUMBER: US/10/957,351
/ CURRENT FILING DATE: 2004-09-30
/ PRIOR APPLICATION NUMBER: US 10/871,602
/ PRIOR FILING DATE: 2004-06-17
/ NUMBER OF SEQ ID NOS: 471
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 357
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: 6xHis, hexahistidine tag
US-10-957-351-357
```

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 8
US-10-895-064-27
; Sequence 27, Application US/10895064
; Publication No. US20060018923A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; APPLICANT: LEUNG, FREDERICK C.
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
; FILE REFERENCE: V0690.0031
; CURRENT APPLICATION NUMBER: US/10/895,064
; CURRENT FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 2918
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: -His tag
US-10-895-064-27

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 9
US-10-950-747-12
; Sequence 12, Application US/10950747
; Publication No. US20060019336A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUD
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/10/950,747
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/782,587
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide tag
US-10-950-747-12

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 10
US-10-989-767A-698
; Sequence 698, Application US/10989767A
; Publication No. US20060018917A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 511582005004
; CURRENT APPLICATION NUMBER: US/10/989,767A
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 10/277,292
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 698
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized 6-His tag
US-10-989-767A-698

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|
|
|
|
|
Db 1 HHHHHH 6

RESULT 11
US-10-903-612B-120
; Sequence 120, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gilte, Sadanand
; APPLICANT: Borge, Vladislav B.
; APPLICANT: Rothenchild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 120

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-903-612B-120
```

```
Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 12
US-10-857-435A-622
; Sequence 622, Application US/10857435A
; Publication No. US20060030007A1
; GENERAL INFORMATION:
; APPLICANT: Byrd, Devon R.N.
; APPLICANT: Esposito, Dominic
; APPLICANT: Potter, Robert Jason
; APPLICANT: Chappell, Thomas
; TITLE OF INVENTION: Peptides for Metal Ion Affinity Chromatography
; FILE REFERENCE: 0942.5790001
; CURRENT APPLICATION NUMBER: US/10/857,435A
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: 60/474,220
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 687
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 622
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-857-435A-622
```

```
Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 13
US-10-861-105-2
; Sequence 2, Application US/10861105
; Publication No. US20060035387A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Peter
; APPLICANT: Kernen, Peter
; APPLICANT: Lu, Hongbo
; APPLICANT: Tran, Huu
; APPLICANT: Zyomyx, Inc.
; TITLE OF INVENTION: Non-Specific Binding Resistant Protein Arrays and
; TITLE OF INVENTION: Methods for Making the Same
; FILE REFERENCE: 020144-001970US
; CURRENT APPLICATION NUMBER: US/10/861,105
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US/10/046,442
; PRIOR FILING DATE: 2001-10-27
; PRIOR APPLICATION NUMBER: US 09/115,455
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US09/353,555
; PRIOR FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: His-6 peptide
US-10-861-105-2
```

```
Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 14
US-10-968-629-13
; Sequence 13, Application US/10968629
; Publication No. US20060040382A1
; GENERAL INFORMATION:
; APPLICANT: Heflitz et al.
; TITLE OF INVENTION: Tagged Epitope Protein Transposable Element
; FILE REFERENCE: 61589
; CURRENT APPLICATION NUMBER: US/10/968,629
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 09/979,338
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: PCT/US00/14687
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,210
; PRIOR FILING DATE: 1999-05-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of 6X
US-10-968-629-13
```

```
Query Match          100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6
```

```
RESULT 15
US-10-498-665-72
; Sequence 72, Application US/10498665
; Publication No. US20060052292A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Hakler, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251us620
; CURRENT APPLICATION NUMBER: US/10/498,665
; PRIOR FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 6
```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide tag
US-10-498-665-72

Query Match 100.0%; Score 48; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 16
US-11-085-864-6
Sequence 6, Application US/11085864
Publication No. US20050246787A1
GENERAL INFORMATION:
APPLICANT: STRETFIELD, STEPHEN J.
APPLICANT: LOVE, ROBERT T.
APPLICANT: BRAY, JEFF
TITLE OF INVENTION: A GLOBULIN-1 REGULATORY REGION AND METHOD OF USING SAME
FILE REFERENCE: AB0002
CURRENT APPLICATION NUMBER: US/11/085,864
CURRENT FILING DATE: 2005-03-22
PRIOR APPLICATION NUMBER: 60/555,720
PRIOR FILING DATE: 2004-03-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-085-864-6

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 17
US-11-158-848-35
Sequence 35, Application US/11158848
Publication No. US20050249703A1
GENERAL INFORMATION:
APPLICANT: Anne Dam Jensen
TITLE OF INVENTION: Interferon gamma polypeptide variants
FILE REFERENCE: 231us410 - INFG variants
CURRENT APPLICATION NUMBER: US/11/158,848
CURRENT FILING DATE: 2005-06-22
PRIOR APPLICATION NUMBER: US/10/116,273
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Tag
US-11-158-848-35

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 18
US-11-040-159-21
Sequence 21, Application US/11040159
Publication No. US2005025552A1
GENERAL INFORMATION:
APPLICANT: Flynn, Peter
APPLICANT: Luehrsen, Kenneth
APPLICANT: Balint, Robert F.
APPLICANT: Her, Jeng-Horng
APPLICANT: Bebbington, Christopher R.
APPLICANT: Yarrancon, Geoffrey T.
APPLICANT: Kalobios, Inc.
TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
FILE REFERENCE: 021167-001730US
CURRENT APPLICATION NUMBER: US/11/040,159
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 60/537,364
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/546,216
PRIOR FILING DATE: 2004-02-23
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 6-His epitope tag
US-11-040-159-21

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
Db 1 HHHHHH 6

RESULT 19
US-11-040-114-9
Sequence 9, Application US/11040114
Publication No. US20050261170A1
GENERAL INFORMATION:
APPLICANT: HANSEN, HANS J.
APPLICANT: MCBRIDE, WILLIAM J.
APPLICANT: GOLDBERG, DAVID M.
APPLICANT: ROSSI, EDWARD A.
APPLICANT: CHANG, CHIEN-HSING KEN
TITLE OF INVENTION: FOLATE CONJUGATES AND COMPLEXES
FILE REFERENCE: 40923-0143US1
CURRENT APPLICATION NUMBER: US/11/040,114
CURRENT FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: 60/538,396
PRIOR FILING DATE: 2004-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 9
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-040-114-9

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 20

US-11-073-605-16
; Sequence 16, Application US/11073605
; Publication No. US20050260161A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ULF
; APPLICANT: ALITRLO, KARI
; APPLICANT: UTELA, MARCO
; TITLE OF INVENTION: METHOD FOR MODULATING REGULATING AND/OR STABILIZING
; FILE REFERENCE: 029065.5347US
; CURRENT APPLICATION NUMBER: US/11/073,605
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 60/550,327
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-073-605-16

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 21

US-11-102-428-8
; Sequence 8, Application US/11102428
; Publication No. US20050260164A1
; GENERAL INFORMATION:
; APPLICANT: OXFORD BIOMEDICA (UK) LIMITED
; TITLE OF INVENTION: GENE REGULATION WITH APPTAMER AND MODULATOR COMPLEXES
; FILE REFERENCE: 674523-2031.WO
; CURRENT APPLICATION NUMBER: US/11/102,428
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/417,456
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 10/008,610
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: PCT/GB02/05901
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0130797.4
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: GB 0201140.1
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: GB 0211409.8
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 10/082,122
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 10/421,947

; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-102-428-8

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 22

US-11-127-004-4
; Sequence 4, Application US/11127004
; Publication No. US20050262596A1
; GENERAL INFORMATION:
; APPLICANT: STREARFIELD, STEPHEN J.
; APPLICANT: LOVE, ROBERT T.
; APPLICANT: BRAY, USEF
; TITLE OF INVENTION: AN EMBRYO PREFERRED PROMOTER AND METHOD OF USING SAME
; FILE REFERENCE: AB0005
; CURRENT APPLICATION NUMBER: US/11/127,004
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: 60/570,665
; PRIOR FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic six
; US-11-127-004-4

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
| | | | |
Db 1 HHHHHH 6

RESULT 23

US-11-000-365-46
; Sequence 46, Application US/11000365
; Publication No. US20050267022A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BUBICI, CONCETTA
; APPLICANT: DESMARIE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
; FILE REFERENCE: 21459-97705
; CURRENT APPLICATION NUMBER: US/11/000,365
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905

```

; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: 6xHis tag
US-11-000-365-46
```

```

Query Match      100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6
```

```

RESULT 24
US-11-032-794-46
; Sequence 46, Application US/11032794
; Publication No. US20050265970A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BOBICI, CONCETTA
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
; TITLE OF INVENTION: CELL DEATH OR APOPTOSIS BY TARGETING JNK
; FILE REFERENCE: 21459-97816
; CURRENT APPLICATION NUMBER: US/11/032,794
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 11/000,365
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: 6xHis tag
US-11-032-794-46
```

```

Query Match      100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6
```

```

RESULT 25
US-11-097-749-40
; Sequence 40, Application US/11097749
; Publication No. US20050267028A1
; GENERAL INFORMATION:
; APPLICANT: VIRJI, MUMTAZ
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES
; FILE REFERENCE: 63221(50221)
; CURRENT APPLICATION NUMBER: US/11/097,749
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: GB0419594.7
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: GB0408390.3
; PRIOR FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: GB2003/004273
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: GB0222764.3
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: 6xHis tag
US-11-097-749-40
```

```

Query Match      100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 HHHHHH 6
        |||||
Db      1 HHHHHH 6
```

```

RESULT 26
US-11-006-031-20
; Sequence 20, Application US/11006031
; Publication No. US20050272114A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Keith V.
; APPLICANT: Klauber, Dieter
; APPLICANT: Los, Georgy V.
; APPLICANT: Bulleit, Robert F.
; APPLICANT: McDougall, Mark
; APPLICANT: Zimprich, Chad
; APPLICANT: Promega Corporation
; TITLE OF INVENTION: Substrates for Covalent Tethering to Proteins
; FILE REFERENCE: 341.035US1
; CURRENT APPLICATION NUMBER: US/11/006,031
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 10/768,976
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,094
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/474,659
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/592,499
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-11-006-031-20
```

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 27

US-11-073-927-6
; Sequence 6, Application US/11073927
; Publication No. US20050271626A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN YUAN
; APPLICANT: SCOTT, MICHAEL LYNN
; TITLE OF INVENTION: USE OF PROLACTIN RECEPTOR ANTAGONISTS IN COMBINATION
; TITLE OF INVENTION: WITH AN AGENT THAT INACTIVATES THE HER2/NEU SIGNALING
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: 035879-0196
; CURRENT APPLICATION NUMBER: US/11/073,927
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 60/550,326
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-073-927-6

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 28

US-11-114-922-91
; Sequence 91, Application US/11114922
; Publication No. US20050282260A1
; GENERAL INFORMATION:
; APPLICANT: HICKS, PAULA M.
; APPLICANT: MCFAHLAN, SARA C.
; TITLE OF INVENTION: POLYPEPTIDES AND BIOSYNTHETIC PATHWAYS FOR THE
; TITLE OF INVENTION: PRODUCTION OF MONATIN AND ITS PRECURSORS
; FILE REFERENCE: 023829-0396
; CURRENT APPLICATION NUMBER: US/11/114,922
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/422,366
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/374,831
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 91
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-114-922-91

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 29

US-11-037-243-149
; Sequence 149, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: His tag
US-11-037-243-149

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
| | | | |
Db 1 HHHHH 6

RESULT 30

US-11-033-039-357
; Sequence 357, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 357
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-033-039-357

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
Db 1 HHHHH 6

RESULT 31

US-11-047-383-32
; Sequence 32, Application US/11047383
; Publication No. US20060003432A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: CLARKE, TERESA
; APPLICANT: KIMBER, MATTHEW
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM ENTEROCOCCUS FAECALIS
; FILE REFERENCE: IPT-318.01
; CURRENT APPLICATION NUMBER: US/11/047,383
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: PCT/CA03/01135
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/400,435
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/453,405
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 32
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-047-383-32

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
Db 1 HHHHH 6

RESULT 32

US-11-124-635-14
; Sequence 14, Application US/11124635
; Publication No. US2006000391A1
; GENERAL INFORMATION:
; APPLICANT: Eigenbrodt, Jr., Charles E.
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF THE HEPATOCYTE GROWTH FACTOR AND METHODS OF
; FILE REFERENCE: 11669.177USU1
; CURRENT APPLICATION NUMBER: US/11/124,635
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: US 60/569,301
; PRIOR FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Poly-His6 Tag

US-11-124-635-14
Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
Db 1 HHHHH 6

RESULT 33

US-11-155-446-3
; Sequence 3, Application US/1155446
; Publication No. US20060003415A1
; GENERAL INFORMATION:
; APPLICANT: BATEMAN, ERIK
; TITLE OF INVENTION: STRUBLE ACANTHAMOEBA PROTEIN EXPRESSION SYSTEMS
; FILE REFERENCE: 61243US(70360)
; CURRENT APPLICATION NUMBER: US/11/155,446
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/582,581
; PRIOR FILING DATE: 2004-06-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6x His
US-11-155-446-3

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHH 6
Db 1 HHHHH 6

RESULT 34

US-11-202-516-22
; Sequence 22, Application US/11202516
; Publication No. US20060008465A1
; GENERAL INFORMATION:
; APPLICANT: Steinaa, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gautam, Anand
; APPLICANT: Dalum, Iben
; APPLICANT: Haaning, Jesper
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; APPLICANT: Rasmussen, Peter
; TITLE OF INVENTION: Novel Methode for Therapeutic Vaccination
; FILE REFERENCE: 4614-0107BUS2
; CURRENT APPLICATION NUMBER: US/11/202,516
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US 09/806,703
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/DK99/00525
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: DK 1998 01261
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: US 60/105,011
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 22
; LENGTH: 6

TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: :
US-11-202-516-22

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 35
US-11-008-570-129
Sequence 129, Application US/11008570
Publication No. US20060014162A1
GENERAL INFORMATION:
APPLICANT: MINOPRIO, PAOLA
APPLICANT: CHAMOND, NATHAIE
APPLICANT: DEGRAVE, WIM M.
APPLICANT: BERREMAN, ARMAND
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF RACEMASES,
TITLE OF INVENTION: DEFINITION OF PROTEIN SIGNATURES, AND A TEST FOR
TITLE OF INVENTION: DETECTING D-AMINO ACID AND FOR SCREENING MOLECULES
TITLE OF INVENTION: CAPABLE OF INHIBITING THE ACTIVITY OF RACEMASE,
TITLE OF INVENTION: ESPECIALLY PROLINE RACEMASE
FILE REFERENCE: 03495.0307-01
CURRENT APPLICATION NUMBER: US/11/008,570
CURRENT FILING DATE: 2004-12-10
PRIOR APPLICATION NUMBER: 10/775,339
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60-446,263
PRIOR FILING DATE: 2003-02-11
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 129
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-008-570-129

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 36
US-11-056-182-19
Sequence 19, Application US/11056182
Publication No. US20060014245A1
GENERAL INFORMATION:
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: HANSEN, HANS J
APPLICANT: CHANG, CHIEH-HSING
APPLICANT: VANAMA, SAILAJA
APPLICANT: ROSSI, EDMUND A.
TITLE OF INVENTION: FUSION PROTEINS CONTAINING RECOMBINANT CYTOTOXIC RNASES
FILE REFERENCE: 40923-0002US1
CURRENT APPLICATION NUMBER: US/11/056,182
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,227
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 19
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-056-182-19

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 37
US-11-153-086-5
Sequence 5, Application US/11153086
Publication No. US20060014669A1
GENERAL INFORMATION:
APPLICANT: KOO, CALVIN
APPLICANT: MULIGAN, RICHARD
TITLE OF INVENTION: A METHOD FOR TREATING CANCER AND INCREASING HEMATOCRIT
TITLE OF INVENTION: LEVELS
FILE REFERENCE: 701039-51133-C
CURRENT APPLICATION NUMBER: US/11/153,086
CURRENT FILING DATE: 2005-06-15
PRIOR APPLICATION NUMBER: 10/467,509
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: PCT/US02/03531
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,834
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6x
US-11-153-086-5

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHH 6
Db 1 HHHHH 6

RESULT 38
US-11-121-612-400
Sequence 400, Application US/11121612
Publication No. US20060025339A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert J
APPLICANT: Mazur, Wieslaw A
TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847MD
CURRENT APPLICATION NUMBER: US/11/121,612
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/376,337
PRIOR FILING DATE: 2002-04-29

```

; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 10/317,252
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 531
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 400
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide sequence
US-11-121-612-400

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 1 HHHHHH 6

RESULT 39
US-11-131-744-9
; Sequence 9, Application US/11131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHMOUD R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADEGHI, MEHRNOOSH
; APPLICANT: LIANG, XIQUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT APPLICATION NUMBER: US/11/131,744
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: 60/621,686
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-9

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 1 HHHHHH 6

RESULT 40
US-11-194-110-20
; Sequence 20, Application US/11194110
```

```

; Publication No. US20060024808A1
; GENERAL INFORMATION:
; APPLICANT: Darzins, Al
; APPLICANT: Encell, Lance
; APPLICANT: Klauber, Dieter
; APPLICANT: Los, Georgyi V.
; APPLICANT: McDougall, Mark
; APPLICANT: Wood, Keith V.
; APPLICANT: Wood, Monika G.
; APPLICANT: Zimprich, Chad
; APPLICANT: Promega Corporation
; TITLE OF INVENTION: Covalent Tethering of Functional Groups to Proteins and Substrat
; FILE REFERENCE: 341.032US1
; CURRENT APPLICATION NUMBER: US/11/194,110
; CURRENT FILING DATE: 2005-07-29
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-11-194-110-20

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 1 HHHHHH 6

RESULT 41
US-11-051-178A-21
; Sequence 21, Application US/11051178A
; Publication No. US20060035296A1
; GENERAL INFORMATION:
; APPLICANT: TAYA, YOICHI
; APPLICANT: TAMAI, KATSUYUKI
; APPLICANT: MINAZAKI, TOSHIAKI
; TITLE OF INVENTION: METHOD FOR DETECTING ACETYLTRANSFERASE AND DEACETYLASE
; TITLE OF INVENTION: ACTIVITIES AND METHOD FOR SCREENING INHIBITORS OR
; FILE REFERENCE: 49979-DIV(71965)
; CURRENT APPLICATION NUMBER: US/11/051,178A
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: 09/618,424
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/JP99/00191
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: JP 10/9171
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-051-178A-21

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
   |||||
Db 1 HHHHHH 6
```

RESULT 42
US-11-129-741-27
; Sequence 27, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KMOK YUNG
; APPLICANT: MOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KMOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INSPECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-129-741-27

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||
Db 1 HHHHHH 6

RESULT 43
US-11-151-762-1
; Sequence 1, Application US/11151762
; Publication No. US20060035533A1
; GENERAL INFORMATION:
; APPLICANT: ZHAO, HUIMIN
; APPLICANT: WOODYER, RYAN
; APPLICANT: SIMURDIK, MICHAEL
; APPLICANT: VAN DER DONK, WILLRED A.
; TITLE OF INVENTION: A HIGHLY ACTIVE XYLOSE REDUCTASE FROM NEUROSPORA CRASSA
; FILE REFERENCE: 21419-99635
; CURRENT APPLICATION NUMBER: US/11/151,762
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,710
; PRIOR FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-151-762-1

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||

Db 1 HHHHHH 6

RESULT 44
US-11-108-088-71
; Sequence 71, Application US/11108088
; Publication No. US20060040353A1
; GENERAL INFORMATION:
; APPLICANT: DAVIDSON, ROBERT
; APPLICANT: GERNGROSS, TILLMAN
; APPLICANT: WILDT, STEFAN
; APPLICANT: CHOI, BYUNG-KWON
; APPLICANT: NETT, JUERGEN
; APPLICANT: BOBROWICZ, PIOTR
; APPLICANT: HAMILTON, STEPHEN
; TITLE OF INVENTION: PRODUCTION OF GALACTOSYLATED GLYCOPROTEINS IN LOWER
; TITLE OF INVENTION: EUKARYOTES
; FILE REFERENCE: GFI-12
; CURRENT APPLICATION NUMBER: US/11/108,088
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/214,358
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/215,638
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/279,997
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US02/41510
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 60/344,169
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/562,424
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 71
; LENGTH: 6
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 6x
US-11-108-088-71

Query Match 100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHHHHH 6
|||||
Db 1 HHHHHH 6

RESULT 45
US-11-123-893-18
; Sequence 18, Application US/11123893
; Publication No. US20060041006A1
; GENERAL INFORMATION:
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: CHO, HANNA
; APPLICANT: ENGLAND, BRUCE
; APPLICANT: GILLETTE, SAM
; APPLICANT: ARTIS, DEAN RICHARD
; APPLICANT: ZUCKERMAN, REBECCA
; APPLICANT: ZHANG, CHAO
; TITLE OF INVENTION: PDE4B INHIBITORS AND USES THEREOF
; FILE REFERENCE: 039363-1109
; CURRENT APPLICATION NUMBER: US/11/123,893
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/569,435
; PRIOR FILING DATE: 2004-05-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 18

```

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-123-893-18

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6

RESULT 46
US-11-179-363-29
; Sequence 29, Application US/11179363
; Publication No. US20060051841A1
; GENERAL INFORMATION:
; APPLICANT: GROSS, RICHARD W.
; TITLE OF INVENTION: IDENTIFICATION, CLONING, EXPRESSION, AND PURIFICATION
; TITLE OF INVENTION: OF THREE NOVEL HUMAN CALCIUM-INDEPENDENT PHOSPHOLIPASE
; TITLE OF INVENTION: A2 FAMILY MEMBERS POSSESSING TRIACYLGLYCEROL LIPASE AND
; FILE REFERENCE: 15060-76
; CURRENT APPLICATION NUMBER: US/11/179,363
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: 60/586,913
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 11/010,558
; PRIOR FILING DATE: 2004-12-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 29
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-179-363-29

Query Match          100.0%; Score 48; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db       1 HHHHHH 6

RESULT 47
US-11-108-001-13
; Sequence 13, Application US/11108001
; Publication No. US20050265962A1
; GENERAL INFORMATION:
; APPLICANT: Desjarlais, John R.
; APPLICANT: Steed, Paul Michael
; APPLICANT: Zalevsky, Jonathan
; APPLICANT: Szymkowski, David Edmund
; TITLE OF INVENTION: PROTEIN BASED TNF-ALPHA VARIANTS FOR THE TREATMENT OF TNF-ALPHA
; FILE REFERENCE: A-68990-7
; CURRENT APPLICATION NUMBER: US/11/108,001
; CURRENT FILING DATE: 2005-04-14
; PRIOR APPLICATION NUMBER: US 10/963,994
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 09/798,789
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/945,150
```

```

; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 09/981,289
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 10/262,630
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/553,908
; PRIOR FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: US 60/510,430
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/509,960
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/528,275
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US 60/523,647
; PRIOR FILING DATE: 2003-11-20
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-11-108-001-13

Query Match          100.0%; Score 48; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db       2 HHHHHH 7

RESULT 48
US-11-222-451-21
; Sequence 21, Application US/11222451
; Publication No. US20060040356A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yaelir
; APPLICANT: Guderman, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Methods of Using a Mycobacterium tuberculosis Coding
; TITLE OF INVENTION: Sequence to Facilitate Stable and High Yield Expression
; FILE REFERENCE: 014058-008010US
; CURRENT APPLICATION NUMBER: US/11/222,451
; CURRENT FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: US/09/684,215
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/158,585
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Met-His tag Gaa
US-11-222-451-21

Query Match          100.0%; Score 48; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HHHHHH 6
        |||||
Db       2 HHHHHH 7

RESULT 49
```

Job time : 30 secs

US-10-950-747-13
; Sequence 13, Application US/10950747
; Publication No. US20060019336A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/10/950,747
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/09/782,587
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide tag
US-10-950-747-13

Query Match 100.0%; Score 48; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
DB 3 HHHHHH 8

RESULT 50
US-10-498-665-73
; Sequence 73, Application US/10498665
; Publication No. US20060052292A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Pedersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bognes, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 0251ue620
; CURRENT APPLICATION NUMBER: US/10/498,665
; CURRENT FILING DATE: 2004-06-10
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide tag
US-10-498-665-73

Query Match 100.0%; Score 48; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHHHHH 6
|||
DB 3 HHHHHH 8

Search completed: March 21, 2006, 11:12:57

THIS PAGE LEFT BLANK